

m151.pep	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
a151	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
	10 20 30 40 50 60
m151.pep	70 80 90 100 110 120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGMPQTRFVTKKALALGL
a151	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGMPQTRFVTKKALALGL
	70 80 90 100 110 120
m151.pep	130 140 150 160 170 180
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFFIVYASGLSGFAKLEETDESN
a151	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFFIVYASGLSGFAKLEETDESN
	130 140 150 160 170 180
m151.pep	190 200 210 220 230 240
	DMRPLEDTILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
a151	DMRPLEDTILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
	190 200 210 220 230 240
m151.pep	250 260 270 280 290 300
	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
a151	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
	250 260 270 280 290 300
m151.pep	310 320 330 340 350 360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDLQKELLTNVALRVEDTADADVFRVSGR
a151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDLQKELLTNVALRVEDTADADVFRVSGR
	310 320 330 340 350 360
m151.pep	370 380 390 400 410 420
	GELHLTILLENMRREGYELAVGKPRVYRDIQKCEPYENLTVDVDPDDNQGAVMEELGR
a151	GELHLTILLENMRREGYELAVGKPRVYRDIQKCEPYENLTVDVDPDDNQGAVMEELGR
	370 380 390 400 410 420
m151.pep	430 440 450 460 470 480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG
a151	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG
	430 440 450 460 470 480
m151.pep	490 500 510 520 530 540
	RHNGVLVSQEQGEAVAYALWNLEDGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGGK
a151	RHNGVLVSQEQGEAVAYALWNLEDGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGGK
	490 500 510 520 530 540
m151.pep	550 560 570 580 590 600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK
a151	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK
	550 560 570 580 590 600
m151.pep	KLDX
a151	KLDX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq  
 1 ATGAAAaaca aaACCAaagt ctgGGacttc cCaccccgcc ttTTCactG  
 51 GctgcttgCC gCATCCctgc CCTTTATGTG gtatagCGCA AAAGCCCGCG  
 101 GcgataTGCT GcaatgGCAC ACGCGCGTCG GGCTGCTCGT CCTTTTCCTG

```

151 CTCGTATTCC GCCTCTGCTG GGGCATTG GGCAGcgATA CCGCCCGTTT
201 CTCccgTtTC GTCGAGGTT GGGCAGGTAT ACGCGGCTAT CTGAAAAAcg
251 gCATTCCCGA ACAtatcCAG CCCGGACACA ACCCCTTGGG CGCACTgatg
301 gtcGTTGCGC TTTTGgccgc cgtcTCATTT CAagtccgca CGGGGCTTTT
351 Tgccgccaat gaaaacacct tcagcaCCAa cggctacctc aaccatttgg
401 tttccgaaca tacgGGCAGC CTTATACGGA AAATCCACCT CAACTTTTTTC
451 AAGCTGCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCATATTC AAAAAGAAAA ACCTCGTCCG CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCGGCGAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 620; ORF 152.ng>:

```

g152.pep
1 MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KAGGDMLOWH TRVGLLVFLF
51 LVFRLCWGIW GSDTARFSRF VRGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAN ENTFTNGYL NHLVSEHTGS LIRKIHLNFF
151 KLLAVFSAVH IAAVAAYRIF KKNLVRPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLLS*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 621>:

```

m152.seq
1 ATGAAAAACA AAACCAAAGT CTGGGACCTC CCCACCCGCC TTTTCCACTG
51 GCTGCTTGCC GCGTCCCTGC CCTTATGTG GTATAGCGCG AAAGCCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTCTG CCTTTTCCTG
151 CTCGTATTTC GCCTCTGCTG GGGCATTG GGCAGCGATA CCGCCCGITT
201 TTCCCGTTTC GTCCAAGGCT GGGCAGGCAT ACGCGGTAT CTGAAAAACG
251 GTATTCGCCA ACACATCCAG CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGGCCGC CGTGTCTTC CAAGTCGGCA CCGGGCTTTT
351 TGCCGCCGAT GAAAACACCT TCAGCACCAA CGGCTACCTC AACCATTG
401 TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCACCT CAACTTTTTC
451 AAGCTGCTCG CCGTTTTTTC TGCAATCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCGTATTC AAAAAGAAAA ACCTCATCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCGGCGAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CTCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 622; ORF 152>:

```

m152.pep
1 MKNKTKVWDL PTRLFHWLLA ASLPFMWYSA KAGGDMLOWH TRVGLFVLFL
51 LVFRLCWGIW GSDTARFSRF VQGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD ENTFTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAIH IAAVAAYRVF KKNLILPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVASLA AAAILLLS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 152 shows 95.4% identity over a 218 aa overlap with a predicted ORF (ORF 152.ng) from *N. gonorrhoeae*:

m152/g152

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFWLLAASLPFMWYSAKAGGDMLOWHTRVGLFVLFLLVFRLCWGIW					
	:     :     :     :     :					
g152	MKNKTKVWDFPTRLFWLLAASLPFMWYSAKAGGDMLOWHTRVGLLVFLLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	:     :     :     :     :					
g152	GSDTARFSRFVRGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAN					
	70	80	90	100	110	120



436

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAIHIAAAYAAYRVFKKKNLILPMI					
	:     :     :     :     :					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFSAVHIAAAYAAYRIFKKKNLVRPMI					
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAASLAAAAILLLSX					
	:     :     :     :					
g152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAILLLSX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

```

a152.seq
1  ATGAAAAACA AAACCAAAGT CTGGGACTTC CCCACCCGCC TTTTCCACTG
51  GCTGCTTGCC GCATCCCTAC CCTTTATGTG GTATAGCGCG AAAACCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTTAT CCTTTTCCTG
151 CTCGTATTCC GCCTCTGCTG GGGCATTTGG GGCAGCGATA CCGCCCGTTT
201 CTCCCGTTTC GTCCGCGGAT GGTCCGGTAT CAGAGAGTAT ATGAAAAACG
251 GTATTCCCGA ACACGTCCAA CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGGCCGC CGTGTGCTTC CAAGTCGGCA CAGGGCTTTT
351 TGCCGCCGAT GTAAACACCT TCAGCACCAA CGGCTACCTC AACCATTTGG
401 TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCATCT CAACTTTTTC
451 AAAGTCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGNCG TCGCCGCATA
501 CCGCGTGTTC AAAAAGAAAA ACCTCGTCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

```

a152.pep
1  MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KTGGDMLQWH TRVGLFILEFL
51  LVFRLCWGIW GSDTARFSRF VRGWSGIREY MKNGIPEHVQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD VNTFSTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAVH IAXVAAYRVF KKKNLVLPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLLS*
  
```

m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVFLFLLVFRLCWGIW					
	:     :     :     :     :					
a152	MKNKTKVWDFPTRLFWLLAASLPFMWYSAKTGGDMLQWHTRVGLFILEFLFLLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNIGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	:     :     :     :     :					
a152	GSDTARFSRFVRGWSGIREYMKNGIPEHVQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAIHIAAAYAAYRVFKKKNLILPMI					
	:     :     :     :     :					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAVHIAAXVAAYRVFKKKNLILPMI					
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAASLAAAAILLLSX					
	:     :     :     :					
a152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAILLLSX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

```

g153.seq
1  atgggggtttg cttacAgtat gacgtatata gaggtCGGGA taccggaggc
51  ggcacccgtc ctttCgtGC CCGAGATgat gcgcctgatG GTGTTtCagg
101 attATGGTTT TttggcCGAA GTGATGTTTG TGctgacTTT cGGCGcgcCG
151 GTTCTGTTtC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GGCAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTCT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AAAGGTTCCG TTCGGGCCCG CGTTTTATCT
351 GATGTTTCGG CTGTCGGTTA TGCTGATTG GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGAA TAATCGGTT
451 CAGACGGCAT CGGAAGGCAA AACCTGTTGC AGCCGCTGCC TGTATTccg
501 cgaAGTgce gaatcccCCT GCGGGGTGTg cgGCGcggaA CTgtacggcg
551 gacggccgaa aagtCTGAGt atttCgtCGG CGTTTCTgac ggcggcggtT
601 GTTTTGATT TCCctgCcaa TATCctgccc attatGAttt cgtccAATCc
651 tgccgcacag GAGGcCAACA CCATCTTTAG CGGCATCGCT TATATGTGGG
701 ACgaggcgga CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTGC TGAAGATTGC GGCAATGTCG GTTTTGATTG CCGCGGCACG
801 GTTCGCTTTG CCGCGGGCGG CAAAGAAATT GTCGCACCTC tacCGCATCA
851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTTGT GATTATTATT
901 TTGATGTGTT CGTTCcacaC TTATGCCGCG CGCGTCATTC CGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTIT GACGATGCTG TCCGCCTATT
1001 ATTTCCAGCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAACGAAA CGGAAAAATA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

```

g153.pep
1  MGPAYSMTYI EVGIPEAAVS LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV MRLRQAMMVD VFFVSTLVAY
101 IKLSSVAKVR PGPAFYLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGNNAV
151 QTASBGKTC SRCLYFRDSA ESPCGVCGAE LYGGRPKSLs ISSAFLTAAY
201 VLYFPANILP IMISSNPAAT EANTIFSGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIAARFAL PAGAKLSHL YRITEAVGRW SMIDIFVII
301 LMCSFHTYAA RVIPGSAAYV FCLVVILTML SAYYFDPRL WDKRASDGA
351 FNETEKYD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

```

m153.seq
1  ATGGCGTTTG CTACGGTAT GACGTATATC GAGGTGCGGA TACCGGGTGC
51  GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACTTT CCGCGCGCCG
151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GACAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTTT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AGAGGTTCCG TTCGGGCCCG CGTTTTATCT
351 GATGTTTCGG CTGTCAGTTA TGCTGATTG GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGGA TAATCGGTT
451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTCCG
501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CGGTGCGGAA CTGTACCGCC
551 GACGGCCGAA AAGTCTGAGT ATTTCGTGCG CGTTTCTGAC GCGGCGGTT
601 ATTTTGATT TCCCTGCCAA TATCCTGCCG ATTATGATT CGTCCAATCC
651 TGCCGCCACG GAGGTCAATA CCATCCTTAA CGGCATCGCT TATATGTGGG
701 ACGAGGGCGA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCG
801 CTTCGCTTTG CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA
851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTTGT GATTATTATT
901 TTGATGTGTT CGTTCACAC TTATGCCGCG CGCGTCATTC CGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

```

m153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV MRLRQAMMVD VFFVSTLVAY

```

101 IKLSSVAEVR FGPAFYLMFA LSVMLIRTSV SVPQHWVFQ IGRLTGDNV  
 151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL ISSAFLTA  
 201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL  
 251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII  
 301 LMCSFHTYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL WDKRASDGIA  
 351 FNETEKHD\*

m153 / g153 96.1% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFDYGFLEAVMPVLTFGAPVLFLLCLYV					
g153	MGFAYSMTYIEVGIPGAASVLSLPEMMRLMVFDYGFLEAVMPVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVMLRQAMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
g153	YAALIRKQAYPALRLATRVMLRQAMVDVFFVSTLVAYIKLSSVAKVRFGPAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVDPQHWVFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
g153	LSVMLIRTSVSVDPQHWVFQIGRLTGNNVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
g153	LYGGRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEANTIFSGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVIII					
g153	AAVIFSASILVPVLKIAAMSVLIAARFALPAGAKKLSHLRYRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHTYAA RVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNETEKHDX					
g153	LMCSFHTYAA RVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNETEKYDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 629>:

a153.seq

1	ATGGCGTTTG	CTTACGGTAT	GACGTATATC	GAGGTCGGGA	TACCGGGTGC
51	GGCATCCGTC	CTTTCGCTGC	CCGAGATGAT	GCGCCTGATG	GTGTTTCAGG
101	ATTATGGTTT	TTTGCCGAA	GTGATGTTTG	TGCTGACCTT	CGGCGCGCCG
151	GTTCTGTTC	TGCTGCTGTG	CCTGTATGTC	TATGCCGCGC	TGATACGGAA
201	ACAGGCGTAT	CCTGCGCTGC	GTTTGGAAC	GCGTGTGATG	GTGCGCTTGA
251	GACAGGCGAT	GATGGTGGAT	GTGTTTTTTG	TTTCCACTTT	GGTGGCGTAT
301	ATCAAGCTCT	CGTCTGTGGC	AGAGGTTCGC	TTCCGATCGG	CGTTTTATCT
351	GATGTTTCGG	CTGTCGGTTA	TGCTGATTCG	GACTTCGGTA	TCGGTTCCCC
401	AGCATGGGGT	GTATTTTCAA	ATCGGGCGGC	TGACGGGGGA	TAATGCGGTT
451	CAGACGGCAT	CGGAAGGTAA	AACCTGTTGC	AGCCGCTGCC	TGTATTCCG
501	CGACAGTGCC	GAATCCCCCT	GCGGCGTGTG	CGGTGCGGAA	CTGTACCGCC
551	GACGGCCGAA	AAGTCTGAGT	ATTTCTGTCG	CGTTTCTGAC	GGCGGCGGTT
601	ATTTTGTATT	TCCCTGCCAA	TATCCTGCCG	ATTATGATTT	CGTCCAATCC
651	TGCCGCCACG	GAGGTCAATA	CCATCCTTAA	CGGCATCGCT	TATATGTGGG
701	ACGAGGGCGA	CAGGCTGATT	GCGGCGGTTA	TTTTCAGCGC	GAGTATTTTG
751	GTGCCGGTAC	TGAAGATTGC	GGCAATGTCG	GTTTGTGATTG	CGTCCGCCCG
801	CTTCGCTTTG	CCAACGGGTG	CAAAGAAATT	GTCGCACCTC	TACCGCATCA

```

851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGAAGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLCLYV YAALIRKQAY PALRLATRV VRLRQAMVD VFFVSTLVAY
101 IKLSSVAEVR FGSFYLMFA LSVMLIRTSV SVPQHWVYFQ IGRITGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL ISSAFLTA
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHYYAA RVIIPGSAAY FCLVVILTML SAYYFDPRL WDKRASDGA
351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVVRLRQAMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRVVRLRQAMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
a153	LSVMLIRTSVSVPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSISSAFLTAAYILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
a153	LYRRRPKSLSISSAFLTAAYILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHYYAARVIPGSAAYFCLVVILTMLSAYYFDPRLWDKRASDGI AFNETEKHDX					
a153	LMCSFHYYAARVIPGSAAYFCLVVILTMLSAYYFDPRLWDKRASDGI AFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CAGGCTCAAG CACGCGTCCG
51  CAAAAACAAC accttctCT CCGCCGCTCG GCTGGTCCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGCGCT
151 GTGTTACGC TCTTGATGGA CAGCGCGGAA GGCATCGAAG TCAACAATAC
201 GGTCAATTAAG GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTTA CTGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGcgtAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT

```

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401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCTA
451 GTGCAGGACA TTCGCCCCGT TACCGCCATC GGGCAAAgcy GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAATCG AAAGCGCGCA TTTGACcccg
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCAACAGG CAGCGGCATC AAATCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTGAGGCG CGATTTTCATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCTT GTCgaATACA AAGGGCTgaA
951 TGTcggCATG GTTTCCGATG TCCCTTATTT TGACCGCAAT gacagCCTGC
1001 ACCtgtTTGA aaacggctgg aTcccGtac gCATCCGCAT cgagcctTCC
1051 CGTTTGAAAA TCAATGCCGA CGAGCAAGC AAAGAGCATT GGAACAACA
1101 ATTCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCGGCAAA ATGATTGAGT TGAACGATCA GCCTCCGCC
1201 TCGCCCAAGC TCGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGGC GCGGTTTGG ATGACTTGCA GGTCAAATG CCGGATTGTC
1301 TGGACaaatT CAACAATCTG CCATTggata aaACCGTTGC CGAATTGAAC
1351 GGCTCGCTCG CCGAACTCAA GTCCGCACTC AAATCCGCCA ATGCCGCCCT
1401 AAGCTCCATT GacaAACTGG TCGgcaTCC GCAGACGCAA AACATCCCGA
1451 ACGAACTGAA CCAAACTCTG AAAGAGTTGC GCATAACCTT CAAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGagacgta caAAATAcgc tgCaAAGTTT
1551 TGACAAAACC TTAAGagagc TtcaACCGT CATTAACTT TTGAaAGAAA
1601 aacCCaaCgc actGATTtTc aacaACAGCA GCAAAGAccc tATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

```

g154.pep
1  MTDNSPPPNQ HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLMLDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FVVVKPRIDQ SGVTGLGLLL SGSYIAFTPG KSGEAKDVFO
151 VQDIPPVTAT GQSGLRRLNI GKNDRIILNVN SPVLYENFMV GQIESAHFDP
201 SDQSVDHYTF IQSPNDKLIH SASRFWLESG INIETTGSGI KLSNAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLBNINAEQS KEHWKQFQT ALNKGILTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATRG GGLDDLQVKL ADLLDKFMNL PLDKTVAELN
451 GSLAELKSAL KSANAALSSI DKLVGNPQTQ NIPNELNQLT KELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSKDIPIK
551 GSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

```

ml54.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGCTCG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTTCATCAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCCGC
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTGCT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCTA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAGCGG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTGACCCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCAACAGG CAGCGGCATC AAATCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTGCGGCG CGATTTTCATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTGCGCC GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCCGACG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAACAAGC AAAGAATATT GGAACAACA
1101 ATTTAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTCCGCA

```

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1201 TCACCTAAGC TGGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCCACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCGCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAAC TTAAGACG TTCAACCCGT GATTAATACT TTGAAAGAAA
1601 AACCCAAACG GCTGATTTT AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

```
m154.pep
1 MTDNSPPFNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL VVKEIRNRGP
51 VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGLTL SGSYIAFTFG KSDEAKDVFG
151 VQDIPPVTAI QSGSLRLNLI GKNDRIILNVN SPVLYENFMV QVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVABL
451 GSLAELKSTL KSANAALSSI DKLVGKPTQ NIPNELNQL KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIK
551 GSR*
```

m154 / g154 97.8% identity in 553 aa overlap

```
10 20 30 40 50 60
m154.pep MTDNSPPFNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL VVKEIRNRGP VVTLLMDSAE
g154 MTDNSPPFNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL VVKEIRNRGP VVTLLMDSAE
10 20 30 40 50 60
70 80 90 100 110 120
m154.pep GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ
g154 GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ
70 80 90 100 110 120
130 140 150 160 170 180
m154.pep SGVTGLGLTL SGSYIAFTFG KSDEAKDVFG VQDIPPVTAI QSGSLRLNLI GKNDRIILNVN
g154 SGVTGLGLTL SGSYIAFTFG KSDEAKDVFG VQDIPPVTAI QSGSLRLNLI GKNDRIILNVN
130 140 150 160 170 180
190 200 210 220 230 240
m154.pep SPVLYENFMV QVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI
g154 SPVLYENFMV QVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI
190 200 210 220 230 240
250 260 270 280 290 300
m154.pep KLSAPLPALL LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ
g154 KLSAPLPALL LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ
250 260 270 280 290 300
310 320 330 340 350 360
m154.pep SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS
g154 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS
310 320 330 340 350 360
370 380 390 400 410 420
m154.pep KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATQG
g154 KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATQG
```

442

	370	380	390	400	410	420
	430	440	450	460	470	480
m154 . pep	GGLDDIQVKLADLLDKFDKLPDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPKQTQ					
	:     :     :     :     :					
g154	GGLDDIQVKLADLLDKFNNLPDKTVAELNGSLAELKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154 . pep	NIPNBNQTLKRLRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	:     :     :     :     :					
g154	NIPNBNQTLKRLRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154 . pep	NSSSKDPIPKGSRX					
	:					
g154	NNSSKDPKPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGCTCG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCCG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCATCAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGCG AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTCTGGCTT GGAAAGCGGC ATCAATATCG
701 AAACACAGG CAGCGGCATC AAATCAATT CCGCCCTCTT GCCTGCCCTG
751 CTGTCGGGCG CGATTTCATT TGATTCGCCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCCG AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT CGGTCGCCTT GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCGGATG TTCCTTATT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTTAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGCACCACA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GGCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGCG
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTCG CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCCACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAACC TTAAAGACG TTCAACCCGT CATTAACACT TTGAAAGAAA
1601 AACCACACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154 . pep
1  MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFQ

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151 VQDIPPVTAI GQSGRLRLNLI GKNDRIILNVN SPVLYENFMV QQVESAHFDP  
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL  
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ  
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS  
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA  
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN  
451 GSLAEKSTL KSANAALSSI DKLVGKPTQ NIPNELNQT LKELRTTQGV  
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDFIPK  
551 GSR\*

m154/a154 100.0% identity in 553 aa overlap

	10	20	30	40	50	60
m154.pep	MTDNSPPPNHQAQARVRKNN	TFLSAVWL	VPLIALIAGGWL	VWKEIRNR	GPVVTL	LLMDSAE
a154	MTDNSPPPNHQAQARVRKNN	TFLSAVWL	VPLIALIAGGWL	VWKEIRNR	GPVVTL	LLMDSAE
	10	20	30	40	50	60
	70	80	90	100	110	120
m154.pep	GIEVNNTVIK	VLSDVGRV	TRIKLRDD	QKGEVTAQL	NADVSG	LIRSDTQFWVVKPRIDQ
a154	GIEVNNTVIK	VLSDVGRV	TRIKLRDD	QKGEVTAQL	NADVSG	LIRSDTQFWVVKPRIDQ
	70	80	90	100	110	120
	130	140	150	160	170	180
m154.pep	SGVTGLGTL	LSGSYIAFT	PGKSDEAK	DVFQVQD	IPPVTAIG	QSGRLRLNLIGKNDRIILNVN
a154	SGVTGLGTL	LSGSYIAFT	PGKSDEAK	DVFQVQD	IPPVTAIG	QSGRLRLNLIGKNDRIILNVN
	130	140	150	160	170	180
	190	200	210	220	230	240
m154.pep	SPVLYENFMV	GQVESAHFDP	SDQSVHYTIF	IQSPNDKLIH	SASRFWLESG	INIETTSGSI
a154	SPVLYENFMV	GQVESAHFDP	SDQSVHYTIF	IQSPNDKLIH	SASRFWLESG	INIETTSGSI
	190	200	210	220	230	240
	250	260	270	280	290	300
m154.pep	KLNSAPLPAL	LSGAISFDS	PKTKNSKNVKS	EDSFTLYDSR	SEVANLPDDR	SLYYTAFFKQ
a154	KLNSAPLPAL	LSGAISFDS	PKTKNSKNVKS	EDSFTLYDSR	SEVANLPDDR	SLYYTAFFKQ
	250	260	270	280	290	300
	310	320	330	340	350	360
m154.pep	SVRGLTVGSP	VEYKGLNVGV	VSDVPYFDRN	DSLHLFENGW	IPVRIRIEPS	RLEINADEQS
a154	SVRGLTVGSP	VEYKGLNVGV	VSDVPYFDRN	DSLHLFENGW	IPVRIRIEPS	RLEINADEQS
	310	320	330	340	350	360
	370	380	390	400	410	420
m154.pep	KEHWKQQFQT	ALNKGLTATI	SSNNLLTGSK	MIELNDQPSA	SPKLRPHTVY	AGDTVIATQG
a154	KEHWKQQFQT	ALNKGLTATI	SSNNLLTGSK	MIELNDQPSA	SPKLRPHTVY	AGDTVIATQG
	370	380	390	400	410	420
	430	440	450	460	470	480
m154.pep	GGLDDLQVKL	ADLLDKFDKL	PLDKTVAELN	GSLAEKSTL	KSANAALSSI	DKLVGKPTQ
a154	GGLDDLQVKL	ADLLDKFDKL	PLDKTVAELN	GSLAEKSTL	KSANAALSSI	DKLVGKPTQ
	430	440	450	460	470	480
	490	500	510	520	530	540
m154.pep	NIPNELNQT	LKELRTTQGV	SPQSPIYGDV	QNTLQSLDKT	LKDVQPVINT	LKEKPNALIF
a154	NIPNELNQT	LKELRTTQGV	SPQSPIYGDV	QNTLQSLDKT	LKDVQPVINT	LKEKPNALIF
	490	500	510	520	530	540



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                    550
m154.pep  NSSSKDPIPKGSRX
          |||||
a154      NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1  atGAAaatcg GtatcCCACG CGAGTCatta tcCGGCGAAA cccgcgtagc
51  ctgcAcgccc gccACCGTTG CCctgctggg caAactAGGC TTTGAAACCG
101 TTGtcgaaAG CGGTGCAggt TTGGCGGCAA GTTTggaCGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGCGGTTT GGGCCTGCCC
201 TTTAATTTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGCTCA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CCTTGCAGCG CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCCCCG ATTTCCCGCG CTCAGGCCTT GGACGCTTGT TCTTCAATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCGGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAGTGC CGCCTGCGCA
501 GGTTTTGGTG ATTGGCGCGG GTGTGGCGGG TTTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGTAAG TTcttGAAAC TCGACTTCCT
651 GCAAGAATCG GCGGCGACGC GAGACGgctA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAAATG AAGCTCTTTG CCGAACAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCGG GGCAAACCCG CTCCTCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCGGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGGCGGC AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAACCG GCAACGCGT GAAATCATC GGCTACACCG ACATGGCAAA
951 CCGCCTTGCC GGACAGTCTT CCCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcgaaATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGcgacg gcgaaATCAC
1101 CTTCCCGCCT CGGccgaTTc aggtTTCgc cgggcccGAG CAAAcgccgt
1151 ctgaAAAagc cgcGCCTGCC GCCAagcccg AgccGaaacc tgmtCCctg
1201 tggAAAAaac tcgCGCCCGC CGCcatcgCC GCCGTATTGG tgctgtgGgt
1251 cggCgcggtc gcacccgcag CATTCTTGAA CCACCTTATC GTCTTCGTCC
1301 TCGCCTGCGT CATCGGCTAC CATGTCGTTT GgaacgTCAG CCACTCGCTG
1351 CACACACCGC TGatgtcggt aaccaaCgcc atctccGGCA tcatggtcgt
1401 cggCGCGCTG CTGCAAAATCG GTCAGGGcaa cggcttcgtT TCgctGCTGT
1451 CGTTTGTTCG CATCTGATT GCCGCGATCA ATATCTTCGG CGGCTTTGCG
1501 GTTACACGGC GTATGCTGAA TATGTTAAG AAAGGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTIY SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTGGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDLQES GSGDGYAKV MSDEFIAAEM KLFQEQAKEV
251 DIIITTAAP GKPAKLITK EMVESMKSGS VIVDLAATGG NCELTRPGEL
301 SVTGNGVKII GYTDMANRLA GSSQLYATN LVNLTLLSP NKDGEITLDF
351 EDVIIRNMTV TRDGEITFPF PPIQVSARPO QTPSEKAAPA AKPEPKPVPL
401 WKKLAPAAIA AVLVLWVGAV APAFLNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLMSVTNA ISGIMVVGAL LQIGQNGFV SLLSFVAILI AGINIFGGFA
501 VTRRMLNMEK KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1  ATGAAAATCG GTATCCACG CGAGTCATTA TCCGCGGAAA CCCGCGTCGG
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGG TTTGAAACCG
101 TTGTCGAAAG CGGTGCAGGT TTGGCGGCAA GTTTGACGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGCGGTTT GGGTCTGCCC
201 TTTGATTTAT AAGGTCAACG CGCCGTCCGA ACAGGAAGT CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

```

```

301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCCG ATTTGCGCGC CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CCGGTACCGC GCCGTAATTG AAGCCGCCAA CGCCTTCGCG
451 CGTTTCTTCA CCGGTCAAAT TACCGCGGCC GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCT
651 ACAAGAATCG GCGCGCAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGCAGCGGC GGCAGCTGCG AACTCACCCG CCCGGGCGAA
901 TTGTCCGTAA CCGGCAACGG CGTGAAATC ATCGGTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCAGCCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCG
1201 CTGTGAAAAA AACTCGCGCC CGCCGTCTAT GCCCGCTCT TGGTACTGTG
1251 GGTGCGCGCG GTGCGACCCG CAGCATTCCT GAACCACTTT ATCGTGTTCG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGCGCGC CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTGTTTTGT TGCCATCTG ATTGCCGGCA TCAACATCTT CGGCGGCTTT
1501 GCGGTAACAC GCGGTATGCT GAATATGTTT AAGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51 QTAGATVADK AAVWVCPLIY KVNAPSEQEL PLLNEGQITV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDFFQES GSGGDGYAKV MSDEFIAAEM KLFQEAQKEV
251 DIIITTAAP GKPAKPLITK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTGNVVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QQTPEKAVP AAKPEPKPVP
401 LWKKLAPAVI AAVLVLWVGA VAPAAFLNHF IVFVLACVIG YVYVWNVSHS
451 LHTPLMSVTN AISGIIVVGA LLQIGQNGF VSLLSFVAIL IAGINIFGGF
501 AVTRRMLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
              10      20      30      40      50      60
m155.pep      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              |||
g155           MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m155.pep      AAVWVCPLIYKVNAPSEQELPLLNEGQITVSFLWPRQNEALVEALRAKKVNALAMDMPVR
              |||:|||||
g155           AAVWACPLIYKVNAPSEGELEPLLKEGQITVSFLWPRQNEALVEALRAKKVNALAMDMPVR
              70      80      90      100     110     120

              130     140     150     160     170     180
m155.pep      ISRAQALDALSSMANISGYRAVIEAANAFGRFFFTGQITAAGKVPPAQVLVIGAGVAGLAA
              |||
g155           ISRAQALDALSSMANISGYRAVIEAANAFGRFFFTGQITAAGKVPPAQVLVIGAGVAGLAA

```

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	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
m155.pep	250	260	270	280	290	300
	KLF AEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
g155	KLF AEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAA-TGGNCELTRPGE					
	250	260	270	280	290	
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	300	310	320	330	340	350
m155.pep	370	380	390	400	410	420
	VTHDGEITFPFPPIQVSAQPQPTPSEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLVWVGA					
g155	VTRDGEITFPFPPIQVSARPQPTPSEKAAAPAKPEPKPVPLWKKLAPAAIAAVLVLVWVGA					
	360	370	380	390	400	410
m155.pep	430	440	450	460	470	480
	VAPAAFLNHFIVFVLACVIGYVWVNVSHSLHTPLMSVTNAISGIIIVVGALLQIQGNGF					
g155	VAPAAFLNHFIVFVLACVIGYHVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIQGNGF					
	420	430	440	450	460	470
m155.pep	490	500	510			
	VSLLSFVAILIAGINIFGGFAVTRRMLNMFKKGX					
g155	VSLLSFVAILIAGINIFGGFAVTRRMLNMFKKGX					
	480	490	500	510		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1  ATGAAATCG GTATCCACG TGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGGCATACCC
201 TTTAATTAT AAGGTTAACG CGCCGTCCGA AGACGAGCTG CCGTGCTCA
251 AAGAAGACA GACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CAATGGACAT
351 GGTGCCCCGC ATTTGCGCGC CGCAGGCTTT GGACGNTTG TCTTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGTGT TCGATACCCG CCTG.AAGTG
601 GCGGAACAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 CCAAGAATCG GCGGCGAGCG GCGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAGATG AAGCTTTTGT CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCGG GGCAAACCCG CGCCCAAGCN
801 NNTNANCAAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGACGGGCG GGCAACTGCG AACTCACCAA ACAGGCGGAA
901 TTGTTTCGTAA CCGCAACGGC CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGACAGT CTTGCGAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGCTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCGCG ACGGCGAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCCAAGC CCGAACCGAA ACCCGTTCCC

```

```

1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTGCGCGCG GTGCGACCCG CAGCATTCTT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCG GCATCATCGT
1401 CGTCGCGCGC CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQTIY SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDXL SXMANISGYR AVIEAANAAG
151 RXFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDFFQES GSGDGYAKV MSDEFIAAEM KLF AEQAKEV
251 DIIITTAaip GKPAKXXXX EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LEVFTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QPTPSEKAAP AAKPEPKPVP
401 LWKKLAPAXI AAVLVLVVGA VAPAAFLNHF IVFVLACVIG YVVVWNVSHS
451 LHTPLMSVTN AISGIIVVGA LLQIGQGNF VSLLSFVAIL IASINIFGGF
501 FVTRRMLNMF RKG*

m155/a155 95.3% identity in 513 aa overlap

      10      20      30      40      50      60
m155.pep  MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
a155      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK
      10      20      30      40      50      60

      70      80      90     100     110     120
m155.pep  AAVWVCPLIYKVNAPSEQELPLLNEGQTIYSFLWPRQNEALVEALRAKKVNALAMDMPVR
a155      AAVWAYPLIYKVNAPSEDELPLLKEGQTIYSFLWPRQNEALVEALRAKKVNALAMDMPVR
      70      80      90     100     110     120

      130     140     150     160     170     180
m155.pep  ISRAQALDALSSMANISGYRAVIEAANAAGFRFTGQITAAGKVPPAQVLVIGAGVAGLAA
a155      ISRAQALDXLSXMANISGYRAVIEAANAAGRXFTGQITAAGKVPPAQVLVIGAGVAGLAA
      130     140     150     160     170     180

      190     200     210     220     230     240
m155.pep  IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDFFQESGSGDGYAKVMSDEFIAAEM
a155      IGTANSLGAVRVFDTRLXVAEQLESMGGKFLKLDFFQESGSGDGYAKVMSDEFIAAEM
      190     200     210     220     230     240

      250     260     270     280     290     300
m155.pep  KLF AEQAKEVDIIITTAaipGKPAKPLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE
a155      KLF AEQAKEVDIIITTAaipGKPAKXXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE
      250     260     270     280     290     300

      310     320     330     340     350     360
m155.pep  LSVTNGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT
a155      LEVFTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT
      310     320     330     340     350     360

      370     380     390     400     410     420
m155.pep  VTHDGEITFPPIQVSAQPQPTPSEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLVVGA
a155      VTRDGEITFPPIQVSAQPQPTPSEKAAPAAKPEPKPVPLWKKLAPAXIAAVLVLVVGA
      370     380     390     400     410     420

```

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```

          430      440      450      460      470      480
m155.pep  VAPAAFLNHFIVFVLACVIGYVVVWNVSHSLHTPLMSVTNAISGIIIVVGALLQIGQGNGF
          |||||||
a155      VAPAAFLNHFIVFVLACVIGYVVVWNVSHSLHTPLMSVTNAISGIIIVVGALLQIGQGNGF
          430      440      450      460      470      480

          490      500      510
m155.pep  VSLLSFVAILIAGINIFGGFAVTRRMLNMFKKGX
          |||||||
a155      VSLLSFVAILIASINIFGGFFVTRRMLNMFKKGX
          490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 643>:

```

g156.seq
1  ATGACTTTCG CCTATTGGTG CATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCTCG CGGTTTCTCG GCACATACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCACCGT TTGCCGCCGC
201 CGTTTGTACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCACAA
251 CGCTTGCCGG ATGTGTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT GCGCTCGCTG ATGTGGGCGG GCGGATTGCG
351 CTGCACCGTC GGACTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 644; ORF 156.ng>:

```

g156.pep
1  MTFAYWCILI ACLLPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQQNGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LERLAFIWCY
101 IADKAALRSL MWAGGFACTV GLFVAAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 645>:

```

m156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGGTTTCTTA GCGCACACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCAC AGCAAAACGG TTTTGAAGCC TTGCACCGT TTGCCGCCGC
201 CGTTTGTACG GCACACGCAA CCGGCAATGC GGCGCAATCG ACCATCAACA
251 CGCTTGCCGT CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAT
301 ATCGCCGACA AAGCCGCTAT GCGCTCACTG ATGTGGGCAG GCGGATTGCG
351 CTGCACCGTC GGGCTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 646; ORF 156>:

```

m156.pep
1  MTFAYWCILI ACLLPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQQNGFEA FAPFAAAVLT AHATGNAAQS TINTLACLFI LERLAFIWCY
101 IADKAAMRSL MWAGGFACTV GLFVAAA*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m156 / g156 96.1% identity in 127 aa overlap

```

          10      20      30      40      50      60
m156.pep  MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA
          |||||||
g156      MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA
          10      20      30      40      50      60

          70      80      90      100     110     120
m156.pep  FAPFAAAVLTAHATGNAAQSTINTLACLFILFRLAFIWCYIADKAAMRSLMWAGGFACTV
          |||||||

```

```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWAGGFACTV
              70          80          90          100          110          120

m156.pep  GLFVAAAX
           |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCAGCCGC
201 CGTTTTCACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTTGT
351 CTGCACCGTC GGGCTGTTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAAARA
51 HAAQQNGFEA FAPFAAAVLTAHATGNAGQA TVNTLAGLFI LRLAFIWCY
101 IADKAALRSL MWVGGEVCTV GLFVAA*

m156/a156  90.6% identity in 127 aa overlap

              10          20          30          40          50          60
m156.pep    MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAARAHAQQNGFEA
           |||||
a156        MTFAYWCILIAYLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAAARAHAQQNGFEA
              10          20          30          40          50          60

              70          80          90          100          110          120
m156.pep    FAPFAAAVLTAHATGNAAQSTINTLACLFILRLAFIWCYIADKAAMRSLMWAGGFACTV
           |||||
a156        FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWVGGEVCTV
              70          80          90          100          110          120

m156.pep    GLFVAAAX
           |||||
a156        GLFVAAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
1  atgaggaacg aggAAAAACg cgcctgcgc cgcgaattgC gCgGgcggcg
51 ttcgcAAATg GGgcgagacg tGCGggCGGC GGCGgCgatA Aaaatcaacc
101 gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTgg
151 cCGATGGGCA AGGAATTGcg TTTGGGCGgc tTgtcCGCG CGGCGCAAAA
201 ACGCgGCGCA AAactctatc tgccttATAT CGAACCgCAC ACGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAAG
401 GCTACCGTTT GGGGCAGGCA GGCGGCTATT ACGATGGGAC GCTTTCGGCG
451 ATGAAATACC GTTTCAGGC GAAAACCGTG GCGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551 TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
1  MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLLKRYI KRGRKIGVYW
51  PMGKELRLGG FVRAAQKRG A KLYLPYIEPH TRRMWFTYP ERGMERERKR
101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGACQLVD RLPREAHDL LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
1  ATGAGGAACG AGGAAAAACG CGCCCTGCGC CGCAATTGC GCGGGCGGCG
51  TTCGCAAATG GGGCGGGACG TCGGGGCGGC GGCAACGGTA AAAATCAACC
101 ACCTGCTCAA ACGTTATATT AAAAAAGGGC GGAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACC GGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAACAAGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTGCGA AAAAGCGTGT
351 GCATGATTTG AACCTCCTGC TTGTGCCAGT GGTCGGTATG GACAGGCTGG
401 GCTACCGCTT GGGACAGGCA GCGGCTATT ACGATGCGAC GCTTTCAGCG
451 ATGAAATACC GTTGCAGGC AAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTGCCGG TCGAGGCGCA CGACCGGTCT TTGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGTTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
1  MRNEEKRALR RELRGRRSQM GRDVRAAATV KINHLKRYI KKGRKIGVYW
51  PMGKELRLDG FVRAAQKRG A ELYLPYIEPR SRRMWFTYP ADGVKQERKR
101 GRAKLHVPQF AGRKKRVHDL NLLVFPVVG DRLGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRSQMGRDVRAAATVKINHLKRYIKKGRKIGVYWP					
g157	MRNEEKRALRRELGRRSQMGRDVRAAAAIKINRLKRYIKRGRKIGVYWP					
	10	20	30	40	50	60
m157.pep	FVRAAQKRGAEKLYLPYIEPRSRMWFTYPADGVKQERKRGRAKLHVPQFAGRKKRVHDL					
g157	FVRAAQKRGAKLYLPYIEPHTRMWFTYPYPERGMERERKRGRAKLHVPQFAGRKIRVHGL					
	70	80	90	100	110	120
m157.pep	NLLVFPVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
g157	SVLLVPLVGIDREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP					
	130	140	150	160	170	180
m157.pep	LDGFVSEAGILCFX					
g157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
1  ATGAGGAACG AGGAAAAACA CGCCTTGC GCAGAGTTGC GCGCGCCCG
51  CGCGCAGATG GGCATCAAG GCGGTTGG GCGGGGCAA ACGATTAAAC
```

451

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAATCGG CGTGATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTATC TGCCTTATAT CGAACCGCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTGCGGATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGCTATT ACATGCGAC GCTTGCAGCG
451 ATGAAATACC GTTTCAGGC AAAAACCGTG GCGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCG GCGAACGCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

```

a157.pep
1 MRNEEKHALR RELRRARAQM GHQRLAAGQ TINRLKRYI KRGRKIGVYW
51 PMGKELRLDG FVRAAQKRGK KLYLPYIEPR SRRMWFTYP ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGACQFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

```

              10      20      30      40      50      60
m157.pep    MRNEEKRALRRELRRRSQMGRDVRAAATVKINHLLKRYIKGRKIGVYWPMGKELRLDG
              |||||:||||| |:|::| || ||:|||||:|||||:|||||
a157         MRNEEKHALRRELRRARAQMGGHQRRLAAGQTINRLKRYIKRGRKIGVYWPMGKELRLDG
              10      20      30      40      50      60

              70      80      90     100     110     120
m157.pep    FVRAAQKRGAEKLYPYIEPRSRMWFTYPADGVKQERKGRKALHVPQFAGRKKRVHDL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a157         FVRAAQKRGAKLYPYIEPRSRMWFTYPESGMERERIRGRAKLNVPQFAGRKIRVHGL
              70      80      90     100     110     120

              130     140     150     160     170     180
m157.pep    NLLLVFVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRLS
              :|||:|:|:| |||||:|||||:|||||:|||||:|||||:|||||
a157         SVLLVPLVGIDREGYRLGQAGGYDATLAAMKYRLQAKTVGVGFACQFVDRLPREPHDLL
              130     140     150     160     170     180

              190
m157.pep    LDGFVSEAGILCFX
              |||||:|||||
a157         LDGFVSEAGILCFX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

```

g158.seq
1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
51 CGGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATCTTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAACCTGCTc
151 aACCGACCA CGCGGCAACT CAATCTGACG GAAGAAGCGC CGCAATATT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTCGCGCT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATCAACGA
351 ACGCTATCCG CATATCcgac TTTGCTCGT TTCTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCCT TACGGGCCGG AGAATTGGAC
451 GATTCCGGGC TGCGTGACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGatgC GCAGGAAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```



801 CTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG  
 851 TATTTTGGGA TTTTITAGTG AAGGAAGTGG GAAAAATAT GAATAGAACG  
 901 AATACCAAT AA

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

g158.pep  
 1 MKTNSEELTV FVQVVEGSGF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL  
 51 NRTRQLNLT EEGAQYFRR QRIQEMAAA ETEMLAVHEV PQGVLRVDSA  
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD  
 151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN  
 201 TWAVLDAQGN FYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE  
 251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNL RLRVFLDFLV KELGKNMNR  
 301 NTK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

m158.seq  
 1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG  
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG  
 101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC  
 151 AACCGCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATTT  
 201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCGG GAAACCGAAA  
 251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG TGTGAGCGT GGATCCGCG  
 301 ATGCCGATGG TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATCAACGA  
 351 ACGCTATCCG CATATCCGAC TTTCGCTCGT TTCTCCGAA GGCTATATCA  
 401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCCCG AGAATTGGAC  
 451 GATTCCGGGC TGCCTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT  
 501 CGCCAGTCCT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG  
 551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT  
 601 ACATGGGCGG TTTTAGATGC GCAGGGAAT CCCTATAAGA TTTACCCGCA  
 651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT  
 701 GCGGTATTGT TTGCTTATCA GATTTTTTGG TTGACAACGA CATCGTGAA  
 751 GGAAAGTTAA TTCCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC  
 801 CTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG  
 851 TATTTTGGGA TTTTITAGTG GAGGAAGTGG GAAACAATCT CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

m158.pep  
 1 MKTNSEELTV FVQVVEGSGF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL  
 51 NRTRQLSLT EEGAQYFRR QRIQEMAAA ETEMLAVHEI PQGVLSVDSA  
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD  
 151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHQC LGFTEPGSLN  
 201 TWAVLDAQGN FYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE  
 251 GKLIPLLAEQ TSDKTHPFNA VYYSKAVNL RLRVFLDFLV EELGNNLCG\*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVEGSGFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTRQLSLT					
g158	MKTNSEELTVFVQVVEGSGFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTRQLNLT					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m158.pep	EEGAQYFRRQRIQEMAAAEETEMLAHVHEIPQGVLSVDSAMPVHLHLLAPLAAKFNERYP					
g158	EEGAQYFRRQRIQEMAAAEETEMLAHVHEVPQGVLRVDSAMPVHLHLLAPLAAKFNERYP					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158.pep	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
g158	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSCLSGCGIVCLS					
g158	SAEDLANHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSCLSSCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSKAVNLRRLRVFLDFLVEELGNNLCGX					
g158	DFLVDNDITEGKLIPLFAEQTSNKTTHPFNAVYYSKAVNLRRLRVFLDFLVKELGKNNMRT					
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158.seq

1	ATGAAAACCA	ATTCAGAAGA	ACTGACCGTA	TTTGTTCAAG	TGGTGGAAAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGCAAGGCG	TGTTGCCCGT	GGATTCCGCG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCCG	CTGGCAGCAA	AATTCAACGA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCGG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGCACG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCGG	CCACCAATGT	TTAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTTAGATGC	GCAGGGAAT	CCCTATAAGA	TTTCACCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTCAGGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTGTGA	TTTTTTAGTG	GAGGAACCTG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158.pep

1	MKTNSEELTV	FVQVVEGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLVNLL
51	NRTTRQLSLT	EEGAQYFRR	QRILQEMAAA	ETEMLAVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFNERYP	HIRLSLVSSE	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQ	LGFTTEPGSLN
201	TWAVLDAQGN	PYKISPHFTA	SSGEILRSCL	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTTHPFNA	VYYSKAVNLR	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVEGSFSRAAEQLAMANSVSRIVKRLEEKLVNLLNRTTRQLSLT					
a158	MKTNSEELTVFVQVVEGSFSRAAEQLAMANSVSRIVKRLEEKLVNLLNRTTRQLSLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRQRILQEMAAEETEMLAVHEIPQGVLSVDSAMPVHLHLLAPLAAKFNERYP					
a158	EEGAQYFRRQRILQEMAAEETEMLAVHEIPQGVLRVDSAMPVHLHLLAPLAAKFNERYP					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158.pep	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1  ATGGAcattc  tgGACAAact  ggtcgatCTC  GCcCaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTTATCT  CTGCATCGAC
151 GCGGAAACTT  CCCCgcGTCC  GGTcGGCACG  GGCGATATTG  TATTTTCCCG
201 GCGCGGCTTG  GGTcATGTGT  TGAGCCACGA  CGGAAAATAC  GGAGAAAGTT
251 TACAACCGGA  CAtACGACAA  AACGGCACAT  TTATGGTCAA  ACAGTGCggc
301 AACGGGCTGG  ATATGAGCCT  GTTTTGCGCC  CGTTTCCGCT  ACGACACCCA
351 CGCCGATTG  ATGAACGGGC  TGCCGGAAAC  CGTTTTCTG  AACATTGCCC
401 ATCCAAGTTT  GCAGTATGTG  GTTCAATGC  TGCAACTGGA  AAGCGAAAAA
451 CCTTTGACGG  GGACGGTTTC  CGTGGTCAAC  GCATTACCGT  CCGTCTGCT
501 GGTGCTTATC  CTGCGCGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAACTCT
551 CGGGCGTATT  GAAAGGTTGG  CAGGACAAAC  GTTGGGACA  TTGATCCAA
601 AAGGTGATAG  ACAAAACCGGA  AGACGAATGG  AATATTGACA  AAATGGTTGC
651 CGCCGCCAAT  ATGTCGCGCG  CGCAACTGAT  GCGCCGCTTC  AAAAGCCAAG
701 TCGGACTCAG  CCCGcACGCC  TTTGTGAACC  ATATCCGCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAAAC  CCCGGATTcG  GTTTGGAGG  TCGCGCTGTC
801 GGTGGGCTTT  CAGTCGGAAA  CGCATTTCCG  CAAGGCGTTC  AAACGGCAAT
851 ATCACGTTTC  GCCGGGGCAA  TACCGGAAAG  AAGGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

```

g160.pep
1  MDILDKLVDL  AQLTGSADVQ  CLLGGQWHET  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLQPDIRQ  NGTFMVKQCG
101 NGLDMSLFCA  RFRYDTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLQLESEK
151 PLTGTVSVDN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201 KVIDKPEDEW  NIDKMVAAN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251 ALLLKTPDS  VLEVALSVGF  QSETHFGKAF  KRQYHVSPGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1  ATGGACATTC  TGGACAAACT  GGTcGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGCAACGCGA  AGGATTGGTA  CACATTGTTA  CATCGGGCAG  CGGCTATCTC
151 TGCATCGACG  GCGAAACTTC  CCCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTCCCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAATGCG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301 CAGTGGCGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCCC  GTTCCGCTA
351 CGACACCCAC  GCCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTCTGA
401 ACATTGCCCC  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGGTTTCC  ATGGTCAACG  CATTGTCGTC

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501 CGTCCTGCTG GTGCTTATCC TGC GCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCCTG
751 CAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTGTGCGGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AggCGGGCAA
901 AAATAA

```

-- This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQSVR HETLQREGLV HIVTSGSGYL
  51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
 101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
 151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
 201 LIQKVIDKPE DEWNVDKMAA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
 251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
 301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

	10	20	30	40	50	60
m160.pep	MDILDKLVDF AQLTGSVDVQ CLLGGQSVRHETLQREGLVHIVTSGSGYLCIDGETSPRP					
	:     :     :     :     :     :     :     :     :					
g160	MDILDKLVDLAQLTGSADVQCLLGGQW---HETLQREGLVHIVTAGSGYLCIDGETSPRP					
	10	20	30	40	50	
	70	80	90	100	110	120
m160.pep	VSTGDIVFFPRGLGHVLSHDGKCGESLQPD MRQHGAFTVKQCGNGQDMSLFCARFRYDTH					
	:     :     :     :     :     :     :     :     :					
g160	VGTGDIVFFPRGLGHVLSHDGKYGESLQPDIRQNGTFMVKQCGNGLDMSLFCARFRYDTH					
	60	70	80	90	100	110
	130	140	150	160	170	180
m160.pep	ADLMNGLPETVFLNIAHPSLQYVVSMLQLESKKPLTGTSMVNALSSVLLVLILRAYLEQ					
	:     :     :     :     :     :     :     :					
g160	ADLMNGLPETVFLNIAHPSLQYVVSMLQLESEKPLTGTSMVNALPSVLLVLILRAYLEQ					
	120	130	140	150	160	170
	190	200	210	220	230	240
m160.pep	DKDVELSGVLKGWQDKRLGHLIQKVIDKPEDEWNVDKMAAANMSRAQLMRRFKSRVGLS					
	:     :     :     :     :     :     :     :					
g160	DKDVELSGVLKGWQDKRLGHLIQKVIDKPEDEWNIDKMAAANMSRAQLMRRFKSQVGLS					
	180	190	200	210	220	230
	250	260	270	280	290	300
m160.pep	PHAFVNHIRLQKGALLLKNPDSVLSVALSVGFQSETHFGKAFKRQYHVSPGQYRKEGGQ					
	:     :     :     :     :     :     :     :					
g160	PHAFVNHIRLQKGALLLKNPDSVLEVALSVGFQSETHFGKAFKRQYHVSPGQYRKEGGQ					
	240	250	260	270	280	290
m160.pep	KX					
g160	KX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
  1 ATGGACATTC TGGACAACT GGTGATTTC GCCCAATTGA CGGGCAGTGT
 51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```

```

101 TGCAACGCGA AGGATTGGTA CACATTGTGA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTTCCTG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAATATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGCAGCA ACGGACAGGA TATGAGCCTG TTTTGCGCCG GTTTCGCGTA
351 CGACACCCAC GCCGATTTGA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCC TCCGAGTTTA CAGTATGTGG TTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCTGCTG GTGCTTATCC TCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTTGTGGT
801 CGCACTGTGC GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAGA AGGCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```

a160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
 51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

m160/a160 100.0% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||
a160      MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          10      20      30      40      50      60

          70      80      90      100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||
a160      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          70      80      90      100     110     120

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLESKKPLTGTVSMVNALSSVLLVLILRAYLEQ
          |||
a160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLESKKPLTGTVSMVNALSSVLLVLILRAYLEQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||
a160      DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          190     200     210     220     230     240

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||
a160      PHAFVNHIRL QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          250     260     270     280     290     300

m160.pep KX
          ||
a160      KX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGGCGCCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGCGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCGG TTTACACGCA GCGGCTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTACAGAA
451 CCGCGCGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACC CGC TGCGCGTTCG
551 TGTTTTACCT TTCCGCAACC GCGGTGGCGA TGTCTGCGgt ttgggcgacg
601 Ctgaccggct ggCACAcccT GTCCTTTcca tcggcagttt ATCgtcCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAcg cGCGcctaca
701 aaGTCGGCGA CAAATTCACG GTTGCCCTCGC tttcctaTat gaccgtcGTC
751 TTTTCCGCCC TGTCTGCCGC ATTTTCTCTg ggcgaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAAA CAGCGGCTGC AAGCCCTCTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVTLGAAAVL RRDTRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSSIFL AVFSFLILKE RISVYTOAVL LLGFAGVVLL LNPFSRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGGCGCCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCGG TTTACACGCA GCGGCTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTACAGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACC CGC TGCGCGTTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCTGCGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCTGTG
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCCTCGC TTTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTCTCTG GCGGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVALGAAAVL RRDxFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTOAVL LLGFAGVVLL LNPFSRSGQE

```

Homology with a predicted ORF from *N. gonorrhoeae*

		10	20	30	40	50	60
m161.pep		MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
		:     :     :     :     :					
q161		MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMFLSTVTLGAAAVL					
		10	20	30	40	50	60
		70	80	90	100	110	120
m161.pep		RRDXFRTPHWKNHLNRSMTGAMLLLFYAVTHLPLATGVTLSYTSISIFLAVFSFLILKE					
		:     :     :     :     :					
q161		RRDTFRTPHWKNHLNRSMTGAMLLLFYAVTHLPLTTGVTLSYTSISIFLAVFSFLILKE					
		70	80	90	100	110	120
		130	140	150	160	170	180
m161.pep		RISVYTQAVLLLGFAVVLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
		:     :     :     :     :					
q161		RISVYTQAVLLLGFAVVLLNPSFRSGQEPALAGLAGGAMSGWAYLKVRELSLAGEPG					
		130	140	150	160	170	180
		190	200	210	220	230	240
m161.pep		WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
		:     :     :     :     :					
q161		WRVVFYLSATGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
		190	200	210	220	230	240
		250	260	270	280	290	300
m161.pep		VASLSYMTVVFSAASAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
		:     :     :     :     :					
q161		VASLSYMTVVFSAASAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR					
		250	260	270	280	290	300
m161.pep	X						
q161	X						

```

a161.seq
1  ATGGATACCG CAAAAAAGA CATTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GCGGCGCTGT TTTACCATT TGAACGTATT GATTAAGAG GCATCGGGACA
101 AATTTGCCCT CGGCAGCGC GAATTGGTCT TTGGCGCAT GCTGTTTTC A
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA CCTTCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCCTTTGGC CACCGCGCTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG CGGGTATTTT CCTTCCGTAT
351 TTTGAAAGAA CGGATTTTCG TTTACACGCA GCGCGTGCTG TCTCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCGCAG CGGTACAGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCCATGTCCG GCTGGGCGTA
501 TTTGAAAGTG TCGCAACTGT TCTTGGCGGG CGAACC CGGC
551 TGTTTTACCT TTCCTGACA GGTGTGGCGA TGTCATCGBT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGCTGTG
651 CATCGGCGTG TCGGCGCTGA TTGCCCACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCCTCG TTTCTATAT GACCCGTGCT
751 TTTTCGGCTC TGTCTGCCG ATTTTTCCTG GCCGAAGAGC TTTTCTGGGA
801 GGAATACTC GGTATGTGCA TCATCATCTC CAGCGGTATT TTGAGCAGCA

```

851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA  
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep  
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVEWRMLFS  
51 TVALGAAAVL RRDTFRTPHW KNHLNRSMSG TGAMLLLFYA VTHLPLATGV  
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPSFRSGQE  
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT  
201 LTGWHTLSFP SAVYLSICGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV  
251 FSALSAAFFL AEELFWOEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR  
301 \*

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSMSGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
a161	RRDTFRTPHWKNHLNRSMSGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGFGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSPSAVYLSICIGVSALIAQLSMTTRAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSPSAVYLSICIGVSALIAQLSMTTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWOEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAAFFLAEELEFWOEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300

m161.pep	X
a161	X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq  
1 ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTTGG TGGTATTGGT  
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAGAAG  
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTTAACGTT TTCCATTtTt  
151 ctgGGTTTtc tgctGATACT CTCGGTCAGC GGTtTGGGAA ACATcagGCT  
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA  
251 TGCTGTTTGC GGCCGGGATG GCGGTGGGCC TGATGTTTTT CGGCGTGGCA  
301 GAGCCGTTGA TGCATTATT TTCGGACATT ACGGTCGGCG CGCCGGAACA  
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACAG  
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC



```

451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAAGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTGTGT TTGGCGGCGG ACCCCACTGT
801 TTACCTGTTG TCGGCATTGC GCGACAACAT AGGGAACATC CTCGGAATC
851 TGGTGCACCT CAGTTTGAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGgC
951 gcCGTTTGTC GGTTTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTCCGGGTT TTGCTCATCC CCGGCTGTG CGCGGTTTTC
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTAA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCCTGTTTTT TGTAACTTCT GCCGACTCCG GGATTTATGT
1251 CTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGCGGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCTT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTACGCTG TGGAAAGGCT
1451 TGAGTGCAGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCC
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTGCTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

```

g163.pep
1  MVILTTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFISIF
51  LGFLLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPALRLS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFGVQV LIIAAVMSLA VVSAISGVGK GVKVLSEINL
251 GLAFLLLFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFEWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLEKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLOS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

```

m163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCCTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGGTGGGTC TGATGTTTTT CGCGGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTGCGTTT
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

```

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651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTTCG GCGACAACAT AGGGAACCTAC CTCGGAAATC
851 TGGTGC GCCT CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTGTTGTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGGGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGCGG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACAGACT GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTGAGCGTC
1651 CGGGTCGATA AAATGTTTCA TCGGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTG ATGTTGTTGG ATGATGTCGG TCAGGAAGCTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

```

m163.pep
1  MVILTLFFV CVLVVLVLT VPDQVQMWLDRAKEVIFTEFSWFYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLEAAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKPLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPEV GLFIARISK RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWG LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDEMYGIK SVQDQVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQDEL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

	10	20	30	40	50	60
m163.pep	MVILTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS					
g163	MVILTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m163.pep	SLGNIRLGRDEDVPEFGFLSWLAMLEAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ					
	:					
g163	GLGNIRLGRDEDVPEFGFLSWLAMLEAAGMGVGLMFFGVAEPLMHYFSDITVGAPEHRQQ					
	70	80	90	100	110	120
	130	140	150	160	170	180

m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSEINLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRSLKTYAYEREHKP
g163	GVKVLSEINLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRSLKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFPALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFPALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKQTASPAHMLQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKHTASPAHMLQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

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201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCCTGTGC TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCCTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCCTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGTCTTGCGT TTTTGCTGCT GTTTTGTGTT TTGGCGCGCG GTCCACTGT
801 TTACCTGTTG TCGGCATTGC GCGACAACAT AGGGAACATC CTCGGAAATC
851 TGGTGCCTCT CAGTTTAAAT ACTTATGCGT ACGAACGGGA ACACAGCCG
901 TGGTTTGAAT CTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTGTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 CGGAGTTTGT CTTCGGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGAAACG CTGCTTTTAA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CTGCGAGTCT ATGACCCTGA TGTTCCTCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGAT
1451 TGAGTGCAGG TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTG ATGTTGTTGG ATGATGTCGG TCAGGAAC TG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

```

a163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHWSVYGT IALALAYFGF
151 RYKLPALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWCWSWAPFV GLFIARISK RTIREFVFGV LLIPGLFGVL
351 WETVFGNTAI WLNDGVAGGV LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFEVTS ADGGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCPSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQ ELSEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTPYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQGEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLFFV CVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS
          |||
a163      MVILTTLFFV CVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS
          10      20      30      40      50      60
          70      80      90     100     110     120
m163.pep  SLGNIRLGRDEDVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ

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|||||
a163 SLGNIRLGRDEVDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
      70      80      90     100     110     120

      130     140     150     160     170     180
m163.pep QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
      |||||
a163 QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
      130     140     150     160     170     180

      190     200     210     220     230     240
m163.pep MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
      |||||
a163 MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
      190     200     210     220     230     240

      250     260     270     280     290     300
m163.pep GVKVLSSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
      |||||
a163 GVKVLSSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
      250     260     270     280     290     300

      310     320     330     340     350     360
m163.pep WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVGVLLIPGLFGLVWETVFGNTAI
      |||||
a163 WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVGVLLIPGLFGLVWETVFGNTAI
      310     320     330     340     350     360

      370     380     390     400     410     420
m163.pep WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
      |||||
a163 WLNDGVAGGVLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
      370     380     390     400     410     420

      430     440     450     460     470     480
m163.pep ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
      |||||
a163 ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
      430     440     450     460     470     480

      490     500     510     520     530     540
m163.pep WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKQTASPMHELQR
      |||||
a163 WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKHTASPMHELQR
      490     500     510     520     530     540

      550     560     570     580     590     600
m163.pep ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
      |||||
a163 ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
      550     560     570     580     590     600

      610     620     630     640     650     660
m163.pep HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
      |||||
a163 HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
      610     620     630     640     650     660

m163.pep X
      |
a163 X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1 ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51 CAAGGCGCGC TTCCTGTTCC CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCCC GTCGAAAAA TCATTGGGAC GGACAAAAGC
151 CGGCCGCGCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCGC ACTTGGGCGG CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTcctg ccgatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAAtc cgttttCCcC ttttccaacG TTTTGAAAAA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTCAAGAT GTTCAACCGC
601 ATCCGCTGTG TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTCC CCCGCGCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCCGTC GTCGCCGTCA ATACGCCCGA ACGGCAAAAA
751 GCCCGCAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801 TGAAGAATTG GTCGAAGTGC CGCGCGGCGA AGTGGGCGAA CTGATCGTCA
851 GGGGCGGTTT GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAACACG GCGGATTTTC TTACCATAGA
951 CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAGAT TTGATTATTT
1001 CCAAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCAT GCGGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTGCG
1151 GCGAGGACGA aatccgccc caccTGCCTA CCGTGCTGGC AAATTTCAAA
1201 ATCCCAAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGCTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1 ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51 RPAGETAEGD AFFENVRRFP EKPDLRQPR INDLAHIIT SGTGHPKGA
101 LISYANLEAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151 SIILVKSVPF FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWENR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLL GYGLSEASPV VAVNTPERQK
251 ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKDD LIISKGQNVY PREIEEIIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1 ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51 CAAAAACGGA AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 AGAATTTATT ACCGCCTATT TCGCCATCTC CGCCATCGGC GCGGTGCGCG
251 TACCGATGAA CACATTTTGT AAAAAACGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGACA
401 AAAGCCGTCC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501 TGATTGGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTC CAACGTTTTC
751 AAACAGACAC TGCTCAAACG CGGACCGGTG TTTTGGGCGG TACCCGCGAT
801 TTACACCGCG ATAGCAAGG CGAAAATCCC TTGGTATTTC AGATGGTTCA
851 ACCGCATTTC CCTGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCGCG GCCAAATTGC TGGAAGGCTA

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951 CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCTGCG CCGGTTTGA AGCCAAAGCC
1051 GTCGATGAAG AATTGGTGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TCGGGGGCTA CCTCAATATG CTGCGCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTGAT
1251 TATTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGD AFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISKDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQTLKRATV FLGVP AIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVPR GEVGLIVRG GSVMRGYLNM PAATDETIVN GWLKTGFVFT
401 IDEGDFIFIV DRKKDLIISK GQNVYPREIE EEIYKLD AVE AAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRLTV LANFKIPKQI HFKDGLPRNA
501 TGVVLRV LK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:  
 Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

m164.pep	60	70	80	90	100	110
	GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARLFASAGLSK					
g164					10	20
					MNTFLKNSEYAYILNDCKARLFASAGLSK	
m164.pep	120	130	140	150	160	170
	ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT					
g164	40	50	60	70	80	90
	ELAGLKAQTPVEKIIWTDKSRPAGETAEGDAFFENVRRFPEKPD LGRQPRINDLAHIIYT					
m164.pep	180	190	200	210	220	230
	SGTTGHPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMAC					
g164	100	110	120	130	140	150
	SGTTGHPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMAC					
m164.pep	240	250	260	270	280	290
	SIILVKSVPFSPSNVLKQTLKRATVFLGVP AIYTAMSKAKIPWYFRWFNRIRLFISGGAP					
g164	160	170	180	190	200	210
	SIILVKSVPFSPSNVLKQALLKRATVFLGVP AIYTAMSKAKIPWYFRWFNRIRLFISGGAP					
m164.pep	300	310	320	330	340	350
	LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVG IPLPGLEAKAVDEEL					
g164	220	230	240	250	260	270
	LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVG IPLPGLEAKAVDEEL					
	360	370	380	390	400	410

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m164.pep  VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164       VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          280      290      300      310      320      330

          420      430      440      450      460      470
m164.pep  LIISKQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164       LIISKQNVYPREIEEEIHKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
          340      350      360      370      380      390

          480      490      500      510
m164.pep  HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164       HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
          400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAAACGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATCCAC
201 GGAATTTATT ACCGCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTG AAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCTCG GCCGCGCTGT CAAAAGAATT
351 GCGGGGCTTG AAGGCGCAA CGCCGTCGA AAAATCATT TGGACGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTGAAGAC
451 GTGCGCGCT TCCCCGAAA ACCCGACTTG GGCCGCCAAC CCGGATAAA
501 TGATTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCT CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TCCCTTTTC CAACGTTTG
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAAATCCC TTGGTATTTC AGATGGTTCA
851 ACCGCATCCG CCGTGTATAT AGCGGCGGAG CACCTTTGCG GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCGCG GCCAAATTGC TGAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGA AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTGA AGTCCCGCGC GCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TCGGGGCTA CCTCAATATG CCGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAAT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKN NGTAVFDGKE KTAYRALKQE AEVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFEKPDLD GRQPRINDLA HIIYTSMTTG HPKGALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQALLKRATV FLGVPALYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVGEIVRG GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDGFIFIV DRKKDLIISK QNVYPREIE EEIYKLDAVE AAIVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRTV LANFKIPKQI HFKDGLPRNA

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501 TGKVLKRVLK EQFDGNK\*

m164/a164 98.3% identity in 517 aa overlap

	10	20	30	40	50	60
m164.pep	MNRTYANFYEMLAACRKN	NGTAVFDGKEKTAYRAL	KQEAEEVAAYLQNI	GVKFGDTVA		
a164	MNRTYANFYEMLTAA	CRKNNGTAVFDGKEKTAYRAL	KQEAEEVAAYLQNI	GVKFGDTVA		
	10	20	30	40	50	60
	70	80	90	100	110	120
m164.pep	LAVSNSTEFITAYFAIS	AGAVPMNTFLKNSEY	AYILNDCKARFLFAS	AGLSKELAGL		
a164	LAVSNSTEFITAYFAV	SAIGAVPMNTFLKNSEY	AYILNDCKARFLFAS	AGLSKELAGL		
	70	80	90	100	110	120
	130	140	150	160	170	180
m164.pep	KAQTPVEKIIWTDKSR	PTGETAEGDAFFEDV	RRFPEKPD	LGRQPRINDLAH	IIYTS	SGTTG
a164	KAQTPVEKIIWTDKSR	PDGEMAE	GDAFFEDVRRFPEKPD	LGRQPRINDLAH	IIYTS	SGTTG
	130	140	150	160	170	180
	190	200	210	220	230	240
m164.pep	HPKGALISYANLFANL	NGIERIFKISK	RDRFIVFLPMFHS	FTLTAMVLLPIY	MACSII	ILV
a164	HPKGALISYANLFANL	NGIERIFKISK	RDRFIVFLPMFHS	FTLTAMVLLPIY	MACSII	ILV
	190	200	210	220	230	240
	250	260	270	280	290	300
m164.pep	KSVFPFSNVLKQ	TLLKRATVFLGVP	AIYTAMSKAKIPWY	FRWENRIRLFIS	GGAPLAEQT	
a164	KSVFPFSNVLKQ	ALLKRATVFLGVP	AIYTAMSKTKIPWY	FRWENRIRLFIS	GGAPLAEQT	
	250	260	270	280	290	300
	310	320	330	340	350	360
m164.pep	ILDFKAKFPRAKL	LEGYGLSEASPV	VAVNTPERQKAR	SVGIPLPGLEAK	AVDEELVEVPR	
a164	ILDFKAKFPRAKL	LEGYGLSEASPV	VAVNTPERQKAR	SVGIPLPGLEV	KAVDEELVEVPR	
	310	320	330	340	350	360
	370	380	390	400	410	420
m164.pep	GEVGELIVRGG	SVMRGYLNMPAAT	DETIVNGWLKTG	DFVTIDEDGFIF	IVDRKKDLISK	
a164	GEVGELIVRGG	SVMRGYLNMPAAT	DETIVNGWLKTG	DFVTIDEDGFIF	IVDRKKDLISK	
	370	380	390	400	410	420
	430	440	450	460	470	480
m164.pep	GQNVYPREIEEEI	YKLDAVEAAVIG	VKDRYADEEIVAF	VQLKEGMDLGENE	IRRHLRTV	
a164	GQNVYPREIEEEI	YKLDAVEAAVIG	VKDRYADEEIVAF	VQLKEGMDLGENE	IRRHLRTV	
	430	440	450	460	470	480
	490	500	510			
m164.pep	LANFKIPKQIHFKD	GLPRNATGKVLK	RVLK	EQFDGNKX		
a164	LANFKIPKQIHFKD	GLPRNATGKVLK	RVLK	EQFDGNKX		
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq  
1 ATGGCTGAAG CGACAGACGT TGTCTGGTG GCGGCGGCA TTATGAGCGC

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51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGat gTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACGcCGgca CGGGGCATTc CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccgac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGC GGAAGGCAAG
301 TTGGAagaCA ATTCCTTCAT CAATGCcgtg ccgcatatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGCTATGAT GTGTTAAAA
401 CGCAGAAACT TTTTGAATAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtcgcCTGAT TATGCGCGGC CGGgacgaaa ACCAACCCGT
501 CGCCGCCAAC TATTCGCCCG Aaggcacgga tgtcgATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCCTCTT CCTCGCGCGG GCGGCGCGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCCCTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CcTGCTGGGc gAaTTGCgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFRTQKLFEN MEFSTDNRKI
151 SDWAPLMRG RDENQPVAAN YSAEGTDVDF GRLTRQMKY LQKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GLPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMRLAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTc CGcGCTGTGc GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTGCg GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTAAAA
401 CCCAAAAACT TTTTGAATAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGCGCGG GCGGCGCGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCGG TGTCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD AFRTQKLFEN MEFSTDNRKI
151 SDWAPLMRG RDENQPVAAN YSAEGTDVDF GRLTRQMKY LQKGVKTEF

```

201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LTRFLFLGA GGGALTLLQK  
 251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSPVPHL  
 301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA  
 351 NMPLTK...

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

	10	20	30	40	50	60
m165.pep	MAEATDVVLVGGGIMSATLGVLKLEPSWEITLIERLEDVALESSNAWNNAGTGHSA					
g165	MAEATDVVLVGGGIMSATLGVLKLEPSWEITLIERLEDVALESSNAWNNAGTGHSA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165	ELNYAPLGADGVINPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m165.pep	HCSYLQKRYDAFKTQKLFENMEFSTDNRKISDWAPLMRGRDENQPVAANYSAEGTDVDF					
g165	HCRYLQKRYDVFKTQKLFENMEFSTDNRKISDWAPLMRGRDENQPVAANYSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m165.pep	GRLTRQMVKYLQGGKGVKTEFNHVEDIKRESGAWVLKTADTRNPDGQLTLTRFLFLGA					
g165	GRLTRQMVKYLQGGKGVKTEFNHVEDIKRESGAWVLKTADTRNPDWQLTLTRFLFLGA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASVGAAPPMSPVPHL					
g165	GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAEOHNAKVYQASVGAAPPMSPVPHL					
	250	260	270	280	290	300
	310	320	330	340	350	
m165.pep	DTRNVDGKRHLMFGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTK					
g165	DTRNVDGKRHLMFGPYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
	310	320	330	340	350	360
g165	ELRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

a165.seq  
 1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC  
 51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTGG GAAATCACCC  
 101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGAAC  
 151 AACGCCGGCA CGGGGCATT CCGCTGTGC GAATTGAACT ATGCGCCGT  
 201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC  
 251 AGTTTCATGT CAGCCGCCAG TTTTGGCGCA CGTTGGTCGC GGAAGCAAG  
 301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT  
 351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA  
 401 CCCAAAACT TTTTAAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT  
 451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT  
 501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTGATTTC GGACGGCTGA  
 551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGCGTAAA AACCGAGTTC

```

601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACGCG CGAACAACAC AACGCCAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACTTATG GATTGCCC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAATACTA CCCCAGGGA AATCCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTG GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCGCAT TGCTGGGCGC GTGCGCGGCG GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AATCCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```

a165.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWTALVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAA N YSAEGTDVDF GRLTRQMVKY LOGKGKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRELFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAQH NAKVYGQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPLMRAGWA
351 NMPLTKYLLG ELRKTEERF ASLLEYYPEA NPDDWELITA GQRVQIIKKD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165/a165 99.7% identity in 356 aa overlap

m165.pep	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC
a165	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED
a165	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED
m165.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF
a165	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF
m165.pep	GRLTRQMVKYLOGKGKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
a165	GRLTRQMVKYLOGKGKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSPVPHL
a165	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSPVPHL

472

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          310      320      330      340      350
m165.pep  DTRNVGDKRHLMFPGPYAGFRSNFLKQGS LMDLPLSIHMDNLYPMLCAGWANMPLTK
          |||||
a165      DTRNVGDKRHLMFPGPYAGFRSNFLKQGS LMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
          310      320      330      340      350      360

          370      380      390      400      410      420
a165      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

```

g165-1.seq
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGCGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTCTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGAAC
151 AACGCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCGCT
201 GGGTgcgac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctggTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAACGAAGAC CACTGCCGTT ACCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtcgCTGAT TATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TATTCCGCCG AAGGCACGGA TGTCTGATTG GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGACCCC
701 GCTTCTCTCT CCTCGCGCGG GCGCGCGCGG CACTGACCCG GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCGGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTG GTCCCTTACG
951 AGGTTTCCGT TCCAACTTCC TCAAGCAAGG CTCGTTTATG GATTGCGCG
1001 GTGCCATCCA TATGGACAAC CTCATCCTTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATAA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTtt gCTCCCTGC TGgaatacta cccGaggcag acccGACGac
1151 tggtaactcat cagcgaggnc acGCGTcata tcattanata tgactCgaaa
1201 ctgcgcgtgc tgcagttgta cgagattgtg ccaCGCGacg ctcgctcgcg
1251 cattctggag cgtcgcgcg catcacgctn tgcgctgata tccgctgatg
1301 acactgctcc gaGCGcgccc gtcttggaag gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

```

g165-1.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALE ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFNAV PHMSLVNED HCRLYQKRYD VFKTKQLFEN MEFSTDRNKI
151 SDWAPLIMRG RDENPVAA N YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GLPVSGLFFR NSNPETAQH NAKVYGOASV GAPPMSVPHL
301 DTRNVGDKRH LMFGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYPRQ TRRLVLITQX TRHIIXYDSK
401 LRLVLQYIIV PRDARSRIE RRGASRXALI SADDTAPSAP VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

```

m165-1.seq
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGCGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTCTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGAAC
151 AACGCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCGCT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCAAAAACCT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATCGCGCGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGTACGGA TGTCTGATTG GGACGGCTGA
551 CGCGCCCAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGACGG GCAGCTCACC CTCCGACCCC
701 GCTTCTCTCT CCTCGCGCGG GCGCGCGCGG CGCTGACCCG GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCGG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG

```

```
851 TGTACGGGCA GGCTTCGTC GCGCGCCGCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTGCGCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TCCAAATCAT TAAAAAGAC
1201 TCCGAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGC
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCCGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCA
1451 AAGTATTGGA TATTAA
```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

```
m165-1.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSAIC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMRGR RDENQPVAA N YSAEGTDVDF GRLTRQMVKY LQKGKVFTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIEPGKGYG GFPVSGLFFR NSNPETAQH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELIT QQRVQIIKID
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*
```

m165-1/g165-1 89.7% identity in 428 aa overlap

	10	20	30	40	50	60
m165-1.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSW	EITLIERLED	VALESSNAWN	NAGTGHSAIC	
g165-1	MAEATDVVLVGGGIMSATLG	VLLKELEPSW	EITLIERLED	VALESSNAWN	NAGTGHSAIC	
	70	80	90	100	110	120
m165-1.pep	ELNYAPLGANGIIDPARALN	IAEQFHVSRQ	FWATLVAEGK	LEDNSFINAV	PHMSLVMNED	
g165-1	ELNYAPLGADGVINPARALN	IAEQFHVSRQ	FWATLVAEGK	LEDNSFINAV	PHMSLVMNED	
	130	140	150	160	170	180
m165-1.pep	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISD	WAPLMRGRDEN	QPVAA	NSAEGTDVDF	
g165-1	HCRYLQKRYDVFKTQKLFEN	MEFSTDRNKISD	WAPLMRGRDEN	QPVAA	NSAEGTDVDF	
	190	200	210	220	230	240
m165-1.pep	GRLTRQMVKYLQKGKVFTEF	NRHVEDIKRES	DGAWVLKTA	DTRNPDGQLT	LRTRFLFLGA	
g165-1	GRLTRQMVKYLQKGKVFTEF	NRHVEDIKRES	DGAWVLKTA	DTRNPDWQLT	LRTRFLFLGA	
	250	260	270	280	290	300
m165-1.pep	GGGALTLLQKSGIEPGKGYG	GFPVSGLFFR	NSNPETAQH	NAKVYQASV	GAPPMSVPHL	
g165-1	GGGALTLLQKSGIEPGKGYG	GLPVSGLFFR	NSNPETAQH	NAKVYQASV	GAPPMSVPHL	
	310	320	330	340	350	360
m165-1.pep	DTRNVDGKRHLMFPGYAGFR	SNFLKQGSIM	DLPLSIHMDN	LYPMLCAGW	ANMPLTKYLLG	
g165-1	DTRNVDGKRHLMFPGYAGFR	SNFLKQGSIM	DLPLSIHMDN	LYPMLRAGW	ANMPLTKYLLG	
	370	380	390	400	410	420
m165-1.pep	ELRKTKEERFASLLEYYPEA	NPDDWELITAG	QRVQIIKIDSEK	GGVLQFGTEI	VAHADGS	
g165-1	ELRKTKEERFASLLEYYPEA	NPDDWELITAG	QRVQIIKIDSEK	GGVLQFGTEI	VAHADGS	
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNNPERADEIIA  
 : III  
 g165-1 ILERRGASRXALISADDTAPSAPVLESVX  
 420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq  
 1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGGCGGCA TTATGAGCGC  
 51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTGG GAAATCACCC  
 101 TGATTGAACG CTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGAAC  
 151 AACCGCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAAC ATGCGCGGTT  
 201 GGGTGC AAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC  
 251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCGC GGAAGGCAAG  
 301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT  
 351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA  
 401 CCCAAAAACT TTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT  
 451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT  
 501 CGCCGCCAAC TACTCCGCGG AAGGCACGGA TGTCGATTTC GGACGGCTGA  
 551 CGCGCCAAAT GGTGAATAT TTGAGGGCA AGGGCGTAAA AACCGAGTTC  
 601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT  
 651 CAAAACCGCC GATACCCGCA ACCCGACGG GCAGCTCACC CTCCGTACCC  
 701 GCTTCTCTT CCTCGGCGCG GCGCGCGGCG CGCTGACCCT GCTGCAAAA  
 751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT  
 801 GTTCTTCCCG AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAG  
 851 TGTACGGGCA GGCTTCCGTC GCGCGCGGCG CGATGTCCGT CCCGCACCTC  
 901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCT GGCCTTACGC  
 951 AGGCTTCCGT TCCAACTTCC TCAAGCAAGG CTCACCTATG GATTGCGCG  
 1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG  
 1051 AATATGCCCG TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA  
 1101 AGAACGCTTC GCCTCCCTGC TGGAACTACTA CCCCAGGCA AACCCGACG  
 1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC  
 1201 TCCGAAAAG GCGCGTGTG GCAGTTGGT ACGGAGATTG TCGCACACGC  
 1251 CGACGGCTCG CTCGCGCAT TGCTGGGCGC GTCGCGGGC GCATCGACCG  
 1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC  
 1351 CCGCTTGGG AAGGCGCTCT GAAAGAGCTG GTACCGGGT ACGCATCAA  
 1401 GTTGAACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA  
 1451 AAGTGTGGA TATTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep  
 1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN  
 51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK  
 101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI  
 151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQGGKGVKTEF  
 201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLCA GGGALTLLQK  
 251 SGIEPEKGYG GFFVSGLFER NSNPETAEOH NAKVYQASV GAPPMSVPHL  
 301 DTRNVGDKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA  
 351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKKD  
 401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT  
 451 PSWEGRLKEL VPGYGIKLNE NPERADEIIA YTAKVLDI\*

a165-1/m165-1 99.4% identity in 488 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLGVLLELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
m165-1	MAEATDVVLVGGGIMSATLGVLLELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
	10	20	30	40	50	60
a165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
m165-1	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
a165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGDENQPVAAANYSAEGTDVDF					
m165-1	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGDENQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGDENQPVAAANYSAEGTDVDF					
m165-1	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGDENQPVAAANYSAEGTDVDF					
	190	200	210	220	230	240

```
a165-1.pep  GRLTRQMVVKYLQGGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
|||||
m165-1      GRLTRQMVVKYLQGGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
a165-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGOASVGAPPMSVPHL
|||||
m165-1      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGOASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
a165-1.pep  DTRNVGDKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
|||||
m165-1      DTRNVGDKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
a165-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQVRQIIKKDSEKGGVLQFGTEIVAHADGS
|||||
m165-1      ELRKTKEERFASLLEYYPEANPDDWELITAGQVRQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
a165-1.pep  LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
|||||
m165-1      LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
a165-1.pep  YTAKVLDIX
|||||
m165-1      YTAKVLDIX
```

**a165-1/p33940**

sp|P33940|YOJH\_ECOLI\_HYPOTHETICAL\_60.2\_KD\_PROTEIN\_IN\_ECO-ALKB\_INTERGENIC\_REGION  
>gi|1736851|gnl|PID|d1016718 (D90850) ORF ID: o372#5; similar to [SwissProt Accession Number  
P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical  
to 490 residues of YOJH\_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct  
identical to GB: ECOHU49\_33  
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548  
Score = 458 bits (1167), Expect = e-128  
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

Query: 3 EATDVLVGGGIMSATLGVLKLEPESWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62  
+ TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL  
Sbjct: 30 QETDVLILGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSALMEL 89

Query: 63 NYAPLGGANGIIDPARALNIAEQFHVSQRQFWATLVAEGKLED-NSFINAVPHMSLVNMEDH 121  
NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+  
Sbjct: 90 NYTPQNADGSISIEKAVAINAEAFQISRQFWAHQVERGVLTPTPSFINTVPHMSFVWGEDN 149

Query: 122 CSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMGRDENQPVAAANYSAEGTDVDFG 181  
++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G  
Sbjct: 150 VNFLRARYAALQQSSLFGRMRYSEDHAQIKAWAPLVMEGRDPQKVAATRTTEIGTDVNYG 209

Query: 182 RLTRQMVVKYLQGGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240  
+TRQ++ LQ K + + V +KR D W + AD +N Q  
Sbjct: 210 EITRQLIASLQKSNFSLQLSSEVRALKRNDNTWTVTVADLKNGTAG-NIRAKFVFIGA 268

Query: 241 XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGOASVGAPPMSVPHL 300  
Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+  
Sbjct: 269 GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVVNHHLAKVYGKASVGAPPMSVPHI 328

Query: 301 DTRNVGDKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360  
DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+  
Sbjct: 329 DTRVLDGKRVLVFGPFATFSTKFLKNGSLWDLMSSTTSNVMPMMHVGLDNFDLVKYLVS 388

Query: 361 ELRKTKEERFASLLEYYPEANPDDWELITAGQVRQIIKKDSEKGGVLQFGTEIVXXXXXX 420  
++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V  
Sbjct: 389 QVMSLSEEDRFALKEYYPQAKKEDWRLWQAGQRVQIIKRDSEKGGVLRALGTEVVSDDQGT 448

Query: 421 XXXXXXXXXXXXXVPLMIRLMHQCFPER--TPSWEGRLKELVPGYGIKLNENPERADEI 478



P+M+ L+ + F +R +P W+ LK +VP YG KLN + . +  
 Sbjct: 449 IAALLGASPGASTAAPIMLNLEKVFGRVSSPQWQATLKAIVPSYGRKLNGDVAATERE 508

Query: 479 IAYTAKVLDI 488  
 + YT++VL +  
 Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq  
 1 atggcggcgg cggaataaaa acgccccctc gctgtcgatt tccagcacat  
 51 agcgtccggt ctgcacggcg gcatagccgc ttttgccctgc ctgatatgggt  
 101 tgcagggcgg aatgcgaaat caggaataca gtcagtttgc cgccgtcttc  
 151 ggcgatattg cccaccagtt tggcaaacaa ggatggcac acgccgtttt  
 201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg  
 251 acgacggcct ccaagtcggt gggatgcttt ccggtcagcc ggacggcggt  
 301 ttgttcgggc aagcctttaa tcggataact gatttgtttt ttgccgtcgt  
 351 tggttttgcc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta  
 401 ttgtcgatgt atttgacttt gaaaaccggt ttcggcgcg tttgtgccgc  
 451 attttgcggc tgttcggcg tattttcgga tttgcgcag gcggcaagca  
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc  
 551 tgatggtttc aaaatgccgt ctgaaatgcc gtctgaaacg tggcaggcgg  
 601 aggttcggac ggcattgggt ttatttcaac gggcggatgc cgaccgcac  
 651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgt tttgcgcgc  
 701 ctgcctgcaa aatctcttcg atttgcaag gattagaggt caatgcgttg  
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep  
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF  
 51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQV GMLSGQPDGV  
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDFDF ENRFRRLCR  
 151 ILRLFRRIFG FAAGGKQQA AOHGKRYFQH SALLMVSKCR LKCR LKRGR  
 201 RFRHVVYFN GRMPTASRTL SNNRSASLRA FCAPACKISS ICEGLEVNAL  
 251 \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq  
 1 ATGGCGGCGG CGGAAATAAA ACGCCCCCTC GCTGTGATT TCCAGCACAT  
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCCTGC CTGATAGGGT  
 101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGCTCTC  
 151 GGCATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT  
 201 CTGCCCAACC TGCCGGACTG TCCTTATCAT CGGTTTCCAT ACATTTGCCG  
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT  
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTCGT  
 351 TGGTTTGGCC TTCGCTGCTT TGTCCCAAAT CCAAACCGGC AATCGCCGTA  
 401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC  
 451 GTTTTGGCGC TGTACCGCCG TATTTCGGA TTTGCCGCaC GGCaArGCAG  
 501 CAGGCAGCCG CCAATACGG CAAArAwGT wTTCAGCAT CCACATCCT  
 551 GATGGTTTCA AAATGCCGTC TGAACCGCG CAGGCGGAGG TTCGGACGGC  
 601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATC9GT ACTTTGTCCA  
 651 ATAATTCGCG TGCTTCTTA CGCGCTTTCG CCGCGCTGC CTGCAAAATC  
 701 TCTTCGATTT GCGAAGGGTC GCGGTCAGC TC GTTGTAG

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep  
 1 MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN \*VIRQFAAVF  
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI  
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRLYR  
 151 VLRLYRRI XG FAATAXQQA AQYKXXXQH STXLMVSKCR LKRGRRRFGR  
 201 HRVHFNGRMP TASGTLNNNS RASLRAFAAP ACKISSICEG SAVSSL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 204 shows 82.0% identity over a 250 aa overlap with a predicted ORF (ORF 204.ng)

from *N. gonorrhoeae*:

m204/g204

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIGLQGGMRNXVIRQFAAVFGDIAHQFGKQ					
	:					
g204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIGLQGGMRNQVISQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
	:      :             :       :       :       :       :					
g204	GMAHAVFRPARRRVL SVGFHTFADDFQVVGMLSGQPDGVLFRQAFNRITDLFFAVVGFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m204.pep	FAALSQIQTGNRRIVDIYDFENRFRRALYRVLRLYRRIXGFAATAXQQAAYGKXXKH					
	:           :             :       :       :       :       :					
g204	FATLSQSQTGNRRIVDVPDFENRFRRALCRILRLFRRI FGFAAGGKQQAAYGKRYFQH					
	130	140	150	160	170	180
	190	200	210	220	230	
m204.pep	STXLMVSKCRLK---RGRRRFGRHRVHFNRMPTASGTLNNSRASLRAFAAPACKISS					
	:             :					
g204	SALLMVSKCRLKCRLKRGRRRFGRHWVFNGRMPTASRTLSNNSRASLRAFCAPACKISS					
	190	200	210	220	230	240
	240					
m204.pep	ICEGSAVSSLX					
	:					
g204	ICEGLEVNAL					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

a204.seq

1	ATGGCGGCGG	CGGAAATAAA	ACGCCCCCTC	GCTGTCGATT	TCCAGCACAT
51	AGCGTCCGTT	CTGCACGCG	GCATAGCCGC	TTTTGCCTGC	CTGATAGGGT
101	TGCAGGCGG	AATGCGAAAT	CAGGTAATCC	GTCAGTTTGC	CGCCGTCTTC
151	GGCGATATTG	CCCACCAATT	TGGCAAACAA	GGTATGGCAC	ACGCCGTTTG
201	CCGCCAGCC	CGAAGGCGCG	CCCTTTCCGT	CGGTTCCAT	ACATTTGCCG
251	ACGACGGCTT	CCAAGTCGTT	GGGATGCTTG	CCGGTCAGCC	GGACGACGTT
301	TTGTTCCGGC	AAGCCTTT..	.....	.....	.....
351	.....	.....	.....	.....	.....
401	.....	.....	.....	.....	.....
451	.....	.....	.....	.....	.....
501	.....	.....	.....	.....	.....
551	.....	.....	.....	.....AAGAG	GTTCCGACGG
601	CATTGGGTTT	ATTCAACGG	GCGGATACCG	ACCGCATCAC	GTACTTTGCC
651	CAATAATTCG	CGTGCTTCTT	TACGCGCTTT	TTGCGCGCCT	GCCTGCAAAA
701	TCTCTTCGAT	TTGCGAAGGG	TCGCGGGTCA	GCTCGTTGTA	G

This corresponds to the amino acid sequence &lt;SEQ ID 702; ORF 204.a&gt;:

a204.pep

1	MAAAEIKRPL	AVDFQHIASV	LHGGIAAFAC	LIGLQGGMRN	QVIRQFAAVF
51	GDIAHQFGKQ	GMAHAVCRPA	RRRALSVGFH	TFADDFQVVG	GMLAGQDDV
101	LFRQAF....	.....	.....	.....	.....
151	.....	.....	.....	.....KRFRGR	.....
201	HWVYFNGRIP	TASRTLPNNS	RASLRAFCAP	ACKISSICEG	SAVSSL*

## m204/a204 54.5% identity in 246 aa overlap

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIGLQGGMRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIGLQGGMRNQVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
a204	GMAHAVCRPARRRALSVGFHTFAADGFQVAGMLAGQPDDVLFROAF-----					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQGTGNRRIVDIYDFENRRFRALYRVLRLYRRXGFAATAQQAAAQYKXXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKGRRRFRGRHVFHNGRMP TASGTLNNSRASLRFAA PACKISSICEG					
a204	-----KRFGRHWVYFNGRIPTASRTLPNNSRASLRFA CAPACKISSICEG					
	110	120	130	140	150	
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

```

g205.seq
1  atgctgaaaa taccttttgc cgtgttgggc ggctgcctgc tgettgccgc
51  ctgcggaata tccgaaaata cgccggaaca gccgcaaat gcggcaciaa
101 ggcgcgcgaa accggttttc aaagtaaat acatcgacaa tacggcgatt
151 gccggtttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgctcg cggcaaatgt
301 atggaacacc cggaagga cgcccttcg ggctggcgcg aaaacggcgt
351 gtgccatacc ttgtttgcca aactgggtgg caatatcgcc gaagacggcg
401 gcaactgac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggctatgc cgccgtgcag aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccgcat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

```

g205.pep
1  MLKIPFAVLG GCLLLAACGK SENTAEQPN AAQSAPKPVF KVKYIDNTAI
51  AGLALGQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNTA EDGGKLTDL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

```

m205.seq
1  ATGCTGAaAw CwTyTTTTGC CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51  tGCGGCAAAAT CCGwAAATAC GGCGGTACAG CCGCAAAACG CGGTACAAAG
101 CGCGCCGAAA CCGGTTTTCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGA TTTGGGACAA AGCAGCGAAG GCAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGA AGCCGTCAGC GGCAAATGTA
301 TGGAACCGA TGATAAGGAC AGTCCGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTGCCAA ACTGGTGGGC AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTGCGATGC CGCCCTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCGCG CGCCGCCATT ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

```
m205.pep
1  MLXTXFAVLG GCLLXCRCGK SXNTAVQPON AVQSAPKPVF KVIYIDNTAI
51  AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101 METDDKQSPA GWAENGVCHT LFAKLVGNIA EDGGKLTDLV VSHAALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

```
m205/g205

      10      20      30      40      50      60
m205.pep  MLXTXFAVLGGCLLXCRCGKSXNTAVQPONAVQSAPKPVFKVIYIDNTAIAGLDLGQSSE
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g205       MLKIPFAVLGGCLLLAACGKSENTAEQPNAAQSAPKPVFKVKYIDNTAIAGLALGQSSE
          10      20      30      40      50      60

      70      80      90     100     110     120
m205.pep  GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKQSPAGWAENGVCHT
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g205       GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT
          70      80      90     100     110     120

      130     140     150     160     170     180
m205.pep  LFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFFRRRH
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g205       LFAKLVGNIAEDGGKLTDLVISHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAFFRRRH
          130     140     150     160     170     180

m205.pep  YX
          |
g205       Y
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

```
a205.seq (partial)
1  TCCGAACCTC TTAAAGGCTT GCCGGAACAA AACGTCGTCC GGCTGACCGG
51  CAAGCATCCC AACGACTTGG AAGCCGTCGT CGGCAAATGT ATGGAAACCG
101 ACGGAAAGGG CGCGCCTTCG GGCTGGGCGG CAAACGGCGT GTGCCATACC
151 TTGTTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG GCAAACCTGAC
201 GGATTACCTG ATTTGCGATT CCGCCCTGCA ACCCTATCAG GCAGGCAAAA
251 GCGGCTATGC CGCCGTGCAG AACGGACGCT ATGTGCTGGA AATCGACAGC
301 GAGGGGGCGT TTTATTTCCG CCGCGCCAT TATTGA
```

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

```
a205.pep (partial)
1  SEPLKGLPEQ NVVRLTGKHP NDLEAVVGKC METDGKGAPS GWAANGVCHT
51  LFAKLVGNIA EDGGKLTDLV ISHSALQPYQ AGKSGYAAVQ NGRYVLEIDS
101 EGAFYFRRRH Y*
```

m205/a205 88.3% identity in 111 aa overlap

```
      50      60      70      80      90     100
m205.pep  KVIYIDNTAIAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC
          | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a205       SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC
          10      20      30

      110     120     130     140     150     160
m205.pep  METDDKQSPAGWAENGVCHTLFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQ
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 709>:

This corresponds to the amino acid sequence <SEQ ID 710; ORF 205-1.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 711>:

This corresponds to the amino acid sequence <SEQ ID 712; ORF 205-1>:

m205-1/g205-1 92.0% identity in 174 aa overlap

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAACGKSSENTAEQPPNAAQSAPKPVFKVKYIDNTA	IAGLALGQSSE				
m205-1	MLKTSFAVLGGCLLLAACGKSSENTAEQPPNAVQSAPKPVFKVKYIDNTA	IAGLDLGQSSE				
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQISYPYIKGLPEQNVRVLTGKHPNDL EAVVGSKMETDGDKDAPSGWAENGVCHT					
m205-1	GKTNDGKKQISYPYIKGLPEQNVRLIRLGKHPGDL EAVSGSKMETDDKDS PAGWAENGVCHT					

a205-1.seq (partial)

1	CCTCTTAAAG	GCTTGC CGGA	ACAAAACGTC	GTCCGGCTGA	CCGGCAAGCA
51	TCCCAACGAC	TTGGAAGCCG	TCGTGCGCAA	ATGTATGGAA	ACCGACGGAA
101	AGGGCGCGCC	TTCGGGCTGG	GCGGCAAAAC	GCGTGTGCCA	TACCTTGTTT
151	GCCAAACTGG	TGGGCAATAT	CGCCGAAGAC	GGCGGCAAA	TGACGGGTTA
201	CCTGATTTCG	CATTCCGCCC	TGCCAACCTA	TCAGGCAGGC	AAAAGCGGTA
251	ATGCGCGCGT	GCAGAACGGA	CGCTATGTGC	TGGAATTCGA	CAGCAGGGGG
301	GC GTTTTATT	TCCGCGCCGC	CCATTATTGA		

a205-1.pep (partial)

1	PLKGLPEQNV	VRLTGKHPND	LEAVVGKCM	EDGKGAPSGW	AANGVCHTLF
51	AKLVGNIAD	GGLKLDYLI	HSALQPYQAG	KSGYAAVQNG	RYVLEIDSEG
101	AFYFRRRHY*				

50 60 70 80 90 100  
 m205-1.pep KYIDNTAIAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHHPGDLEAVSGKCMEE  
 |||||  
 a205-1 PLKGLPEQNVVRLTGKHPNDLEAVVGKCMEE  
 10 20 30

110 120 130 140 150 160  
 m205-1.pep TDDKDSFAGWAENGVCHTLFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNG  
 || : |||||  
 a205-1 TDGKGAPSGWAANGVCHTLFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNG  
 40 50 60 70 80 90

170 180  
 m205-1.pep RYVLEIDSEGAFYFRRRHYX  
 |||||  
 a205-1 RYVLEIDSEGAFYFRRRHYX  
 100 110

g206.seq

1	atgttttccc	ccgacaaaac	ccttttccct	tgtctcggcg	cactgctcct
51	cgctcatgc	ggcacgacct	ccggcaaaca	ccgccaaccg	aaacccaaac
101	agacagtcg	gcaaattcaa	gccgtccgca	tcagccacat	cggccgcaca
151	caaggctcg	aggaactcat	gctccacagc	ctcggactca	tcggcacgcc
201	ctacaatat	ggcggcgaca	gcaccgcaac	cggtctcgac	tgacgcggca
251	tgattcaatt	ggtttcaaaa	aacgccctca	acgtcaagct	gccgcgcacc
301	gccgcgcaca	tggcggcggc	aagccgcaaa	atccccgaca	gcgcctcaa
351	ggcggcgac	atcgatttct	tcaacaccgg	cggcgcacac	cgtctatcac
401	acgtcggact	ctacatcggc	aacggcgcaat	tcatcatcgc	ccccgcgacg
451	ggcaaaaaca	tcaaaaccgc	aaaactctcc	acacggtttt	acgccaaaaa
501	ctaccttgga	gcgcatacgt	tttttacaga	atga	

g206.pep  
1 MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT

51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPR  
 101 ARDMAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS  
 151 GGTIKTEKLS TPFYAKNYLG AHTFFTE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 717>:

m206.seq  
 1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT  
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC  
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA  
 151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC  
 201 CTACAAATGG GCGGCGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA  
 251 TGATTCAATT CGTTTACAA AAGCCCTCA ACGTCAAGCT GCCGCGCACC  
 301 GCCCGCGACA TGGCGGCGGC AAGCCGAAA ATCCCGACa GCCGCyTCAA  
 351 GCGCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC  
 401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCAGCAGC  
 451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTT ACGCCAAAAA  
 501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

m206.pep..  
 1 MFPPDKTLFL CLSALLLASC GTTSKGHRQP KPKQTVRQIQ AVRISHIDRT  
 51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQVYK NALNVKLPR  
 101 ARDMAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS  
 151 GGTIKTEKLS TPFYAKNYLG AHTFFTE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSKGHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
g206	MFSPDKTLFLCLGALLLASC GTTSKGHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQVYK NALNVKLPR TARDMAASRKIPDSRXKAGD					
g206	LGLIGTPYKWGGSSTATGFD CSGMIQVYK NALNVKLPR TARDMAASRKIPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
g206	IVFFNTGGAHRYSHVGLYIGNGEFIHAPSGKTIKTEKLSTPFYAKNYLGAHTFFTE					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

a206.seq  
 1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT  
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC  
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA  
 151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC  
 201 CTACAAATGG GCGGCGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA  
 251 TGATTCAATT CGTTTACAAA AAGCCCTCA ACGTCAAGCT GCCGCGCACC  
 301 GCCCGCGACA TGGCGGCGGC AAGCCGAAA ATCCCGACA GCCGCCTTAA  
 351 GCGCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC  
 401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCAGCAGC  
 451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTT ACGCCAAAAA  
 501 CTACCTCGGC GCACATACTT TCTTACAGA ATGA

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQAVRISHIDRT	QGSQELMLHS			
a206	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQAVRISHIDRT	QGSQELMLHS			
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD	CSGMIQFVYKNALNVKLPRT	ARDMAAASRKIPDSRXKAGD			
a206	LGLIGTPYKWGGSSTATGFD	CSGMIQFVYKNALNVKLPRT	ARDMAAASRKIPDSRLKAGD			
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGN	GEFIHAPSSGKTIKTEKLS	TPFYAKNYLGAHTFFTEX			
a206	LVFFNTGGAHRYSHVGLYIGN	GEFIHAPSSGKTIKTEKLS	TPFYAKNYLGAHTFFTEX			
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
1  atgctgcggc atttaggaaa cgacttcgcc ttggcgcgct tgttttcga
51  tgctgcggtt gatgtgccac tgctgggcga tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcggttcag ataggtttg gcgaacatcg ttgccgccat aatgatgggc
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgccag tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcatc gcttgctgtt gcgccatacg
451 gtcgtcgccg tatttttctt tgatggtctg cagttcgggt gcggcgccac
501 gcattttcgc catcgaacgg taggagcggt tggatcaatg atacgtacg
551 gctttgacga tgatggtcaa aacgacgatt gccagcccc agttgcccgt
601 aatgtgtgac agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgctggc gatgtttgag
701 ataacggatg tggtttgagg accggcatac aggttgaccg ccattttcgg
751 ttttgcccc cggttgagg tagcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
1  MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDHPVENQT GREEEHEDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPAQP
101 RCLAQFYGGE QCFVQADEDG DLQQHRTAA QRVDFLVFEK LHHRLRLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQEPE ERRCEPVYFT VVFCQLQVVG DVCDNGCGLR TGIQVDRHFR
251 FWPPGWDSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
1  ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGGTT GTTTTTCGAT
51  GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAAGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTCGCC TGTCATCGGT CGGTCGGCGG
201 CGGTTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGTAATCCA ACCCAGCCAA
```



```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGGCGGCACG
501 CATTTTCGCC ATAGAGCGGT AAGAGCGGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTCGGCG ATGTTTGCGA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCTG TGCGGCGTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTGCCTTTAG GTTGAGAAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGTTCGGGG TTTTGGCGAT GTATTGCGCC
951 TCGGATTTGC CGGATTGGC ATCGTCGTCC AAGTCGGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
1 MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ ISLGEHRCRH NDQDQVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDGDL DLQQRQAAAA QRVDFLVCVK LHHRLLLRHT
151 VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW IQYGFDDG* NDNRPAPVAD
201 DVVQLVQEP EERGEPVYFA VVFGQLQVVG DVCDGCGGLR AGVEVDGGFG
251 FAPFWMAAKG TLTLLVLSLS LRLMSMLHS PAAQTLCLPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSP V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng)

from *N. gonorrhoeae*:

m209/g209

m209.pep	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR
g209	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVENQTGREEEEHDGENQRHDFHHFR
	10 20 30 40 50 60
m209.pep	LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAAEVGNPTQPRCLAQFYGGEQCPIQSDG
g209	LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAAEVGNPAQPRCLAQFYGGEQCPVQADEG
	70 80 90 100 110 120
m209.pep	DLQQRQAAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
g209	DLQQRQTAQAQRVDFLVFEKLHHRLLLRHTVVAVFFFDGLQFGCGGTHFRHRTVGGVGVQW
	130 140 150 160 170 180
m209.pep	IQYGFDDDGXNDNRPAVADDVVQLVQEP EERGEPVYFAVVFGQLQVVGQDVCDGCGGLR
g209	IQYGFDDDGQNDPCPAPVADNVVQLVQEP EERRCEPVYFTVVFQQLQVVGQDVCDGCGGLR
	190 200 210 220 230 240
m209.pep	AGVEVDGGFGF-APFWMAAKGTLTLVLSLSLRLMSMLHSPAAQTLCLPLGWRIQVDMK
g209	TGIQVDRHFRFWPPGWDSG
	250 260 270 280 290 299

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGCGT TGTTTTTCGA

```

```
51  TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGATC
101  ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151  AACCAGAGGC ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTCGGCG
201  GCGGGTTCAG ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251  AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCCAGCCA
301  AGGTGCCTGG CGCAATTCTA CGGAGGCGAA CAATGCCCAA TACAATCCGA
351  TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401  ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGTCT GCGCCATACG
451  GTCGTCGCGG TATTCTCTTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501  GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551  GCTTTGACGA TGATGGTTAA AACGATAATC GCCAGCCCC AGTTGCCGAT
601  GATGTTGTGC AGTTGGTTCA AAAGCCAAAA GAGGGGGGAG GCGAACCACT
651  GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTGTGCGGC GATGTTGCG
701  ATAACGGATG TGGTCTGTGG GCCGGCGTAG AGGTTGATGG AGGCTTCGGT
751  TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGGTGTGTGA
801  CAGCTTGTGC TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGGCGC
851  AAACGCTTTG TCCGCCTTTG GGTGGAGGA TCCAGGTGGA CATGAAGTGG
901  TGTTCATCA TGCCGAGCCA GCCGGTCGGG GTTTGCGGA TGTATTCGGC
951  CTCGGATTG CCGGATTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```
a209.pep
1  MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEHDGE
51  NQRHDFHHER LHRVGRRRVQ IGLGEHRCRH NDQDVVGVG AAEVGNPTQP
101  RCLAQFYGGE QCPIQSDGDL DLQQRQAAA QRVDLVCVK LHHGLLRHT
151  VVAVFLFDGL QFGRGGTHFR HRTVRGVGQW IQYGFDDG* NDNRPAPVAD
201  DVVQLVQKPK EGGGEPVYFA VVFGQLQVVG DVCNCGCLW AGVEVDGGFG
251  FAPFWIAAKG TLTLVLYSL LRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301  CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*
```

m209/a209 95.6% identity in 341 aa overlap

```
10 20 30 40 50 60
m209.pep MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEHDG ENQRHDFHHER
|||||
a209 MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEHDG ENQRHDFHHER
10 20 30 40 50 60

70 80 90 100 110 120
m209.pep LHRVGRRRVQ IGLGEHRCRH NDQDVVGVG AAEVGNPTQP RCLAQFYGGE QCPIQSDGDL
|||||
a209 LHRVGRRRVQ IGLGEHRCRH NDQDVVGVG AAEVGNPTQP RCLAQFYGGE QCPIQSDGDL
70 80 90 100 110 120

130 140 150 160 170 180
m209.pep DLQQRQAAA QRVDLVCVK LHHGLLRHT VVAVFLFDGL QFGRGGTHFR HRAVRGVGQW
|||||
a209 DLQQRQAAA QRVDLVCVK LHHGLLRHT VVAVFLFDGL QFGRGGTHFR HRTVRGVGQW
130 140 150 160 170 180

190 200 210 220 230 240
m209.pep IQYGFDDG XNDNR PAPVADDV VQLVQEP EERGGE PVYFA VVFGQLQVVG DVCNCGCLR
|||||
a209 IQYGFDDG XNDNR PAPVADDV VQLVQKPK EGGGEPVYFA VVFGQLQVVG DVCNCGCLW
190 200 210 220 230 240

250 260 270 280 290 300
m209.pep AGVEVDGGFG FAPFWIAAKG TLTLVLYSL LRLMSIRQS PAAQTLCPPL GWRIQVDMKW
|||||
a209 AGVEVDGGFG FAPFWIAAKG TLTLVLYSL LRLMSIRQS PAAQTLCPPL GWRIQVDMKW
250 260 270 280 290 300

310 320 330 340
m209.pep CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSGVX
```

```

|||||
a209      CSIMPSQPVGVLRMYSASDLPLDASSKSEKLTFWKLP SGVX
           310      320      330      340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

```

g211.seq
1  atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atggtgcggc
51  ggtgggaaac ggggtcgata agtttggcgc tgggtgctgat aatcaggttg
101 agtttttggg aggaaacctg attgtagtcg gcgcgtccgg gcgtgccgct
151 gtaacggtag ccgtggcgca attcgagcgt gcgtttgttg tccttcagcg
201 agaagttacc ttctttggcg aagatgatgt tgcgcgccgc gtttttgtcc
251 tgttcgcgca ggaacaggtt tttcatgatg ccggattcgg tgtcaaaggt
301 ttcgacgaaa taaaccctgc cgttgcgctt gcccaagtta ttgaactcgc
351 cggcttcac caaagacaat tcctgcttct gtttcaaaat ttcggcatat
401 tcgcggctgc gcagctctgc ccacggatc acccaaagct gcatgacggc
451 aatcaggatg gcaaacggca cggcaaacgt catgacgggg cgtatccact
501 gtttcaacgc caatccgcag gatag

```

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

```

g211.pep
1  MLRIAAANQL GGRNGAAVGN GVDKFRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVLQREVT FFGEDDVVAA VFVLFQAEQV FHDAGFGVKG
101 FDEINPAVAL AQVIELAGFH QRQFLLLQD FGIFAAALC PRYHPKLHDG
151 NQDGKRHGKL HDGAYPLFQR QSAG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

```

m211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTCTGATG AGTTTGGCGC TGGTGCTGAT AATCAGGTTG
101 AGTTTTTGGG AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGGTAG CCGTGGCGCA ATTCGAGCGT GCGTTTGTG TCCTTCAGCG
201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTCGCGGCC GTTTTGTCC
251 TGTTCGCGCA GGAACAGGTT TTTCATGATG CCGGATTCGG TATCGAAGGT
301 TTCGACAAA TAAACCCTGC CGTTGCGCTT GCCCAAAGT TTGAACCTGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAACCGGCA CCGCAAAGT CATCACGGG CGTATCCATT
501 GTTCAATGC CAATCCGCAG GATAG

```

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

```

m211.pep
1  MLRVAAANQL GGRNGTAVGN GVDEFGRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVVQREVT FFGEDDVVAA VFVLFQAEQV FHDAGFGIEG
101 FDKINPAVAL AQTVELACLH QRQFLLLQD FSVFAAAXLC PRYHPKLHDG
151 NQNGKRHGKL HHRAYPLFQC QSAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

```

m211/g211
           10      20      30      40      50      60
m211.pep  MLRVAAANQLGGRNGTAVGNQVEFLEGNLIVVGASGRAAVTVAVAQFER
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g211       MLRIAAANQLGGRNGAAVGNQVEFLEGNLIVVGASGRAAVTVAVAQFER
           10      20      30      40      50      60
m211.pep  AFVVVQREVTFFGEDDVVAAVFVLFQAEQVFHDAGFGIEGFDKINPAVALAQTVELACLH
           70      80      90     100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 731>:

This corresponds to the amino acid sequence <SEQ ID 732; ORF 211.a>:

m211/a211 99.4% identity in 174 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 733>:

g212.seq (partial)

1	atggacaatc	tcgtatggga	cggcattccc	gacatccgca	cactcgacca
51	ataatccgcg	aaacacgcac	acccgctcaa	cctgattgtc	tgccctccccg
101	aaccatcagat	tcccgatttt	caaacgcgac	aagatgtctc	ggactcggaa
151	tgcgctctga	agcaccgttt	ggatcaggca	accagtgcc	tcagttcga
201	cagcatcaac	ctcatcgaac	acatcctgcc	cgatgtccgc	ttctggtctg
251	ttcccccttc	agcaaccccc	cgacctgcag	aacatttcca	cacattttcc
301	tggcagaccg	aagccatccc	gcaaaccgaa	agcaagtccg	acaaacctcg
351	gtttgcactt	ccacaaacat	ccgaacggaa	aaaaccggaa	cacgtcctcg

```

401 tcatcgggtgc aggcattgcc ggcgcacga ccgcccacgc cttagcatca
451 cacggcatttt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctcggacaca tcctgcccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacggcg aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtcc
851 gcacctcctt cagccatccg ctgatcgaa tatatgaaaa cacaacgtta
901 accggcattt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacatttacc gccacacaca tcatctactg caccggcgcg cacagcccct
1001 gcctgcccga aaccaaccte gccgccctac ccctcaggca aatacgcgga
1051 caaacggcc tcacaccgtc caccctgtt tccgaacaac tgcgttgcg
1101 cgtttcaggc gaaagctaca tcagcccgct gtggcacgga ctgactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacgcga agcattggca caccttaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQTIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RIHEHFHHIS
101 WTEAIPQTE SKSDKPWFAL PQTSEKPKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSAEA
251 EKIAGIPLNT PYAEPLCGLY WQHGVLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNEA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCGCTCAA CCTGATTATC TGCCTCCCCG
101 ATAATCAGAT TCCCGATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCCTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCT CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCCTG
351 GTTTGCACCT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGGCATATCC GCGCGGGCAA CCGCCACGCG CTTAGCATCA
451 CACGGCATT TCCGTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCCG
501 CAGCGGCAAC CGCAAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAACTTTTG CTTGCCGGCT ACGGCTACAC CAAACGCCTG
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTGCTCC
851 GCACCCTCCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCCTTG
901 ACCGACATT CCCACGACGG GGAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCCGA AACCAACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCGTTT TCCGAACAAC TCGTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTTCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCGACACACC TTCCCTAGT CGGCGCACTC
1351 GGCGACATTG CCGCATGCG GCAGACCTAC ACCAACTCG CGCTGGACAA
1401 AAACCTACCG ATCGACACCC CATGCCATA CCTGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CGGCACCCGC GGAATCGCCA CCGCCCCAT CTGCGCGGCC

```

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1501 GmCAwTGCAG CCCAAATCaT AGGCyTGCCC CATCCCTTTT yAcAAcGCCT  
 1551 gCGCCACGCC cTAcACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA  
 1601 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep  
 1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE  
 51 CRLKHLRDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS  
 101 WQTEAIPQTE SKPDKPFAL POTSERQKPE HILVIGAGIS GAATAHALAS  
 151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL  
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA  
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL  
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG  
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA  
 401 EEASNRQALA HLNPALESSE FAANPNQKH QGHAAIRCDS PDHLPVGLAL  
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLEN AYVNTAHGTR GLATAPICAA  
 501 XXAAQIXGLP HPFXQLRHA LHPNRTIIRA IVRKDLTP\*

Computer analysis of this amino acid sequence gave the following results:

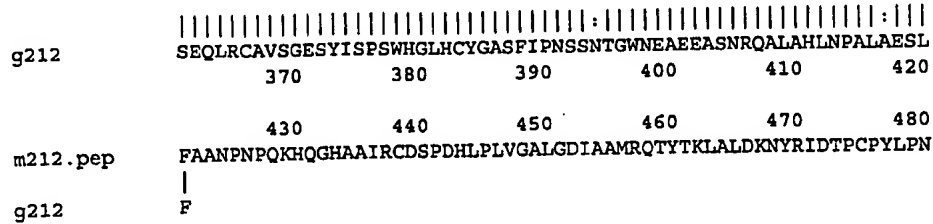
Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng)  
 from *N. gonorrhoeae*:

m212/g212

	10	20	30	40	50	60
m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLII CLPDNQIPDFQTAQDASDAECRLKHLRDQA					
g212	MDNLVWDGIPDIRTLDQITRKHAHPLNLIVCLPDNQIPDFQTAQDASDSECLKHLRDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPDKPFAL					
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRRLHEHFHHISWQTEAIPQTESKSDKPFAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m212.pep	PQTSERQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
g212	PQTSERKKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
	190	200	210	220	230	240
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTPL					
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNL AALPLRQIRGQTGLTPSTPF					
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAEEASNRQALAHLPALSESSE					

490



-- The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 737>:

a212.seq

```

1   ATGGACAATC TCGCATGGAA CGGCATTCCC GACATCCGCA CACTCGACCA
51  AACCATCCGC AAACACGCAC ACCCGCTCAA CCTGATTGTC TGCCTCCCCG
101 ATAATCAGAT TCCCAATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGCTCTGA AGCACCGTTT GGATCAGGCA ACCCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTGATTGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCGC CGCCTGCACG AACACTTCCA CCACATTTC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGTAAGCCCG ACAAAACCTG
351 GTTTGCACCT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGAGC GGCATATACC GGCGCGGCAA CCGCCCACGC CTAGCATCA
451 TACGGCATT TCCGTACCGT ATTGGAAGCC CGAAAAGCCG CCAAGCCGCG
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAATCTCG CCGCACGACA
551 CCGAACAAAC CGAACTGCTG CTTGCCGGCT ACGGCTACAC CAAACGCCTG
601 CTCGGACATA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAAAC ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACGCA GGCAGAAGCC
751 GAAAAAATCG CCGGCATCCC TCTGAACAG CCCTACGCCG AACCATTATG
801 CGGACTGTTT TGGCAGTACG GCGTATGGCT CAATCCTCCC ACATTCTGTC
851 GCGCCCTCCT CAGCCATCCG CTCATTGGAC TACACGAAGA CACACCGTTA
901 ACCGACATTT CCCACGACGG GGAAGAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTATAC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCTT
1001 ACCTACCCGA AACCAACCTC GCCACCCTGC CCCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TCGGTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCAGGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTTCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCCGACCACC TTCCCTAGT CCGCGCACTC
1351 GCGGACATTG CCGCTATGCA ACAAACTTAC GCCAACTCG CGCTGGACAA
1401 AACTATCGC ATCGATGCCC CCTGCCCGTA CCTGCCCAAT GCCTACGCCA
1451 ACACCGCCCA CGGCACACGC GGGCTTGCCA CCGCCCCCAT CTGCGCGGCC
1501 GCCGTTGCAG CCGAAATCCT AGGCTTGCCC CATGCCCTCT CAAAACGCCT
1551 GCGCCACGCC CTACACCCCA ACCGCGCCAT CATCCGCGCC ATCGTCAGAA
1601 GGAAGGATCT AACCCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 738; ORF 212.a>:

a212.pep

```

1   MDNLAWNGIP DIRTLDQIR KHAHPLNLIV CLPDNQIPNF QTAQDASDAE
51  CRLKHLRDLQA TQCLQFDSIN LIEHILPDVR FWLVPPSRR RLHEHFHHIS
101 WQTEAIPQTE SKPDKPWFAL POTSERQKPE HILVIGAGIS GAATAHALAS
151 YGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITQAEA
251 EKIAGIPLNT PYAEPLCGLF WQYGVWLNPP TFVRALLSHP LIGLHEDTPL
301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL ATLPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGFIP NSSHTGWNEA
401 EEASNRQALA HLNPALESSE FAANPNPQKH QGHAAIRCDSPDHLPLVGAL
451 GDIAAMQQTY AKLALDKNYR IDAPCPYLPN AYANTAHGTR GLATAPICAA
501 AVAAEILGLP HPLSKRLRHA LHPNRAIIRA IVRRKDLTP*

```

m212/a212 93.7% identity in 539 aa overlap

```

10      20      30      40      50      60
m212.pep MDNLVWDGIPDIRTLDQIRKHAHPLNLIVCLPDNQIPNFQTAQDASDAECLKHLRDLQA
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a212      MDNLAWNGIPDIRTLDQIRKHAHPLNLIVCLPDNQIPNFQTAQDASDAECLKHLRDLQA

```

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	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
a212	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
a212	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
a212	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
a212	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
a212	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
a212	370	380	390	400	410	420
m212.pep	430	440	450	460	470	480
a212	430	440	450	460	470	480
m212.pep	490	500	510	520	530	540
a212	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

```

g214.seq
1  atgatacaaa agatatgtaa gctatttggt ttaattgtaa tttttgcaac
51  ttctcccgt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagcgtc aacatttcgg cctcgtgtgt
201 caacgtcaca cgcggcaggc aaaggcggcg aatccgtgag ggcggaaggt
251 tcgcccgtcc gcttcagcca aacgttggac gggggcaaa ggcagggtgcg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaaag actgtcgttc
351 tgaccggcaa tgccaaagtg cagcgcggcg gcgacgttgc cgaaggtgcg
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcggtt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep



```
m214.seq (partial)
1 ATGATACAAA AGATATGTAA GCTATTGTGT TTAATAGCAT TTTTTCGGC
51 GTCCCCCGCT TTGCCCCCTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTCT GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GAAAACGTCA TCATCAGACA GGGTACGCTC AATATTCCG CGCCCCGCGT
201 CCAATTGTCA CGCGCGCGCA AAGGCGCGCA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTCAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGC GC
301 GGACAGGCAA ACAACGTTGC TTATTCACTT GCAGGCAGCA CCGTAGTCTT
351 AACC GGTAAT GCCAAAGTAC AGCGCGCGCG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...
```

```
m214.pep (partial)
  1  MIQKICKLFV LIAFFSASP AFAQSDSRQ IQIEADQGS LDAQNSTTFS
51  GNVVIRQGT L NISAARVNT RGRQRRRRE GGRFASPLQ DIGRRQRHGA
101 RTGKQRCLF I CRQHRSLNR* CQSTARRRC RRCGDYIQH NRSLYHQRQH
151 KI...
```

```

m214/g214
      10      20      30      40      50      60
m214.pep  MIQKICKLFLVLIAFFSASPALQSDSRQPIQIEADQGSLDQANQSTTFSGNVVIRQGT
|||:|||:::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g214      MIQKICKLFLVIVIFATSPALQSDSRRIQIEADQGSLDQANQRTTFSGNVIIRQGT
      10      20      30      40      50      60

      70      80      90     100     110     120
m214.pep  NISAARVNVTRGRQRRRIREGGRFASPLQPDIGRRQRHGARTGKQRCFLICRQHSNLRX
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g214      NISASCNVNTRGRQRRRIREGGRFARPLQPNVGRGQRDGA RSGKQRYLFLRRKHCRSDRQ
      70      80      90     100     110     120

      130     140     150
m214.pep  CQSTARRRCRRRCGDYIQHQNRSLSYHQ RQHKI
|||:||| ||| |||:|||:|||:|||:|||:|||
g214      CQSAARRRCRRRCGHYLQHQNRSLYHQ RQHEIGCEIRFQNRQGRRHAPAFKHTKNRITPM
      130     140     150     160     170     180

g214      PSETETQFRRLPTMPRRDY
      190     200

```

```
a214.seq
1  ATGATACAAA  AGATATGTAA  GCTATTTTGTT  TTAATAGCAT  TTTTTCGGC
51  GTCCCCCGCT  TTTGCCCTTC  AAAGCGACAG  CAGGCAGCCT  ATTCAGATTG
101 AGGCCGACCA  AGGTTCGCTC  GATCAAGACA  ACCAAGACAC  CACCAATTAG
151 GGAACGTCG  TCATCAGACA  GGGTACGCTC  AATATTTCG  CCGCCCGGT
201 CAATGTTACA  CGCGGC.GGC  AAAGCGCGCG  AATCCGTGAG  GCGCGAAGT
251 TCGCCAGTCC  GCTTCAGCCA  GACATTGGAC  TGCGGCAAAG  CACGGTGGC
301 CGGACAGCCA  AACTACGTTG  CTTATTCATC  TCGAGCAGC  ACCGTAGTCT
```

493

```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTGCCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNV T RGXQRRRIE GGRFASPLQ P DIGRRQRHGA
101 RTGKQRC LFI CRQHRSLNR* CQSTARRRCR RCGDYIQH Q NRSLYHQ RQH
151 KIRRKIRFQ I RQGQRRYPAF EYAKIRIIPM PSET*TWFR HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m214.pep	MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L					
a214	MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L					
	10	20	30	40	50	60
	70	80	90	100	110	120
m214.pep	NISAARVNV TRGQRRRIE GGRFASPLQ PDIGRRQRH GARTGKQ RCLFICRQ HRSINRX					
a214	NISAARVNV TRGXQRRRIE GGRFASPLQ PDIGRRQRH GARTGKQ RCLFICRQ HRSINRX					
	70	80	90	100	110	120
	130	140	150			
m214.pep	CQSTARRRC RRCGDIQH QNRSLYHQ RQH KI					
a214	CQSTARRRC RRCGDIQH QNRSLYHQ RQH KIRRKIR FQIRQG RRYPAFEY AKIRIIPM					
	130	140	150	160	170	180
a214	PSETXTWFR HLPTEILKRY LX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTTCGAAC
51  TTCTCCCGCT TTTGCCCTTC AAAGCGACAG CAGACGGCCC ATCCAAATCG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGTAC CACATTAGC
151 GGCAATGTCA TCATCAGACA GGGTACGCTC AACATTTCCG CCTCGCGCGT
201 CAACGTCACA CGCGGCGGCA AAGCGGCGCA ATCCGTGAGG GCGGAAGGTT
251 CGCCCGTCCG CTTCAGCCAA ACGTTGACG GGGGCAAAGG GACGGTGCGC
301 GGTCAGGCAA ACAACGTTAC CTATTCCTCC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAAGTGC AGCGCGGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAAA ACCGAAGTCT ATACCATCAA CCGCAGCACG
451 AAATCGGGTG CGAAATCCGC TTCCAAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
1  MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISASRVNV T RGGKGGSVR AEGSPVRF S Q TLDGGKGTVR
101 GQANNVTYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTK TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCG CCGCCCGCGT

```

494

```

201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAATCCGC TTCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

```

m214-1.pep
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGTVR
101 GQANNVAYSS AGSTVVL TGN AKVQRGGDVA EGAVITYNTK TEVYTISGST
151 KSGAKSASKS GRVSVVIQPS STQKSE*

```

m214-1/g214-1 93.8% identity in 176 aa overlap

```

m214-1.pep      10      20      30      40      50      60
MIQKICKLFVLIAFFSASPAFALQSDSRQPIQIEADQGS L DQANQSTTFSGNVVIRQGT L
|||||:|||||:|||||:|||||:|||||:|||||
g214-1          10      20      30      40      50      60
MIQKICKLFVLIVIFATSPAFALQSDSRRIQIEADQGS L DQANQSTTFSGNVIRQGT L

m214-1.pep      70      80      90      100     110     120
NISAARVNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGT VRGQANNVAYSSAGSTVVL TGN
|||||:|||||:|||||:|||||:|||||:|||||
g214-1          70      80      90      100     110     120
NISASRVNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGT VRGQANNVYSSAGSTVVL TGN

m214-1.pep     130     140     150     160     170
AKVQRGGDVAEGAVITYNTKTEVYTISGSTKSGAKSASKS GRVSVVIQPSSTQKSEX
|||||:|||||:|||||:|||||:|||||:|||||
g214-1         130     140     150     160     170
AKVQRGGDVAEGAVITYNTKTEVYTINGSTKSGAKSASKTGRVSVVIQPSSTQKTEX

```

g214-1/p38685

```

sp|P38685|YHBN_ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF_0185 [Escherichia coli]
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185
Score = 97.1 bits (238), Expect = 6e-20
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

```

```

Query: 19  PAFALQSDSRQPIQIEADQGS L DQANQSTTFSGNVVIRQGT L NISAARVNVT R--GGKGG 76
          PAF+  D+  QPI IE+DQ SLD      TF+GNV++ QGT+ I+A +V VTR  G +G
Sbjct: 24  PAFAVTGD TDQPIHIESDQQLDMQGNVVTFTGNVIVTQGTIKINADKV VVTRFGGEQ GK 83

Query: 77  ESVRAEGSPVRF SQ TLDGGKGT VRGQANNVAYSSAGSTVVL TGN AKVQRGGDVAEGAVIT 136
          E +  G P F Q D GK V G A+ + Y A  VVLTGNA +Q+  +G IT
Sbjct: 84  EVIDGYGKPATFYQM DNGK-PVEGHASQMHYELAKDFVVL TGNAYLQQVD SNIKGDKIT 142

Query: 137 YNTKTE 142
          Y K +
Sbjct: 143 YLVKEQ 148

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

```

a214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTCGCTC GATCAAGCCA ACCAAAGCAC CACATTACAGC
151 GGAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCGCGT
201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAATCCGC TTCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

```

a214-1.pep
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS

```

51 GNVVIRQGTI NISAARVNVT RGGKGGESVR AEGSPVRFSQ TLDGGKGTVR  
 101 GQANNVAYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTK TEVYTISGST  
 151 KSGAKSASKS GRVSVVIQPS STQKSE\*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKLFVLI	AFFSASP	AFALQSDSR	QPIQIEAD	QGS	LDQANQSTTFSGNVVIRQGTI
m214-1	MIQKICKLFVLI	AFFSASP	AFALQSDSR	QPIQIEAD	QGS	LDQANQSTTFSGNVVIRQGTI
	70	80	90	100	110	120
a214-1.pep	NISAARVNVT	RGGKGGES	VRAEGSP	VRFSQ	TLDGGKGT	VRGQANNVAYSSAGSTVVLTGN
m214-1	NISAARVNVT	RGGKGGES	VRAEGSP	VRFSQ	TLDGGKGT	VRGQANNVAYSSAGSTVVLTGN
	130	140	150	160	170	
a214-1.pep	AKVQRGGD	VAEGAVIT	YNTKTEV	YTI	SGSTKSGAKS	ASKSGRVS
m214-1	AKVQRGGD	VAEGAVIT	YNTKTEV	YTI	SGSTKSGAKS	ASKSGRVS

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq  
 1 atgaaagtaa gatggcggta cggaattgcg ttccattga tattggcggg  
 51 tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa  
 101 tcgaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc  
 151 ttggacgga ggcggtttga cgaacagggg tacttgaaag aacatttgag  
 201 cgcgaaaggt gcgaaacagt ttcccgaata cagcgacatc cattttgatt  
 251 cgccgcattc cgtgttcttc caagaaggca ggctgttgta cgaagtcggc  
 301 agcgatgaag ccgtttacca taccgaaaac aaacagggtc ttttataaaa  
 351 caacgttgtg ctgacaaaaa ccgccgacgg caggcggcag gcgggtaaa  
 401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaac  
 451 gatacgctg tcagtttcca atatggcggc tcgcacggtc aggcgggcgg  
 501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga  
 551 aagccgcgat ttatgataca aaagatatgt aa

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep  
 1 MKVRWRYGIA FPLILAVAG SLSAWLGRIS EVEIEEVRNL PDEPQYTMDS  
 51 LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPHLVFF QEGRLLYEVG  
 101 SDEAVYHTEN KQVLFKNNV LTKTADGRRQ AGKVEATEKLH VDTESQYAQT  
 151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAAYDT KDM\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)  
 1 ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT  
 51 CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA  
 101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTGAG CGCGAAGGCG  
 151 GCGAAACAGT TTCCGAAAAG CAGCGACATC CATTGTGATT CGCCGCATCT  
 201 CGTGTCTTTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC AGCGACGAAG  
 251 CCGTTTACCA TACCGAAAAC AAACAGGTTC TTTTAAAAA CAACGTTGTG  
 301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA  
 351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAAAC GATACGCCTG  
 401 CAGTTTCCA ATATGGTGCA TCGCACGGTC AGGCGGGCGG CATGACTTAC  
 451 GACCACAWWA CAGGCATGTT GAACCTCTCA TCTAAAGTGA AAGCCACGAT  
 501 TTATGATACA AAAGATATGT AA

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)  
 1 ..SLSAWLGRIS EVEIEEVRNL PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG  
 51 AKQFPENSDI HFDSPHLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNNV  
 101 LTKTADGRRQ AGKVEATEKLH VDTESQYAQT DTPVSFQYGA SHGQAGGMTY

496

151 DHXTGMLNFS SKVKATIYDT KDM\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

```

m215/g215
--
m215.pep          10      20      30      40
                  SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG
g215              MKVRWRYGIAFPLILAVALGSLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG
                  10      20      30      40      50      60

m215.pep          50      60      70      80      90      100
                  YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
g215              YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
                  70      80      90      100      110      120

m215.pep          110     120     130     140     150     160
                  LTKTADGKRQAGKVEAEKLVHVDTESQYAQTDTVPVSFQYGASHGQAGGMTYDHXTGMLNFS
g215              LTKTADGRRQAGKVEAEKLVHVDTESQYAQTDTVPVSFQYGASHGQAGGMTYNHKTGMLNFS
                  130     140     150     160     170     180

m215.pep          170
                  SKVKATIYDTKDMX
g215              SKVKAAYDTKDM
                  190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

```

a215.seq
1  ATGAAAGTAA GATGGCGGTA CGGAATTGCG TTCCCATTTGA TATTGGCGGT
51 TGCCTTGGGC AGCCTGTCGG CATGGTTGGG ACGCATCAGC GAAGTCGAGA
101 TTGAAGAAGT CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACGGA
151 TTGGATGGCA GCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTGAG
201 TTCGAAGGGC GCGAAACAGT TTCCCGAAAG CAGCGACATT CATTTCGACT
251 CACCGCATCT CGTGTCTTTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC
301 AGCGATGAAG CCGTTTACCA TACCGAAAAC AAACAGGTTC TTTTAAAAA
351 CAACGTTGTG CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG
401 TTGAAGCCGA AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC
451 GATACGCCTG TCAGTTTCCA ATATGGTGCA TCGCACGGTC AGGCGGGCGG
501 CATGACTTAC GACCACAAA CAGGCATGTT GAACCTCTCA TCTAAAGTGA
551 AAGCCACGAT TTATGATACA AAAGATATGT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 756; ORF 215.a&gt;:

```

a215.pep
1  MKVRWRYGIA FPLILAVALG SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS
51 LDGRRFDEQG YLKEHLSSKG AKQFPESDI HFDSPHLVFF QEGRLLYEVG
101 SDEAVYHTEN KQVLFKNNVV LTKTADGKRQ AGKVEAEKLVH VTESQYAQT
151 DTPVSFQYGA SHGQAGGMTY DHKTGMLNFS SKVKATIYDT KDM*

```

m215/a215 98.3% identity in 173 aa overlap

```

m215.pep          10      20      30      40
                  SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG
a215              MKVRWRYGIAFPLILAVALGSLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG
                  10      20      30      40      50      60

m215.pep          50      60      70      80      90      100
                  YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV

```

```

|||||:|||||
a215      YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
              70      80      90      100      110      120

              110      120      130      140      150      160
m215.pep  LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHTGMLNFS
              |||||||
a215      LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHTGMLNFS
              130      140      150      160      170      180

              170
m215.pep  SKVKATIIDTKDMX
              |||||||
a215      SKVKATIIDTKDMX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

g216.seq (partial)

```

1  ..atgatatcga tttcgagctc ggtacccagc gacgaaatca cgcgccatcat
51  ccccgcactc aaacgcaaag acattaccct cgtctgcatc accgcccgc
101 ccgattcaac catggcgcgc catgccgata tccacatcac cgcacgggt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttgggcgacg cgttggcggt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgcccg cagcctcggc
301 aaacgcctgc ttttgccgct tgccgacatt atgcacaaag gcggcgccct
351 gcccgcctgc cgactcggca cgccttgaa aggagccatc gtcagcatga
401 gcgagaaaagg tttgggcatg tggcggggaa cggacgggca aaggctgtct
451 gaaaggcctt tttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

g216.pep (partial)

```

1  ..MISISSVPS DEITAIIPAL KRKDITLVC I TARPDMAR HADIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVLL RARAFTPDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGA I VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

```

1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT
51  GCACGCCGAA GCGGAAGGCT TGCGCGAAAT TGCAGCGGAA TTGAACAAAA
101 ACTTCGTCTT TGCGGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGCGACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGCGCA TTTGGGTATG ATTGTGGACA TCGACGTGGT CGTCGCGATT
301 TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCAGCCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACGCGG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTCT TCCTGCTGCG CgcACGCGCG TTCACGCCCC
551 ACGATTTCGC CTTGAGCCAT CCTGCCGSCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCCTGC CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CTTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

m216.pep

```

1  MAMAENGKYL DWAREVLHAE AEGLEIAAE LXKNFVLAAD ALLHCKGRV

```

m216/g216

```

              70      80      90      100      110      120
m216.pep    TMASTGTPAFFVHPAEAAHGDLGMIVDXDVVVAISNSGESDEIAAIIPALKRKRDITLVCI
              ::|||:|||||||||||||||||
g216         MISISSVPSDEITAIIPALKRKRDITLVCI
              10      20      30

              130     140     150     160     170     180
m216.pep    TARPDSMARHADIIHITASVSKEACPLGLAPTSTTAVMALGDALAVVLLRRAFTPDDF
              |||||||||||||||:|||||||||||||||||
g216         TARPDSMARHADIIHITASVSQEACPLGLAPTSTTAVMALGDALAVVLLRRAFTPDDF
              40      50      60      70      80      90

              190     200     210     220     230     240
m216.pep    ALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQGRL
              |||||||||||||||:|||||||||||||
g216         ALIHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKGAIVSMSEKGLGMWAGTDGQRLS
              100     110     120     130     140     150

```

a216.seq

```

seq
1      ATGGCGATGG CAGGAAACGA AAAATATCTT GATTGGGCAC GCGAAGTGT
51     GCACACCGAA GCGGAAGGCT TGC CGCGAAAT TGCGGCGGAT TTGGACGAAA
101    ACTTCGCCCT TGCGGCGGAC GCGTTGTGTG ACTGCAAGG CAGGGTCGTT
151    ATCACGGGCA TGGGCAAGTC GGCAGATATC GGGCGCAAAA TGCGGGCAAA
201    CATGGCCTCG ACCGCGACGC CGCGCTTTT CTCTCACCTT CGGGAAGCGG
251    CACACGGCGA TTTGGGCTAG ATTGTGGACA ACAGCTGGT CGTCGCGATT
301    TCCAATTCCG GTGAAAGCGA CGAAATCGCC GCCATCATCC CCGCGCTCAA
351    ACGCAAAGAT ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401    TGGCGCGCCA TTCCGACATC CACATCACCG CGTCGGTTTC CAAAGAGCC
451    TGCCCGCTGG GGGTGTCCCC GACCACGAGC ACCACGGTCC TTATGGCTTT
501    GGGCGCATGC TTGCGGTTG TCCTGCTGCG CGCCCGCGCG TTCACGCCG
551    ACGACTTCGC CTTGAGCCAC CCTGCCGGCA GCCTCGGCAA ACGCCTACTT
601    TTGCGCGTTG CCGACATTAT GCACAAAGGC GCGCGCTCGT GTCCGCTCCG
651    ACTCGGCACG CCGTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701    TGGGCATGTT GCGCTGAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751    ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801    TCTTTTGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCGCCGG
851    AACGCTTCGC CACCGAAGCG CTGAAAGTCA TGCAGGCAAA CCGTGTGAAC
901    GGCCTTCTGG TTACCGATGC AGATAGCGTG CTGATCGGCG CATCTGAATAT
951    GCACGACCTT TTGGCGGCGC GGATTGTATA G

```

a216.pep

```

1  MAMAGNEKYL DWAREVLHTE AEGLEIAAD LDENFALAAD ALLHCKGRVV
51  ITGMGKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDGDM IVDNDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITRA DSTMARHADI HITASVSKEL
151 CPLGLAPTMS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRL
201 LRVDAMHMKG GGLPAVRLLGT PLKEAISVMS EKLGLMLAVT QDQGRLLKGVF
251 TDGDLRLRLFQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN

```

301 GLLVTDADGV LIGALNMHDL LAARIV\*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENGKYLDWAREVLHAAEAGLREIAAELXKNFVLAADALLHCKGRVVITGMVKSCHI					
a216	MAMAGNEKYLDWAREVLHTEAAGLREIAADLDENFALAADALLHCKGRVVITGMGKSGHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIIPALKRRKD					
a216	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDNDVVVAISNSGESDEIAAIIIPALKRRKD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITAREPDSTMARHADIIHTASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARA					
a216	ITLVCITAREPDSTMARHADIIHTASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLEAIVSMSEKGLGMLAVT					
a216	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLEAIVSMSEKGLGMLAVT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRCLKGVFTDGLRRLFQECDNFTGLSIDEVMHHPKTI SAERLATEALKVMQANHVN					
a216	DGQGRCLKGVFTDGLRRLFQECDNFTGLSIDEVMHHPKTI SAERLATEALKVMQANHVN					
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADGV LIGALNMHDL LAARIVX					
a216	GLLVTDADGV LIGALNMHDL LAARIVX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcggatg acggtttgtt gcggaactg tccgaaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt ttctgaggtt ttggactgcc
101 ttttggtcat cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga cgcgcgagg ttgccgcat atccgggcaa
201 tatccgacag ggtttcgagg aaggcggcaa aacgtccgaa catggcgggtt
251 tgattcacgt cggcatacca cgcgctgaca tctgcccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgccgcgca tttctccgtc caatccccc
401 tggacgttca aatcggaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcgc aaacggcgca acacgggcgc ggtttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttccagca agtcggacac gcactccaac
551 gcataaaaaa acggttgccg gcggctgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgtata ggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPPYPGNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAHFSV QSPMDVQIGN HIVQKRQIVP
151 GQSETAQHGR GFQKREHFAD FKTAQQQVGH ALQRIKKRLP AADFHVNRGI

```



201 ROCLRAGLRL SEHGFHKRRI GFDIRG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 765>:

m217.seq

82	1	ATGGCGGATG	ACGGTGTGCG	GCGGCAACTG	TCCGGAAAAA	TGCGCCAATT
51		CGGTTTCCCG	CTrCCATTTG	ACCCATTTCGT	TTTCAAGGTT	TTGCACTGAC
101		TTTTGTGCAT	CGGCTTCFAG	TTGGAACAAT	GTTTCAAGCA	AATCCCGGCA
151		ACGCGCCACC	CATTTCGCGA	CCGTGTGCGG	CTGCGCCCAT	ATCCGTACAA
201		TATCCGTGAG	GGTTTCGAGG	AAGGCGGCBA	AACGTCCGAA	CATGGCGGTT
251		TGATTACAGT	CGGCATACCA	CGCGCTGACA	TCCTGCCACA	TCGGATTGCC
301		GCCTTTGGGC	AGCATCCAGC	CCAATATCAT	GCGTCTTACC	GCTGTGTTCC
351		AGGTGAACAG	CTGATCCGTG	CCGCGCGCGA	TTTCTCCGTG	CAAAACCCAG
401		TGGACGTTCA	AATCGGCAAC	CATGTCTGTG	AAAGCGGATA	AATCGTCTCT
451		AGTCAGTCCG	AAACGGCGCA	ACACGGGCGC	GGTTTCTAAA	AGCACAAGCA
501		CTTTATCGAC	TTCAAATCGG	CTTTCACAAC	AGTCGAACAG	GCATGACAAA
551		GCATGAAGCA	GCGGTTGGCG	GCGGCTGATT	TTACAGTCTG	ACACGGAATA
601		CGGCAATGCC	TGCGCACCGG	GctGCGCCTT	TCCGAACACG	GCTTCGATAA
651		AAGGCGTATA	GGAATCGATA	TTCGGGGTTA	A	

This corresponds to the amino acid sequence <SEQ ID 766; ORF 217>:

m217.pep

```

1  MADDGVRRL  SGKLRQFGFR  LPDPFPVFKV  LDLLLVIGFS  LEQCFKQIPA
51  TRHPFADRCG  LPPYPYNIRQ  GFEEGGKTSE  HGGLIHVGTP  RADILPHRIA
101 AFGQHPAQYH  AFYRLLPGEQ  LKRAAQHFVS  QTPVDVQIGN  HVVQKRXLVL
151 SQSETAQLHR  GFXXKHKFID  FKSAAQQVEQ  AXQSMKQRLA  AADFHVXHGI
201 RQCLRTGLRL  SEHGQDKRRI  GFSDIRG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng)

from *N. gonorrhoeae*:

m217/g217

	10	20	30	40	50	60
m217.pep	MADDGVRRLSGKLRQFGFRLPFDPFVFKVLDXLVLVIGFSLEQCCKQIPATRHPPFADRCG					
	:     : :: :     :     : :     :					
g217	MADDGLLRQLSEKPSQSALFLFPDPFVFEVLDCLLVLVIGPGLKQCFKQIPATRHPPFADRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m217.pep	LPPYPYNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
	:     :     :     :     :     :					
g217	LPPYPGNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRVA AFGQHPAQYHTVCRLLPGKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGNHVQKRXIVLSQSETAQHG RGFXXHKHFIDFKSAFQQVEQ					
	:     :     :     :     :     :					
g217	LIRAAAHFSVQSPMDVQIGNHIVQKRQIVPQSETAQHG RGFQKREHFADFKTAFQQVGH					
	130	140	150	160	170	180
	190	200	210	220		
m217.pep	AXQSMKQRLAAADFHVXHGI RQCLRTLRLSEHGFDKRRIGFDIRGX					
	:     :     :     :					
g217	ALQRIKKRLPAADFHVNRGIRQCLRAGLRLSEHG FHKRRIGFDIRG					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 767>:

a217.seq

1 GTGGCGGATG ACGGTGTGCA GCGGCAACTG TCCGAAAAT TGCGCCAATT  
51 GGGTTTCCGC CTGCCATTG ACCAATTCGT TTTCGAGGCT TTGGACTGCC  
101 TTTTGGTCAT CGCCTTCGAC TTGGAACAAT GTTTCAGCA AATCCCGGCA  
151 ACGCGCCACC CATTCTGCAA CCGTCGCAGG TTGCCGCCAT ATCCGTACAA

```

201 TATCCGTCAG GGTTCGAGG AAGCGGGCAA AACGTCCGAA CAGGGCGGTT
251 TGGTTCACGT CGGCATACCA CGCGCTGACC CCCTGCCACA TCGGATTGCC
301 GCCTTCGGGC AGCATCCAGC CCAATATCAT GCGTCTTACC GCGTGCTTCC
351 AGGTGAACAG CTGATCCCGT CCGCCGCGCA TTTCTCCGTC CAACCCCGCA
401 CGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGCA AATCGTCTC
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAARCA GCGGCTGTGC GCGGCTGATT TTCACATCCG AAACGGAATA
601 CGGCAATGCC TGCGGCGCGG GCTGCGCCTG TCCGAACACG GCTTCGATAA
651 CAGGCGTATA GGATTCGATA TTCGGGGTTA A

```

a217.pwp

**m217/a217 90.3% identity in 226 aa overlap**

g218.seq

g218.pep

1 MVAVDPYTAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

502

51 IMVVSGLYLW WAKQRGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF  
 101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK  
 151 EVPWILELMP MPVSGTTVGE NGINPTEPNN IGRRPFPRAG NRFQRALSVE  
 201 FAQRRGRGMD FVAGFYEL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

m218.seq  
 1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG  
 51 CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC  
 101 TCGGTGCGGC AGGCGATTAT CTTTGGGAAA CGGCAGCTTC ACTGACCATT  
 151 ATTATGGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGC GCGGCAT  
 201 CAAGGCGATG CTGCTGCCGT CAAAAGGCAT GGCGCGTTCT TGGTGGCGGA  
 251 ATCTGCACGG CACGTTTGA ACTTGGGTGT CGTTGATTTT GCTGTTGTC  
 301 TGCTGTGCGG GTATTGCTTG GCGGGGTATT TGGGGCGGCA AGTTCGTACA  
 351 GGCTTGGAGT CAGTTCCTG CCGGTAAATG GGTGTGCGAA CCGAACCCCG  
 401 TTTCACTCGT GCCGACCCAC GCGGAGGTAT TGAATGACGG CAAGGTTAAG  
 451 GAAGTGCCGT GGGTTTGA GCTTACGCCT ATGCTGTGTT CAGGGACGAC  
 501 yGtgGGCAAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAACCG  
 551 TCGACCGCTT TCGCGGnGA AATCGGTTT AAAGGGCGTT ATCAGTTGAA  
 601 TTTGCCCAAA GCGGAGGAC GCGTATGGAC TTTGTCGAG GATTCTATGA  
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep  
 1 MVAVDPYTAK VVSTMPRNQG WYYTMDEIHS DMMLGAAGDY LLETAASLTI  
 51 IMVVSGLYLW WVKRRGIKAM LLPSKXARS WWRNLHGTFG TWVSLILLLF  
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK  
 151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRALSVE  
 201 FAQRRGRMD FVAGFYEL

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/g218

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMDEIHS DMMLGAAGDYLLETAASLTIIMVVSGLYLW					
g218	MVAVDPYTAKVVNTMPRNQGWYHTMDEIHGDMMLGAAGDYLLETAASLTIIMVVSGLYLW					
	10	20	30	40	50	60
70	80	90	100	110	120	
m218.pep	WVKRRGIKAMLLPSKXARSWWRNLHGTFGTWVSLILLFCLSGIAWAGIWGGKFVQAWS					
g218	WAKQRGIKAMLLPPKSRARSWWRNLHGAFGTWVSLILLFCLSGIAWAGIWGGKFVQAWN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKVPPWVLELTPMPVSGTTVGKDGINPDEPMT					
g218	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKVPPWVLELMPMPVSGTTVGENGINPTEPNN					
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRFQRALSVEFAQRRGRMDFVAGFYEL					
g218	IGNRRPFRAFNRFQRALSVEFAQRRGRGMDFVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

a218.seq  
 1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG  
 51 CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC  
 101 TCGGTTTCGAC AGGTGATTAT CTTTGGAAA CGGCTGCATC GCTGACGATT  
 151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT  
 201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GGCGCGTTCT TGGTGGCGGA  
 251 ATCTGCACGG CGCGTTTGA ACTTGGGTGT CGTTGATTTT ACTGTTGTTT  
 301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA  
 351 GGCTTGGAGT CAGTTCCCGG CAGGCAAATG GGGTGTGCGA CCGAACCCCTG  
 401 TTTCAGTCGT GCCGACCCAC GGCGAGGTAT TGAATGACGG CAAGGTTAAG  
 451 GAAGTGCCGT GGGTTTTGGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC  
 501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAACCG  
 551 TCGACCGTTT TCGCGG.GA AATCGGTTT AAAGGGCGTT ATCAGCTGAA  
 601 TTTGCCCAAA GGCGAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA  
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep  
 1 MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI  
 51 IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLF  
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK  
 151 EVFWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRLSAE  
 201 FAQRRGRMD FVAGFYEL

m218/a218 95.9% identity in 218 aa overlap

m218.pep	10	20	30	40	50	60
	MVAVDPYTAKVVSTMPRNQGWYYTMDIHS DMMLGAAGDY LLETAASLTIIMVVSGLYLW					
a218						
	10	20	30	40	50	60
	MVAVDPYTAKVVSTMPRNQGWYYAMDEIHS DMMLGSTGDY LLETAASLTIIMIISGLYLW					
m218.pep	70	80	90	100	110	120
	WVKRRGIKAMLLPSKXARSWWRNLHGTFGTWVSLILLFCLSGIAWAGIWGGKFVQAWS					
a218						
	70	80	90	100	110	120
	WVKRRGIKAMLLPPKGRARSWWRNLHGAFGTWVSLILLFCLSGIAWAGIWGGKFVQAWS					
m218.pep	130	140	150	160	170	180
	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKVPPVLELTPMPVSGTTVGK DGINPDEPMT					
a218						
	130	140	150	160	170	180
	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKVPPVLELTPMPVSGTTVGK DGINPDEPMT					
m218.pep	190	200	210			
	LETVDRFARXNRFQRLSAEFAQRRGRMD FVAGFYEL					
a218						
	190	200	210			
	LETVDRFARXNRFQRLSAEFAQRRGRMD FVAGFYEL					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 775>:

```
g219.seq
1   atgacggcaa ggtaaggaa gtgccgtgga ttttggagct tatgcctatg
51  cctgtctcag ggacgactgt gggtagaaac ggcatatacc ccaccgagcc
101 caataacatt ggaaaccgtc gaccgtttcg cgcggaatc cggtttcaaa
151 gggcggtatc agttgaattt gcccgaaggc gagggacggg tatggacttt
201 gtcgcaggat tctatgagtt atgacatgat cagcccgttt gccgaccgca
251 cggtagatat cgaccagtac agcggcgaga ttcttgccga catccgtttt
301 gacgattaca acccgttcgg caaatttatg gcggcaagca ttgcgctgca
351 tatggggact ttgggctggg ggagcgtggt gggaacgtc gtgttctgcc
401 ttgccgtgat ttttatcggc atcagcggct gcgtgatgtg gtggaaacgc
451 cgtccgtccg gcgtggcggg cattgttctt ccggcgcaaa aaatcaaaact
501 gcccgctctg tggcgatgg cattgccgct gctgttgatt gcactgcttt
551 tccccgaccg gctgcttgcc attgccgtga tttggctggt ggataccttg
601 ctgctgtcgc ggattcctgt gttgaggaaa tggtttaaat ga
```

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

```
g219.pep
1   MTARLRKCRG FWSLCLCLSQ GRLWVKALT PPSPITLETV DRFAREIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGEILADIRF
101 DDYNPFGKFM AASIALHMGT LGWWSVLAV VFCLAVIFIG ISGCVWWKRW
151 RPSGVAGIVP PAQIKLPVW WAMALPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

```
m219.seq
1   ATGACGGCAA GGTTAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACyGt gggcaaaagc ggcatatacc CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGCTTTCG GCGGnGAAAT CGGTTTCAAA
151 GGGCGTTATC AGTTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCCTTT GCCGACCGCA
251 CGGTACATAT CGACCAGTAC AGCGGCAAAA TCCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT CTGGGCTGGT GGAGCGTGTG GCGGAACGTC TTGTTCTGCC
401 TTGCCGTCAT TTTTATCGGT ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGACCG GAGCGGTGGG CATCGTTCCG CCGGCGCAGA AAGTCAAGCT
501 GCCGGTTTGG TGGATGATGG CATGCGCGCT ATTGGCAATC GCACTGCTCT
551 TCCCCGACCTC ACTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

```
m219.pep
1   MTARLRKCRG FWSLRLCLFQ GRXWAKTALT LTRXHWKPS TALRGEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMGT LGWWSVLAV LFCLAVIFIG ISGCVWWKRW
151 RPTGAVGIVP PAQKVKLPVW WMMALPLLLI ALLFPTSLLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

m219/g219

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRLCLFQGRXWAKTALTLSRXHWKPS TALRGEIGFKGRYQLNLPKG					
	:     :     :     :     :					
g219	MTARLRKCRGFWSLCLCLSQGRLWVKALTTPSPITLETVDRFAREIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMGT					
	:     :     :     :     :					
g219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFMAASIALHMGT					

505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPTGAVGIVPPAQKVKLPVWMMALPLLAI					
	:     :     :     :     :					
g219	LGWWSVLANVVFCLAVIFIGISGCVMWKRRPSGAVGIVPPAQKIKLPVWAMALPLLII					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFVKX					
	:     :     :					
g219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRKWFK					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219.seq
1   ATGACGGCAA GGTTAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCATATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTCG GCGG.GAAAT CGGTTTCAAA
151 GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCCGAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CCGTGCATAT CGACCACTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTT GCGGAACGTT TTGTTCTGCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAACGC
451 CGTCCGTCGG GCGCGGTGGG CATGGTTCCG CCGGCGCAAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CGGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
  
```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219.pep
1   MTARLRKCRG FWSLRCLCFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSDQ SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV LFCLAVIFIG ISGCVMWKR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLR WFK*
  
```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRCLCFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
	:     :     :     :					
a219	MTARLRKCRGFWSLRCLCFQGRWAKTVLTLSRXHWKPSTVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDQSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	:     :     :     :					
a219	EDGVWTLSDQSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPTGAVGIVPPAQKVKLPVWMMALPLLAI					
	:     :     :     :					
a219	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPSGAVGMVPPAQKIKLPVWAMAVPLLI					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFVKX					
	:     :     :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFVKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```
g221.seq
1  atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
51  gatcgggcga gccgtaaatc adatcgacgc tgacggattt gaacctgccc
101 tcacggggcg catcgatgac ttctttggtt tcttcgtagc tttggatgcg
151 gttgactgcc gcctgcactt tggggtcgaa atcctgaatg ccgacgctca
201 tgcggttgaa gccgagtcgt ccgagcatga ggacgggtgc gcggctgact
251 ttgcgcgggt cgatttcgat ggaatattcg ccggacggta tcagttcgaa
301 atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351 aggtcgccgt gccgccgccg aagtgcagtt gggcaagctg gtgccgtccg
401 ttcagatgtg gagcgagcag ttccatttct ttttcaagat attcgatgta
451 ggtatcgccg cggcttttgt ctttgggtgat gattttgttg cagccgcagt
501 agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag ggaagcgggt
551 ttgtttaa
```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```
g221.pep
1  MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FFGFFVALDA
51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101 MPADHAEDTF DLFVAQKGRR AAAEVQLGKL VPSVQMWEQ FHFFFKIFDV
151 GIGAAVFVGD DFVAAAVVAD GVAERNVNVK GKRFV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```
m221.seq
1  ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTG ACCGCCGCTT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TGCGGAAGAC
301 ACGTTCGATC TGTTCTGTCG TCAAAAAGGt GCGTGCCCGC CCGAAGTGCA
351 GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCCATT
401 TCTTTTTCAA GATATTCGAT GTAGGCATCG GCGCGGCTTT TGTCTTTGGT
451 GATGATTTTG TTGCAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501 TGTGAATGTA AAGGGAAAGC GGTGTGTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```
m221.pep
1  MXVLMXRSLV RQAVNQIDAD GFEPFRFARRI DDFGFFVTL DAVDRRLHFG
51  VEILNADAH VEAESAIEDH GVAADFARVD FDGVFAGGDX LEMFAYHAED
101 TFDLFVAQKG ACPAEVQLGK LVPSVQMWE QFHFFFKIFD VGIGAAVFVG
151 DDFVAAAVVA DGVAERNVNV KGKRFV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng) from *N. gonorrhoeae*:

m221/g221

	10	20	30	40	50
m221.pep	MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDAVDRRLHFGVE				
	: :                :				
g221	MHDHGAMDRRLPAFGSLMRRVAVNXIDADGFEPCLTGGIDDFFGFFVALDAVDCRLHFGVE				
	10	20	30	40	50
	60	70	80	90	100
m221.pep	ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLFVAQKGA-				
g221	ILNADAHAVEAESAEHEDGVAADFARVDFDGI FAGRYQFEMFADHAEDTFDLFVAQKGRR				
	70	80	90	100	110
	120	130	140	150	160
	170				

```
a221.seq
1  ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTGTAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATCGG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTCGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCCGCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGGGAAGAC
301 ACGTTCGATT TGGTCGTCGC TCAAAAAGGT CGGCGTGCCG CCGCCGAAGT
351 GCAGTTGGGC AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTCC
401 ATTTCTTTTT CAAGAAATTC GATGTAGGCA TCGCGCGCGG TTTTGTCTTT
451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGAACG
501 GAATGTGAAT GTAAAGGGAA AGCGGTTTGT TTAAT
```

a221.pep

1	MVVLMLRSLV	RQAVNQIDAD	GFEPRFARRI	DDFFGFFVTL	DAVDRRLHFG
51	VEILNDAHAH	VEAESAEHD	GVAADFARVD	FDGVFAGGD*	LEMFAYHAED
101	TFDLVVAQKG	RRAAAEVQLG	KLVPVSQMW	EQFHFFKKF	DVGIGAAFVE
151	GDDEFVAAAV	ADGVAERNVN	VKGKRFV*		

a221 95.5% identity in 177 aa overlap  
 m221.pep  
 MXVLMXRSLVRQAVNQIDADGFEPFRARRIDDFGFFVTLDVDRRLHFGVEILNADAHA  
 a221  
 MVVLMRLRSLVRQAVNQIDADGFEPFRARRIDDFGFFVTLDVDRRLHFGVEILNADAHA  
 m221.pep  
 VEAESAEHEDGVAADFARVDFDGVFAGGDYLEMFAYHAEDTFDLFVAQKGA-CPAEVQLG  
 a221  
 VEAESAEHEDGVAADFARVDFDGVFAGGDYLEMFAYHAEDTFDLVVAQKGRRAAAEVQLG  
 m221.pep  
 KLVPSPVQMWSEQHFHFFKIFDVGIGAAVFVGDDFVAAAVVADGVAERNVNVKGRFVX  
 a221  
 KLVPSPVQMWSEQHFHFFKIFDVGIGAAVFVGDDFVAAAVVADGVAERNVNVKGRFVX

g223.seq

```
1 atgcgaattca ggcaccagggt agtggtagtt ggtgtcgaac catttggtca
51 ttctgatggc gaatttggtct ttgtgtccgc gcgccagttg gaagaattgt
101 tccaaaggca ggttttggtc atcgaagccg aaacggggcg gaatcgcgcc
151 cgtggatact tgcaggtcga ggatgtgatg gtagaaagtg aaatcacgta
201 cagcaacgta atcagcgtta ggagcagctt ggtgtttcca gtttttctcg
251 ccaggtcttt tggcaacgtc gagcagctct tgttcactga tctctttgcg
301 ccagtatctt tcttgggcga atttcaattc acggaaggcg ccgacacgcg
351 qqaacattctga
```

g223.pcp..



1 MEFRHQVVVV GVEPFGHFDG ELVFVAARQL EELFQRQVLA IEAETGGNRA  
 51 RGYLQVEDVM VESEITYSNV ISVRSSLVFP VFLAQVFGNV EQLLFTDLFA  
 101 PVFFLGFEQF TEGADTREAA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 789>:

m223.seq  
 1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTGGGTCA  
 51 TTTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT  
 101 TCCAAAGACA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC  
 151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCCTAC  
 201 GGCAACGAAA TCGGCGTTGG CAGCGACCTG GTGTTTCCAG TTTTCTCGC  
 251 GCAAGTCTTT AGCAACAGCC AGCAATTCTT GCTCGCTGAT TTCTTTGCGC  
 301 CAGTATTTT CTTGTGCGAA TTTCAATTCG CGGAAGGCGC CGACACGCGG  
 351 GAAGCCTGA

This corresponds to the amino acid sequence <SEQ ID 790; ORF 223>:

m223.pep  
 1 VEFRHQVVVV GVEPFGHFDG ELVFVTARQL EELFQRQVLA VEAAGGNRA  
 51 GGDQVEDVM VESEIXYGNV IGVGSDLVFP VFLAQVFSNS QQFLADFFA  
 101 PVFFLCEQF AEGADTREAA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 223 shows 80.7% identity over a 119 aa overlap with a predicted ORF (ORF 223.ng) from *N. gonorrhoeae*:

m223/g223

	10	20	30	40	50	60
m223.pep	VEFRHQVVVV	GVEPFGHFD	SELVFVTAR	QLEELFQRQ	VLA	VEAAGGNRAGGD
g223	MEFRHQVVVV	GVEPFGHFD	GELVFVAAR	QLEELFQRQ	VLA	IEAETGGNRARGYLQVEDVM

	70	80	90	100	110	120
m223.pep	VESEIXYGNV	IGVGSDLVFP	VFLAQVFSNS	QQFLADFFA	PVFFLCEQF	AEAGADTREAX
g223	VESEITYSNV	ISVRSSLVFP	VFLAQVFGNV	EQLLFTDLF	APVFFLGFEQ	FTEGADTREAX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 791>:

a223.seq  
 1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTGGGTCA  
 51 TTTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT  
 101 TCCAAAGATA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC  
 151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCGCCTA  
 201 CGCAACGTA ATCGGCGTTG GCAGCGGCTT GGTGTTTCCA GTTTTCTCG  
 251 CGCAAGTCTT TAGCAACAGC CAGCAATTCT TGCTCGCTGA TTTCTTTGCG  
 301 CCAGTATTTT TCTTGTGCGA ATTTCAATTC GCGGAAGGCA CCGACACGCG  
 351 GGAAGCCTGA

This corresponds to the amino acid sequence <SEQ ID 792; ORF 223.a>:

a223.pep  
 1 VEFRHQVVVV GVEPFGHFDG ELVFVTARQL EELFQR\*VLA VEAAGGNRA  
 51 GGDQVEDVM VESEIAYGNV IGVGSLVFP VFLAQVFSNS QQFLADFFA  
 101 PVFFLCEQF AEGDTREAA\*

m223/a223 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
m223.pep	VEFRHQVVVV	GVEPFGHFD	SELVFVTAR	QLEELFQRQ	VLA	VEAAGGNRAGGD
a223	VEFRHQVVVV	GVEPFGHFD	SELVFVTAR	QLEELFQRQ	VLA	VEAAGGNRAGGD

	70	80	90	100	110	120
m223.pep	VESEIXYGNV	IGVGSDLVFP	VFLAQVFSNS	QQFLADFFA	PVFFLCEQF	AEAGADTREAX
a223	VESEIAYGNV	IGVGSLVFP	VFLAQVFSNS	QQFLADFFA	PVFFLCEQF	AEAGDTREAX

70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgccgtccgc cccgcccttg cgcacgagtt gaccaacctg ctcagcagcc
101 gcgagcagat tctcagacag tttgccgaag acgaacagcc cgttttaccc
151 gtcaaccgag cccccgcccg gcggcggggc aatgccgacg aactcatcgg
201 cggcgcgatg gggcttaacg aacagccccg tgtacgcgtc aaccgagccn
251 ccgccccggc ggcgggcaat gccgacaaac tcatcggcag cgcgatgcgg
301 cttttgggta ttgcctaccg ctacggcgcg acatcggtgt ctaccggttt
351 tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401 acctgccgcg cagtcggcg gaacaggcgc ggatggcgcg acccgttgcc
451 cgaagcgaat tgcagcccg ggatatggtg tttttccgca cgctcggcgg
501 cagccgcatt tccccgtcg gactttatat cggcaacaac cgcttcatcc
551 acgcgccgcg cacggggaaa aatatcgaaa tcaccagcct gagccacaaa
601 tattggagcg gcaaatatgc gttcgccgcg cgggtcaaga aaaacgaccc
651 gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQVLPV
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIETISLSHK
201 YWSGKYAFAR RVKKNDSRF LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1  ..TTTCAAACC CGGCAGTTTG GGCGGTTTGT TGGCTGAWGT TTGCCGTCCG
51  CCCC GCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101 TTCTCAGACA GTTTGCCGAA GACGAACAGC CCGTTTACC CATCAACCGA
151 GCCCCGCCCC GGCGGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201 GGGGCTTAAC GAACAGCCCC TTTTACCGT CAACCGAGTC CCCGCCCGGC
251 GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAACGAA
301 CAGCCCGTTT TACCGTCAA CCGAGCCCC GCGCGCGGG CGGGCAATGC
351 CGACGAACTC ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCGCT
401 ACGGCGGCAC ATCGGTTTCT ACCGGTTTGT ACTGCAGCGG CTTTATGCAG
451 CACATCTTCA AACCGCCCAT GGGCATCAAC CTGCCGCGCA CGTCGGCAGA
501 ACAGGCACGG ATGGGTACGC CGGTTGCCCG AAGCGAATTG CAGCCCGGAG
551 ATATGGTGT TTTCCGACG CTCGCGGCA GCGCATTC CCATGTCCGA
601 CTTTATATCG GCAACAACCG CTTTATCCAC GCGCCGCGCA CGGGGAAAAA
651 TATCGAAATC ACCAGCCTGA GCCACAAATA TTGGAGCGGC AAATACGCGT
701 TCGCCCGCCG GGTCAAGAAA AACGACCCGT CCCGCTTCT GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1  ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQVLPINR
51  APARRAGNAD ELIGSAMGLN EQVLPVNRV PARRAGNADE LIGNAMGLNE
101 QPVLVNRAP ARRAGNADEL IGNAMLLGI AYRYGGTSVS TGFDCSGFMQ
151 HIFKRAMGIN LPRTSAEQAR MGTPVARSEL QPGDMVFFRT LGGSRISHVG
201 LYIGNNRFIH APRTGKNI EI TSLSHKYWSG KYAFARRVVK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

m225/g225

```

          10      20      30      40      50
m225.pep  FSNPAVWAVLWLXFAVRPALADELTNLSSREQILRQFAEDEQVLPINRAPARRAG
          | : ||||| ||||| ||||| ||||| ||||| ||||| : |||||
g225      MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQVLPVNRAPARRAG
```

510

	10	20	30	40	50	60
m225.pep	60	70	80	90	100	110
	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
	:       :					
g225	NADELIG-----			GAMGLNEQPVVRVNRAXARRAGNA		
		70	80	90		
m225.pep	120	130	140	150	160	170
	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
	:     :					
g225	DKLIGSAMRLGLIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225.pep	180	190	200	210	220	230
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIETSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIETSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225.pep	240	249				
	VKKNPSRFLNX					
g225	VKKNPSRFLN					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225.seq
1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCCCGCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGGC GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCGC CCGGCGGGG
351 GGGCAATGCC GACGAACCTCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCCCCCGCCC GCGGGCGGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTTGA CTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAA ACGCGTTCCG
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVARS ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNPSRFLN *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225.pep	FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG				
	:				
a225	MDSFFKPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG				
	10	20	30	40	50
	60	70	79	80	
m225.pep	NADELIGSAMGLNEQPVLPVNR-----				VPARRAGNA

511

```

a225      |||||
          NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
          70      80      90      100      110      120

m225.pep  90      100      110      120      130      140
          DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
          |||||
a225      DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
          130      140      150      160      170      180

m225.pep  150      160      170      180      190      200
          MQHIFKRAMGINLPRTSAEQARMGTFVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
          |||||
a225      MQHIFKRAMGINLPRTSAEQARMGTFVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
          190      200      210      220      230      240

m225.pep  210      220      230      240      249
          IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDRPSRFLNX
          |||||
a225      IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDRPSRFLNX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

```

g225-1.seq
1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgccgtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag ttgcccgaag acgaacagcc cgttttaccc
151  gtcaaccgag ccccccgcgc gcgggcgggc aatgccgacg aactcatcgg
201  cggcgcgatg gggccttaacg aacagcccg tgtacgcgtc aaccgagccn
251  ccgcccggcg ggcgggcaat gccgacaaac tcacggcgag cgcgatgcgg
301  cttttgggta ttgcctaccg ctacggcgcg acatcggtgt ctaccggttt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401  acctgcgcgc cagtcgcggc gaacaggcgc ggatgggcgc accggttgcg
451  cgaagcgcaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501  cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551  acgcccgcgc cagggggaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gtteggccgc cgggtcaaga aaaacgaccc
651  gtcacgcttt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

```

g225-1.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FADEQPVLP
51  VNRAFPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101  LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNDRSRF LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

```

m225-1.seq
1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTGTG GGCTGATGTT
51  TGCCGTCCGC CCGGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101  GCGAGCAGAT TCTCAGACAG TTGCCCgaag ACGAACAGCC CGTTTACCC
151  ATCAACCGAG CCCCCGCGCG GCGGCGGGGC AATGCCGACG AACTCATCGG
201  CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGAGTCC
251  CCGCCCGGCG GCGGGGCAAT GCCGACGAAC TCATCGGCAA CGCGATGGGG
301  CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGCCCCCG CCGGCGGGG
351  GGGCAATGCC GACGAATCA TCGGCAACGC GATGGGACTT TTGGGTATTG
401  CCTACCGCTA CGGCGGCACA TCGGTTTCTA CCGGTTTGA CTGCAGCGGC
451  TTCATGCAGC ACATCTTCAA ACGCGCATG GGCATCAACC TGCCGCGCAC
501  GTCGGCAGAA CAGGCACGGA TGGGTACGCC GGTGCCCCGA AGCGAATTGC
551  AGCCCGGAGA TATGGTGTG TTCCGCACGC TCGGCGGCAG CCGCATTTC
601  CATGTCGGAC TTTATATCGG CAACRACCGC TTCATCCAGC CGCCGCGCAC
651  GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGAGCGGGCA
701  AATACGGGTT CGCCCGCGCG GTCAAGAAAA ACGACCCGTC CCGCTTCTG
751  AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQPVLPV NRVPARRAGN ADELIGNAMG
101 LNEQPVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKNDPSRFL
251 N*
```

m225-1/g225-1 84.9% identity in 251 aa overlap

```

      10      20      30      40      50      60
m225-1.pep MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g225-1     MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPVNRAPARRAG
          10      20      30      40      50      60

      70      80      90     100     110     120
m225-1.pep NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g225-1     NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA
          70      80      90

      130     140     150     160     170     180
m225-1.pep DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g225-1     DKLIGSAMRLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR
          100     110     120     130     140     150

      190     200     210     220     230     240
m225-1.pep SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPARTGKNIEITSLSHKYWSGKYAFARR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g225-1     SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPARTGKNIEITSLSHKYWSGKYAFARR
          160     170     180     190     200     210

      250
m225-1.pep VKKNDPSRFLNX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g225-1     VKKNDPSRFLNX
          220
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```
1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTGCGCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCC GCCCG GCGGGCGGGC AATGCCGAGC AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTT ACCCGTCAAC CGAGTCCCGC CCCGGCGGGC
351 GGGCAATGCC GACGAACTCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTTACC CGTCAACCGA GCCCCCGCCC GCGGGGCGGG CAATGCCGAC
451 GAACATCATG GCAACGCGAT GGGACTTTTG GGTATTGCTT ACCGCTACGG
501 CCGCACATCG ATTTCTACCG GTTTTGACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCARAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA
```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAIYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVAR S ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHPARTGKNI
251 EITSLSHKYW SGKYAFARRV KKNDPSRFLN *
```

a225-1/m225-1 88.6% identity in 280 aa overlap

```

      10      20      30      40      50      60
a225-1.pep MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG
          |||||
m225-1     MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG
          |||||
      10      20      30      40      50      60

      70      80      90     100     110     120
a225-1.pep NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
          |||||
m225-1     NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA
          70                      80  90

      130     140     150     160     170     180
a225-1.pep DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
          |||||
m225-1     DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
          100    110    120    130    140    150

      190     200     210     220     230     240
a225-1.pep MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
          |||||
m225-1     MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
          160    170    180    190    200    210

      250     260     270     280
a225-1.pep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKNDPSRFLNX
          |||||
m225-1     IHAPRTGKNIEITSLSHKYWSGKYAFARRVKNDPSRFLNX
          220    230    240    250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

```

g226.seq
1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccggatacc caattctcct tcccgcctcg tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccgcc
451 tttctgttgc ctccgcctct cctgcgcgcg ctcggcccgc atacattgcg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggc ctttctcct Cggggcctcg cccctcccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

```

g226.pep
1  MSEILRQPSV LLFLTLAVYA LAIVRTRTG NIFCNPVLS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRRIFNQ WLPVIVSOLA
101 GSVTGIVTGM YFAAWLGPDT QSFPPRLQY LLFTPSGIPI HTLYARVLPP
151 FLLPPPLLPR LGPHTLRRFT ILPKLRPFK PLLPVVLSL PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

```

m226.seq
1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACAGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGGTTACAA

```

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501 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCCGTTGGT ATGTCGCTCG  
 551 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC  
 601 CGTATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC  
 651 CGCGCTGATT GCGCCGCTGC TCATCCCGT TTTGGGATT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

m226.pep  
 1 MNEILRQPSV LLFLTLAVYA LAIVRTRTG NIFCNPVLVS TIVLIAYLKI  
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA  
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT  
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR  
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

	10	20	30	40	50	60
m226.pep	MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
g226	MSEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m226.pep	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSOLAGSVTGIVTGM YFAKWLGAER					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVSOLAGSVTGIVTGM YFAAWLGPDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m226.pep	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG					
g226	QFSFPRLQYLLFTPSGIPHTLYARVLPPFLPPPLPRLGPHTLRRFTILPKKLRPFK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

a226.seq  
 1 ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC  
 51 CGTGTACGCG CTTCGATTG TCGTGCGCAC GCGCACGGGT AATATCTTCT  
 101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC  
 151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATT  
 201 CTGGCTCAAG CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC  
 251 GCCGTAAAT CTTCACCAA TGGCTGCCCG TCATCGTTTC GCAGCTTGGC  
 301 GGCAGCGTTA CGGGCATTGT TACGGGGATG TATTTTGCCA AATGGCTGGG  
 351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAATC  
 401 CTATCGCCAT CGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC  
 451 GCCGCCACCG TCATCATTGC CGGCCTGGTC GGACAGATTG CCGGTTACAA  
 501 AATGTTGAAA AACACGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG  
 551 GCACGGCTTC GCACGCGATG GGCATTGCCG CCTCGCTCGA ACGCAGCCGC  
 601 CGCATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC  
 651 CGCGCTGATT GCGCCGCTGC TTATCCCGT TTTGGGATT TGA

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

a226.pep  
 1 MNEILRQPSI LLFLTLAVYA LAIVRTRTG NIFCNPVLVS TIVLIAYLKI  
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA  
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT  
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR  
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF \*

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

515

```

m226.pep      MNEILRQPSVLLFLTAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
a226          |||||:|||||
              10      20      30      40      50      60

              70      80      90      100     110     120
m226.pep      AAQFIDFWLKPAVVVLAVPLYQNRRIENQWLPVIVSQLAGSVTGIVTGMVFAKWLGAER
a226          |||||:|||||
              70      80      90      100     110     120

              130     140     150     160     170     180
m226.pep      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVVG
a226          |||||:|||||
              130     140     150     160     170     180

              190     200     210     220     230
m226.pep      MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
a226          |||||:|||||
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1  atgaacatca tccgcgcgct cctcatcatc ctcgctgcc tcgccgccgg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccggc agcatcgctcg
101 gcatggcgct gctgtttgct cttttgcagg cgggttggt caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgctgttctc
201 cgtgccgccc tgcgtggcgg tcatcagcta tttggatttg attgccgacg
251 attggttttc gatactggtt tccgctcccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1  MNIIRALLII LGCLAAGETA VFLAGIKLEG SIVGMGVLF LQAGWLKTS
51  WLQQLTDALM ANLTFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1  ..ACGTCTTkgc TGCAACAGCT TACCGACGCG CTGATGTCGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTG GATTGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCCG CCTCCGCCAG cACTTTGTGC
151 GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1  ..TSXLQQLTDA LMSNLTFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

m227/g227

```

m227.pep      TSXLQQLTDALMSNLTFLVPPCVAVISYL
g227          TAVFLAGIKLP GSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTFLVPPCVAVISYL
              20      30      40      50      60      70

              40      50      60

```



516

```

m227.pep    DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
            |||||
g227        DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
            80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51 CGAAACCGCC GTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101 GCATGGGCGT ACTGTTTGGC CTTTTCAGG CGGGTTGGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCC TGGCTGGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATGGGTTTC GATACTGGT TCCGCCTCCG CCAGCACTT GTGCGTACTG
301 CTGGTTACAG GCAAGGTTCA CCGCTGGATA CGGAGCATTA TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLEA LQAGWVKTS
51 WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep                                10      20      30
                                TSXLQQLTDALMSNLTFLVPPCVAVISYL
                                || |||||
a227      TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTLFLVPPCVAVISYL
            20      30      40      50      60      70

m227.pep                                40      50      60
            DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
            |||||
a227      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
            80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCCGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCCGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

517

```

a228.pep
1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51  VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

m228/a228 100.0% identity in 107 aa overlap

```

          10      20      30      40      50      60
m228.pep  MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD
          |||
a228      MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD
          10      20      30      40      50      60

          70      80      90      100
m228.pep  AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX
          |||
a228      AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX
          70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

```

g229.seq
1  atggctgccg tatcgggcgg cggtgcggtc ttcctgataa tgcttcaca
51  tattgcccgc gttcagcgtc agccgccagc gttcgcccaa gcgtcgggag
101 aaatcgccat tgaagccgcc ggcgaaattg tatcggtgc cgcccaagag
151 gttttgcccg acaaacggca cggtgccgaa cgagcgcgtt accgaacggt
201 tttgatggcc gaacgacagg cgcaggttct gttcggtgaa atctttgtta
251 tcccaataat gcacgccgcg gctgatgccg ccgtagagga aatgatgcc
301 gcccgattg atttcgcgcg acacgcccaa gccgtagcgc aaaccgtgtg
351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaaat
401 tcaatcgttt ttctcgacga agcgttgttt atagcggatt aacaaaaatc
451 aggacaaggc ggcggggcgc aggcagtacg gatggtacgg aaccggttcg
501 cccggtgctt ggacgcctta gggaaccgtt ccttttgagc cggggcgggg
551 caaccgttac cggtttttgt tcatccgcca tattgtgttg a

```

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

```

g229.pep
1  MAAVSGGGAV FLIMLPHIAR VQROPFAFAQ ASGEIGIEAA GEIVSAAAOE
51  VLPDKRHGAE RARYRTVLMA ERQAQVLF AE IFVIPIMHAA ADAAVEEMMP
101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRF FGR SVVYSGLT KI
151 RTRRRAAGST DGETPVRPVL GRLREPFPLS RGGATRTGFC SSAILC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

```

m229.seq (partial)
1  ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
51  GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC
151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCGC CTGATGCCGC
201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTGCGCGCA CACGCCTAAG
251 CCCTAGCGCA AACCGTGTGC CTTTGCGGC AGGCTGTCCG CGGTTTTTCGT
301 CCAGCTTCTG CCCGCAAAAT CAATCGTTTT TTCGGACGAA GCGTTGTTTA
351 TAGCGGATTA ACAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
401 AATAGTACGG AACCGATTCA CTTGGTGCTT CAGCACCTTA GAGAATCGTT
451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

```

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

```

m229.pep (partial)
1  ..AQALGEIGIE AAEIVSAAA KEVLLDKRHD AERARYRTVF IAERQAQALF
51  AEIFVIPIMH AAAADA AVEE MPPARIDFAR HAXALAQTV LRLQAVGGFR
101 PASARKFNRF FGRSVVYSGL TKIRTRQRSA DSTNSTEPIH LVLQHLRESR
151 SLFCSSAILC *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 229 shows 80.5% identity over a 169 aa overlap with a predicted ORF (ORF 229.ng) from *N. gonorrhoeae*:

m229/g209

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      MAVVSGGGAVFLITLPHIAHVQRQPPAFAQASGEIGIEAADEIVSAAAXEVLPDKRHGAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFVIMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      RARYRTVLMARQAQVLF AEIVFVIMHAAA-DA AVEEMMPARIDFARHAQAVAQTVCLL
                70      80      90      100     110

                                100     110     120     130     140
m229.pep      RQAVGGFRPASARKFNRFGRSVVYSGLT KIRTRQRSADSTNSTEPIHLVLQHLRE----
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      RQAVGGFRPASARKFNRFGRSVVYSGLT KIRTRRRAAGSTDGTEPVRPVLGRRLREPFFPL
                120     130     140     150     160     170

                                150     160
m229.pep      -----SRSLFCSSAILCX
                :|: ||| ||| ||| |||
g229      SRGGATRTGFCSSAILC
                180     190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

```

a229.seq (partial)
1  ATGGCTGTCG TATCGGGCGG CGGTGCGGTC TTCCTGATAA CGCTTCCACA
51 TATTGCCACG GTTCAGCGTC AGCGGCCA. GTTCGCTCAA GCGTCGGGAG
101 AAATCGGCAT TGAAGCCGCC GACGAAATTG TATCGGCTGC CGCCTAAGAG
151 GTTTGTGCTG ATAAACGGCA CGATGCCGAA TGAGCGCGTT ACTGAACGGT
201 TTTTATAGCC GAGCGACAGG CGCAGGCTCT GTTCGCTGAA ATCTTTGTTA
251 TCCTAATAGT GCACGCCGCC GCCGCTGATG TCTCCGTAGA GGAAATGATG
301 CCGGCCCGCA TTGATTTCGC GCGACACGCC CAAGCCGTAG CGCAAACCGT
351 GTGCCTTTTG CGGCAGGCTG TCGGCGGTTT TCGTCCAGCT TCTGCCTGCA
401 AATTCAATCG TTTTTTCGGA CGAAGCGTTG TTATAGCGG ATTAACAAA
451 ATCAGGACAA GGCGACGAAG CGCAGACAGT ACAGATAGTA CGGAACCGAT
501 TCACCTGGTG CTTACGACC TTAGAGAATC GTCTCTTGA GCTAAGGCGA
551 GGCAACGCCG TACTGGTTT TGTTCATCCA CTATA

```

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

```

a229.pep (partial)
1  MAVVSGGGAV FLITLPHIAH VQRQPPXFAQ ASGEIGIEAA DEIVSAAA*E
51  VLLDKRHDAE *ARY*TVFIA ERQAQALFAE IFVILIVHAA AADVSEEMM
101 PARIDFARHA QAVAQTVCLL RQAVGGFRPA SACKFNRFEG RSVVYSGLTG
151 ITRRRRSADS TDSTEPIHLV LQHLRESSL* AKARQRTGF CSSTI

```

m229/a229 85.6% identity in 167 aa overlap

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a229      MAVVSGGGAVFLITLPHIAHVQRQPPXFAQASGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFVIMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a229      XARYXTVFIAERQAQALFAEIVFVILIVHAAAADVSEEMMPARIDFARHAQAVAQTVCLL
                70      80      90      100     110     120

```

519

	100	110	120	130	140	149
m229.pep	RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---					
	:     :     :     :     :     :					
a229	RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX					
	130	140	150	160	170	180
	150	160				
m229.pep	-----RSLFCSSAILCX					
	:      :					
a229	AKARQRRTGFCSTI					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

g230.seq

```

1 atgttccatt ccatcgaaaa atacagaaca cccgcccag tcttattagg
51 cctgattgca ttaacttttg tcggcttcgg cgtcagcacg gtttcccatc
101 cgggcgccga ctacatcgtc caagtggcg acgaaaaaat cagcgagcac
151 tcaatcaaca acgcatgca gaacgagcag gcggacggcg gcagcccttg
201 gcgcgacgcg gtgttccaat ccctgctgca acgcgcctac ctgaaacagg
251 gcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtcacgc
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtgtg
401 tcgaagaaat ccgcgatcag tttgccttgc agaatttggg aagcctcgtc
451 caaaacggcg tattggtcgg cgacgcgcag gcggaacagc tgatcaggct
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcategcccc agtcaaagcg tctgaagccg atttgcagaa attttataat
601 gcgaacaaaa aagactatct gctgccgcag gcggtcaaat tggaatatgt
651 cgcccttgaa ctgaaggatt ttgcagacaa gcagaccgtc agtgaacgg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgtttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaag gcggttgccg acttcaacaa ggcaaaaaga aagctgggcg
851 acgatgcgtt caatcatccc tcctcgcttg ccgaagccgc caaaaacagc
901 ggtttgaaag tggaaaccca agaaacttgg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaat acctaataa tgccgtattc agcgacgacg
1001 tattgaagaa aaaacacaat tccgaagtgc tgaccatcaa cagcgaaacc
1051 gcgtgggtcg tccgcgccaa agaagtccgc gaagaaaaaa acctactgtt
1101 tgaagaagcc aaagatgcgg tgcgtcaggc ctatatccgt accgaagccg
1151 ccaaactttt gaaaacaatg taa

```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

g230.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51 SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMGI SVSSEIQKM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMSE DQFVEEIRDQ FALQNLVSLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFPY
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEK AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINA VF SDDVLKKKHN SEVLTINSET
351 AWVVRKEVR EEKNLLFEEA KDAVRQAYIR TEAKLLKTM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

m230.seq (partial)

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCAGC GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC

```

520

```

451 CAAACGCGC TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTCCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGg
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTGCGAA ACGAATTGAA
801 AATGAAAAAG GCGGTGCGCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGC.GT CAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTCGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCT...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPDPA VFQSLQRAY LKQGAJLMI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSD QFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKQFN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELMKK AVADFNKAKE KLGDVAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRKEVR EEKTLPPAEA KDAVRQAYIR TEAAKL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

m230/g230

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGSPDPAVFQSLQRAYLKQGAJLMI SVSSEQIKQIIVDDPNFHDANGKFDHALLN					
g230	ADGGSPWRDAVFQSLQRAYLKQGAJLMI SVSSEQIKQMIIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m230.pep	RYLSQRHMSDQFVEEIRDQFALQNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN					
g230	QYLSQRHMSDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m230.pep	PDEFIAQVKVSEADLQKQFNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230	PDEFIAQVKASEADLQKQFNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m230.pep	ERVARLPANEAKPSFEQEKA AVENELMKKAVADFNKAKEKLGDVAVNHPSSLAEAAKNS					
g230	ERVARLPANEAKPSFEQEKA AVENELMKKAVADFNKAKEKLGDVAVNHPSSLAEAAKNS					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRakevr					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRakevr					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPFaeAKDAVRQAYIRTEAAKL					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq (partial)

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCAACGTCAT TATGCTGAA GACCAAGTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGACGGTC AACCACACCA TCCGTTCCGA CACTTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAAA AAGACTACCT GCTTCCCAA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAGAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAAACTTGG CTGAGCAGGC AGGATGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT

```

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep (partial)

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVSTVSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAklmgi SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHNSVLTINSET
351 AWVVRakevr EEKTLPFaeA KDAVRQAYIR TEAAKL

```

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGPSRDAVFQSLQRAYLKQGAklmgiSVSSEQIKQIIVDDPNFHdANGKFDHALLN					
a230	ADGGGPSRDAVFQSLQRAYLKQGAklmgiSVSSEQIKQIIVDDPNFHdANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

m230.pep  RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a230      RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN
          130      140      150      160      170      180

          190      200      210      220      230      240
m230.pep  PDEFIAQVKVSEADLQKFYNANKKDYLKPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a230      PDEFIAQVKVSEADLQKFYNANKKDYLKPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
          190      200      210      220      230      240

          250      260      270      280      290      300
m230.pep  ERVARLPANEAKPSFEQEKAAVENELKMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a230      ERVARLPANEAKPSFEQEKAAVENELKMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS
          250      260      270      280      290      300

          310      320      330      340      350      360
m230.pep  GLKVVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a230      GLKVVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR
          310      320      330      340      350      360

          370      380
m230.pep  EEKTLPF AEAKDAVRQAYIRTEAAKL
          |||||||||||||||||||||||||||||||
a230      EEKTLPF AEAKDAVRQAYIRTEAAKL
          370      380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

```

g230-1.seq
1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCCGCCCAAG TCTTATTAGG
51  CCTGATTGCA TTAACTTTGG TCGGCTTCGG CGTCAGCACG GTTTCCTATC
101 CGGCGCCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATG
301 ATTTGTGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGTCTGAA GACCACTTGG
401 TCGAAGAAAT CCGCGATCAG TTTGCCCTTG AGAATTTGGT AAGCCTCGTC
451 CAAACCGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCACACCA TCCGTTTCGA CACTTTC AAC CCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAAT TGGAATATGT
651 CGCCTTGAAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGGCTTTGAA GAGCGCGTGG CGCGTTTGCC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAGAAAGC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAGCTGGGCG
851 ACGATGCGTT CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAACACAGC
901 GGTTTGAAAG TGGAAACCCA AGAAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCGCGC ATGCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TGCGTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACTTGC CGAAAACAAAG GCAAAAGAAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCAG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAACCCGCG AAACGGCAAA CCCGCCTATG TCAGACTGAC CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAGGC GCAGGCAGTC ACGCCTCCGG AGGATATTGC
1401 CGCACAGCTT CCTCTGCGA AACAGGCTTT GCGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CCTGCTGATC CGCTATTCA ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGGCGAT GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

```

g230-1.pep
1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAALMGI SVSSEKIQOM
101  IVDDPNFHDA NGKFSHALLS QYLSQRHMSDQFVEEIRDQ FALQNLVSLV

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151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWE VSVLGAQAR QSMPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TPPEDIAAQL PPAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNG GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

```

m230-1.seq
1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCAGC GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACCGG GTGTTCCAAT CCTGCTGCA ACGCGCTTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAAAT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGCTGAA GACCAAGTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTCCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACCGG
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTGGC GGCAATGAA
751 GCGCAACCTT CTTTCGAGCA GGAAAAAGCC GCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GCGTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGAGC
1001 TATTGAAGAA AAAACACAA TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCTGCGCTT
1101 TGCCGAAGCC AAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTTG CGAAAACAG GCAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTGCAAGT ACAGGCTGTA ACCCGCGCG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GCGGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CTGTGTGATA CGTTATTTC ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTCAAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

```

m230-1.pep
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGAKLMI SVSSEIQIKI
101 IVDNPNFHDA NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRKEVR EEKTLFPAEA KDAVRQAYIR TEAAKLAENK AKDVLTQLNG
401 GKAVDVKWE VSVLGAQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPEDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNG GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

	10	20	30	40	50	60
m230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230-1	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230-1.pep	ADGGGSPSRDAVFQSLQRAYLKQGAKLMI SVSSEIQIKIIVDDPNFHDANGKFDHALLN					
g230-1	ADGGSPWRDAVFQSLQRAYLKQGAKLMI SVSSEIQIKQMIIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m230-1.pep	RYLSQRHME DQFVEEIRDQ FALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRNRTIRSHTFN					



a230-1.seq

1	ATGTTCCATT	CCATCGAAAA	ATACGAACG	CCCGCCCAAG	TCCTTTTGGG
51	CCTGATTGCA	TTAACCTTCG	TCGGCTTCGG	GGTCAGCACG	GTATCCCATC
101	CGGGTGCCGA	CTACATCGTC	CAAGTGGGGG	ACGAAAAAT	CAGCGACCAC
151	TCCATCAACA	ACGCCATACA	GAACGAAACG	GCGGACGGCG	GCGGCGCTTC
201	GCGCGACGGG	GTTGTCCAAT	CCCTGCTACA	ACGCGCCTTAC	CTGAACACAGG
251	GCGCGAAGCT	GATGGGCATT	TCGGTTTCTT	CCGAACAAAT	CAAGCAGATT
301	ATCGTGGACG	ATCCCAATTT	CCACGACGCA	ACGCGCAAT	TGCAGCACGC
351	GCTTTTAAAC	CGCTACTCTT	CCCAACGTCA	TATGTTCAAA	GACCAGTTTG
401	TCGAAGAAAT	CCGCGATCAG	TTTGCCCTGC	AGAATTTGGT	AAACCTCGTC
451	CAAAACGGCG	TATTGGTCGG	CGACGCGCAG	GCGGAACACG	TCGTCAGGCT
501	GACGCAAGTC	AACCCGACCA	TCGGTTCCGA	CACTTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAAGTG	TC'TGAAGCCG	ATTTGCAGAA	GTTTTATAAC
601	GCAAAACAAA	AAGACTACTT	GC'TTCCCAAA	GCGGTCAAAT	TGGAATATGT
651	CGCCTTGAAT	CTGAAGAGT	TTGCAACAA	ACAGACCGTC	AGCGAAACAC
701	AAGTAGAAAA	TGCGTTTGA	GAGCGCGTGG	GCGGTTTGCC	GCGAAATGAA
751	GCCAAACCTT	CTTTGCAGCA	GGAAAAAGCC	GCGCTCGAAA	ACGAATTTGA
801	AATGAAAAAG	GCGGTTGGCG	ACTTCAATA	GGCAAAAGAA	AAGCTGGGCG
851	ATGACGCGTT	CAACCATCCT	TCCTCGTTG	CCGAAGCCCG	CAAAAACAGC
901	GGTTTGAAG	TCGAAACCCA	AGAAACTTGG	CTGAGCAGCG	AGGATGCGCA
951	AATGTCCGGT	ATGCCCGGAA	ACCATGATCA	TGCGCTATTG	AGCGACGCG
1001	TATTGAAGAA	AAAAACAAAT	TCCGAAGTGC	TGACCATCAA	CAGCGAAACC
1051	GCGTGGGTCG	TCCGCGCCAA	AGAAGTCCCG	GAAGAGAAAA	CCCTGCGGTT
1101	TGCCGAAGCG	AAAGACGCGG	TAGCTCAGCG	TTATATCCCT	ACCGAAGCCG
1151	CCAAACTTGC	GAAAAACRAG	GCAAAAGACG	TGCTTACCGA	ACTGAACGGC
1201	GGCAAGGGTGT	TTGACGTGAA	ATGGTCGGAA	GTGTCCGTTT	TGGGCGCACA
1251	GCAGGCAAGG	CAGTCCATGC	CGCCCGAGCG	TTATGCGGAA	CT'GCTGAAG
1301	CAAAACCCGC	AAACGGCAAA	CCCGCTACG	TACGGCTGAT	CGGCTCTGGC
1351	GCACCGGTGA	TATCGTAGT	AGCGGCTGTA	ACCCCGCCGG	ATGATATCGC
1401	CGCAGAGCTT	CGCCTTGCAA	AACAGGCTTT	GCGCRAACAG	CAGTCTGCCA
1451	ATACTTTCGA	CTTGTGTATA	CGTTATTTC	ACGGCAAAAT	CAACAGAGCC
1501	AAAGGAGCGC	AATCGGTCGA	CAACGGCGAC	GGTCAGTAA	

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

## a230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFGVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGAKLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRAKEVR EEKTLFPAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQQAQ QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEQAV TPPDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDGD GQ*

```

## a230-1/m230-1 99.8% identity in 512 aa overlap

	10	20	30	40	50	60
a230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFGVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
m230-1	MFHSIEKYRTPAQVLLGLIALTFVGFGVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a230-1.pep	ADGGGSPSRDAVFQSLQRAYLKQGAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
m230-1	ADGGGSPSRDAVFQSLQRAYLKQGAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
a230-1.pep	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRIRSHFTN					
m230-1	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRIRSHFTN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a230-1.pep	PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE					
m230-1	PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a230-1.pep	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
m230-1	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
	250	260	270	280	290	300
	310	320	330	340	350	360
a230-1.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRAKEVR					
m230-1	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRAKEVR					
	310	320	330	340	350	360
	370	380	390	400	410	420
a230-1.pep	EEKTLFPAEAKDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVWKSEVSVLGAQQAQ					
m230-1	EEKTLFPAEAKDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVWKSEVSVLGAQQAQ					
	370	380	390	400	410	420
	430	440	450	460	470	480
a230-1.pep	QSMPEAYAE LLKAKPANGKPAYVRLIGLPAPVIVEQAVTPPDDIAAQLPLAKQALAAQ					
m230-1	QSMPEAYAE LLKAKPANGKPAYVRLIGLPAPVIVEQAVTPPDDIAAQLPLAKQALAAQ					
	430	440	450	460	470	480
	490	500	510			
a230-1.pep	QSANTFDLLIRYFNGKIKQTKGAQSVNDGQGX					
m230-1	QSANTFDLLIRYFNGKIKQTKGAQSVNDGQGX					
	490	500	510			

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

527

**a231.seq** (partial)

```

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTGCGCGTT CAAAGCCGTG CCGTGCTTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTG GTGTGGAACA
501 CCGCGACGCT GACTTTCCTG CCTCCGCGC CCGCGCGCAG GTTGTGCGGC
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCGGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCCG CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

**a231.pep** (partial)

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPOKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFFP RLNLVGIIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 I

```

**m231/a231** 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPOKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFPG					
a231	QSRVSLPNAQPFAGHIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFFPRLNLVGIIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

**g231-1.seq**

```

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTGCGCGTT CAAAGCCGTG CCGTGCTTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTGCGCTG ATAGCGGTG GTTTCAAACa
501 CaCgTaCaat gagtttcgtA ccctccGCCG ccgcgcgCAG GTTGTcgcGC
551 GAACgTGTAC CGTAagcgtg TTtcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTTta tGTttcgcgc cgtcgcCgtc gATGACGTGA AGGGtatcGC
651 CgtcATAGAC TTTGGACACC Gtgcctgcgt AGctGTGGCC GGAtttcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

**g231-1.pep**

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPOKCR
51 ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```

```
101 SFPQSFAPFF RLNLVGIIVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 AGGYLRHFAL IAVGFKHTYN EFTRLRRRAQ VVARTCTVSV FHLRCVDIRH
201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFR
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

```
m231-1.seq
1  ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGCGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCGCGTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTCG GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CGCCCCGCTC CTGCACTGCG ATCAGGTTCA AATCGGTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTG GTATCGAACA
501 CGCGCACGCT GACTTTCCTG CCTCCGCCG CGCGCGCGAG GTTGTCGCGC
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGCTC GATAACGTGA AGGCTGTCGC
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

```
m231-1.pep
1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR
51  ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF
101 SFPQSFAPFF RLNLVGIIVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGIEHAHA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*
```

g231-1/m231-1 87.0% identity in 262 aa overlap

g231-1.pep	10	20	30	40	50	60
m231-1	10	20	30	40	50	60
g231-1.pep	70	80	90	100	110	120
m231-1	70	80	90	100	110	120
g231-1.pep	130	140	150	160	170	180
m231-1	130	140	150	160	170	180
g231-1.pep	190	200	210	220	230	240
m231-1	190	200	210	220	230	240
g231-1.pep	250	260				
m231-1	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

```
a231-1.seq
1  ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGCGTTGCG CGTCTCCGCA AAAATGCAGG
```

```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTC AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTGTCGAACA
501 CCGGAGCGCT GACTTTCCTG CCTTCCGCGC CCGCGCGCAG GTTGTGCGGC
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GCGCGCTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGGTC GATAACGTGA AGGTTGTCGC
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTGCGC
701 GATGCTCGGC GCGGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGCTCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGCGGACGGG AAGCCATTTT
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

```

a231-1.pep
  1 MSKRKSINRP YOKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
 51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAACP AVRPRLRIF
101 SFQSFAPFP RLNLVGIIG KIRLILFFS ITFIMPRRPV LHLHQVIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCAS	PQKCRARGFQTAFV				
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCAS	PQKCRARGFQTAFV				
	10	20	30	40	50	60
	70	80	90	100	110	120
a231-1.pep	QSRVSLPNAQPFAHGIHPILIAPAACPFAVRPRLRIFSFPQSFAFP	RLNLVGIIG				
m231-1	QSRVSLPNAQPFAHGIHPILIAPAACPFAVRPRLRIFSFPQSFAFP	RLNLVGIIG				
	70	80	90	100	110	120
	130	140	150	160	170	180
a231-1.pep	KIRLILFFSITFIMPRRPVHLHLQVQIGFADRNLRHFALVAVGVEHADA	DFPAFRRAQ				
m231-1	KIRLILFFSITFIMPRRPVHLHLQVQIGFADRNLRHFALVAVGVEHADA	DFPAFRRAQ				
	130	140	150	160	170	180
	190	200	210	220	230	240
a231-1.pep	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNLVKGVAIDFGHRACVAVAG	FRRCSAAGG				
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNLVKGVAIDFGHRACVAVAG	FRRCSAAGG				
	190	200	210	220	230	240
	250	260	270	280	290	300
a231-1.pep	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLH	IFQMPMPSEH				
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLH	IFQMPMPSEH				
	250	260	270	280	290	300
	310					
a231-1.pep	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

```

g232.seq
  1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatcctggt
 51 tggtcagatt ttgggaacgg cggttgccgg cgcgcgcct tatattgtcg
101 ggatactggt tttgctggtc gccgtcggag gaacggccgg cagcctggtt

```

530

```

151 atgccgtccg tacccgccaa ggctgccgat acccaaatcg agtggaaatat
201 tgtcccggtg acaaaatccc tgctgcgtga aacgggtcgg cacaatcccc
251 tttttaccgc cattatcggc atctcgtggt tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg cgggcaacga
351 taatgttttt aacctgatgc ttgctttgtt ttccatcggt attgccgccg
401 gttcggtagt gtgtgccaaag ttcggcaggg aacggctgat gttggcttgg
451 gtaacggttg gtgcgttggg ttcgacgggt tgcggcctgg ttttgggtg
501 gctgacgcac ggacaccggt ttgaagggct gaacggcatt ttttggtttt
551 tatcgcaagg atgggcatac cccgtgatgg cggtgatgac gctgatcggc
601 tttttcggcg gatttttctc cgttcgctc tatacctggc tgcaaacgcg
651 cagcagcgag acttttcggc cccgcgcgt tgcgcgcaac aatatcgta
701 acggcatctt tatggtttcc gccgccgtt tgagcgcggg attgctgttt
751 ttggttgaca gcatttccct gctgtatctg attgtcgcct tgggcaatat
801 tccgttggcg gtatttttga ttaagcgcga aaggcgggtt ttaggcgcgg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g232.pep

```

1  MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51  MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HNPVFTAIIG ISWFWFGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGLNGI FWFLSQGWAY PVMAMVTLIG
201 FFGGFFSVPL YTWLQTASSE TFRARAVAN NIVNGIFMVS AAVLSAVLLF
251 LFDSISLLYL IVALGNIPLA VFLIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m232.seq

```

1  ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTCTG CCATCCTGTT
51  CGGTCAGATT TTGGGAACGG CGGTGGCAGG TGTACCGCCT TATATTGTCTG
101 GGATACTGGT TTTGCTGGTC GCCGTGGGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGAATAT
201 TGTCCGTGGC ACAAATCCC TGCTGCGTGA AACGGTGGCG CACAAGCCCG
251 TTTTACCAGC CATTATCGGT ATTCGTGGT TTTGGTTTGT CGGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTT AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAKGG AACGCCTGAT GTTGGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTGACGGTT TCGCGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CCGTGATGAC GCTGATCGGC
601 TTTTTCGGCG GATTTTTCTC CGTTCGCTC TATACCT(g)TG CAAACCGCCA
651 TAGCGAGATT TCCGCGCCCG GCCGTTGCCG CCAACAATAT CGTTAACGGT
701 ATTTTATGTT TTTCCGCTGC CGTTTGTGAG GCGGTGTTGC TGTTTGTGTT
751 TGACAGCATT TCCTTGTTGT ATCTGATTGT CGCTTTGGGC AATATCCGT
801 TGTCGGTATT TTTGATTAAG CGCGAAAGGC GGTTTTTAGG CGCGGCGGCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m232.pep

```

1  MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51  MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HKPVFTAIIG ISWFWFGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGLNGI FXFLSQGWAY PVMAMVTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

```

              10      20      30      40      50      60
m232.pep  MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
|||||
g232      MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```

531

	10	20	30	40	50	60
m232 . pep	70	80	90	100	110	120
	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPFVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	70	80	90	100	110	120
m232 . pep	130	140	150	160	170	180
	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	130	140	150	160	170	180
m232 . pep	190	200	210	220	230	
	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAVAANNIVNGIFMVS					
	190	200	210	220	230	240
m232 . pep	240	250	260	270	280	289
	AAVLSAVLLFLFDSISLLYLIALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLIALGNIPLAFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```

a232 . seq
1  ATGTACGCTA AAAAAGGCGG TTTGGGACTG GTTAAAAGCC GCCGTTTCGC
51  ACCTCTTTTC GCTACGCAGT TTCTCGGCGC GTTCAACGAC AATGTGTTC
101 AAACCGCGCT GTTTGTGATG ATTGGGTTT ACGGTTTGGG GCAAAACGGC
151 TTCCTGCCTG CCGGACAGAT GTTGAACCTG GCGCGCTTGC TGTATTATTT
201 GCCGTATTTC CTGTTTTCCT CGCTGTCGGG GCAGTTGGGT AACAAATTCG
251 ACAAGGCCGT TTTGGCGCGT TGGGCCAAGG TGCTGGAAT GATCATTATG
301 GCGGTGGCGG CATACGGGTT TTATATCCGG TCTGCCCCGC TGCTTTTGGC
351 GTGCTCTGTT TGCATGGGCG CGCAATCGAC GCTGTTCCGG CCGCTGAAAT
401 ACGCCATCCT GCCCGATTAT CTCGACGACA AAGAGTTGAT GATGGGCAAC
451 AGCCTGATTG AATCGGTGAC GTTTGTCGCC ATCCTGTTGC GTCAGATACT
501 GGGGACTGCG GTGGCAGGTG TACCGCCTTA TATTGTCGGG ATACTGTTT
551 TGCTGGTCGC CGTAGGAGGC ACGGTCGGCA GCCTGTTTAT GCCGTCCGTA
601 CCCGCCAAGG CTGCCGATAC ACAAATTGAG TGGAATATTG TCCGGGGTAC
651 AAAATCCCTG CTGCGTGAAA CGGTGCGGCA CAAGCCCGTT TTTACGCCCA
701 TTATCGGTAT TTCGTGGTTT TGGTTTGTG GCGCGGTTA TACCACGCAA
751 CTGCCGACCT TTACCCAAAT CCATCTAGGC GGCAACGACA ATGTTTTCAA
801 CCTGATGCTT GCCCTGTTT CCATCGGTAT TGCCGCCGGT TCGGTACTGT
851 GTGCCAAGTT CAGCAGGAA CGGCTGAGGT TGGCTTGGGT AACGGTTGGT
901 GCGTTGGGTT TGACGGTTTG CGGCTTGGT TTGGTGTGGC TGACGCACGG
951 ACACCGTTTT GAAGGGCTGA ACGGCATTTT TTGGTTTTTA TCGCAAGGAT
1001 GGGCATATCC CGTGATGGCG GTGATGACGC TGATCGGCTT TTCGGCGGA
1051 TTTTCTCCG TTCGCTCTA TACCTGGCTG CAAACCGCCA GTAGCGAGAC
1101 TTTCCGCGCC CGCGCCGTTG CCGCCAACAA TATCGTTAAC GGTATTTT
1151 TGGTTTCCGC TGCCGTTTTG AGCGCGGTGT TGCTGTTTTT GTTTGACAGC
1201 ATTTCTTGT TGTATCTGAT TGTGCTTTG GGCAATATTC CGTTGTCCGT
1251 ATTTTGTATT AAGCGCGAAA GGCGTTTTT AGGCGCGGCG GCAATCAGGA
1301 AAAAACCTTG A

```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```

a232 . pep
1  MYAKKGGGLGL VKSRRFAPLF ATQFLGAFND NVFKTALFVM IGFYGLGQNG
51  FLPAGQMLNL GALLFILPYF LFSSLSGQLG NKFDKAVLAR WAKVLEMIIM
101 AVAAYGFYIR SAPLLLACLF CMGAQSTLFG PLKYAILPDY LDDKELMMGN
151 SLIESGTFAV ILFGQILGTA VAGVPPYIVG ILVLLVAVGG TVGSLEMPV
201 PAKAADTQIE WNIVRGTKSL LRETVRHKPV FTAIIGISWF WFGAVYTTQ
251 LPTFTQIHLG GNDNVFNML ALFSIGIAAG SVLCAKFSRE RLRLAWVTVG

```



532

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPVMA VMTLIGFFGG  
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAAVL SAVLLFLFDS  
 401 ISLLYLIVLAL GNIPLSVFLI KRERREFLGAA AIRKKP\*

m232/a232 95.9% identity in 290 aa overlap

				10	20	30
m232.pep				MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLCMGAQSTLFGPLKYAILPDYLDKELMMGNSLIESGTFVAILFGQILGTAVAGVPP					
	120	130	140	150	160	170
	40	50	60	70	80	90
m232.pep	YIVGILVLLVAVGGTVGSLEMPSPVAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
a232	YIVGILVLLVAVGGTVGSLEMPSPVAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
	180	190	200	210	220	230
	100	110	120	130	140	150
m232.pep	ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNMLALFSIGIAAGSVLCAKFSXERLMLAW					
a232	ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNMLALFSIGIAAGSVLCAKFSRERLRLAW					
	240	250	260	270	280	290
	160	170	180	190	200	210
m232.pep	VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFXFLSQGWAYPVMAVMTLIGFFGGFFSVPL					
a232	VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFWFLSQGWAYPVMAVMTLIGFFGGFFSVPL					
	300	310	320	330	340	350
	220	230	240	250	260	
m232.pep	YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVLALGNIPLS					
	:    ::					
a232	YTWLQTASSETFRARAVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVLALGNIPLS					
	360	370	380	390	400	410
	270	280	289			
m232.pep	VFLIKRERREFLGAAAIRKKPX					
a232	VFLIKRERREFLGAAAIRKKPX					
	420	430				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq  
 1 atgaaacgca aaaatatcgc gctgattccc gccgccggca tcgggggtgcg  
 51 ttccggtgcg gacaaaccca agcaatatgt cgaaatcgga agcaaaaccg  
 101 ttttagaaca tgtacttggg atttttgaac ggcatgaggc cgctcgatttg  
 151 accgtcgttg tcgtctcgcc cgaagacacg tttgccgata aggttcagac  
 201 ggcatattcca caggttcggg tgtggaaaaa cggaggacag acccgcgccg  
 251 aaactgtccg caacggtgtg gcaaaactgt tggaaaccgg tttggcggcg  
 301 gaaaccgaca atattctggt acacgatgcc gcccgctgct gcctgccgtc  
 351 tgaagctctg gcgcggttga tagaacaggc gggcaacgcc gccgaaggcg  
 401 ggatttttggc agttcccgtt gccgatacgc tcaagcgcgc agaaagcgga  
 451 caaatcagtg caactgtcga ccgttcgggg ctttggcagg cgcaaacgcc  
 501 gcagcttttt caagcgggtt tgctgcaccg cgcattggct gcggaaaact  
 551 tgggcggcat taccgatgaa gcgtccgccg tggaaaaact ggggtgtcgt  
 601 ccgctactga tacagggcga cgcgcgcaat ttgaaactga cgcagccgca  
 651 ggacgcatac atcgtcaggc tgctgctcaa tgccgtctga

This corresponds to the amino acid sequence &lt;SEQ ID 858; ORF 233.ng&gt;:

g233.pep  
 1 MKRKNIALIP AAGIGVRFGA DKPKQYVEIG SKTVLEHVLG IFERHEAVDL  
 51 TVVVVSPEDT FADKVQTAFP QVRVWKNGGQ TRAETVRNGV AKLLETGLAA  
 101 ETDNILVHDA ARCLPSEAL ARLIEQAGNA AEGGILAVPV ADTLKRAESG

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR  
 201 PLLIQGDARN LKLTQPDAY IVRLLLNAV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)  
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGCA TCGGGGCGCG  
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG  
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTTG  
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC  
 201 GGCATTTCCT CAGGTTCTGGG TGTGGAAGAA CGGCCGACAG ACCCGCGCCG  
 251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGGCGCGC  
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC  
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGGCG  
 401 GGATTTTGGC AATTCCCAT TCCGATACGC TCAAGTGC GCACGGTGGG  
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)  
 1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL  
 51 TVVVVSPEDT FADKVQTAFF QVRVWKNNGQ TRAETVRNGV AKLLETGLAA  
 101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG  
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
g233	MKRKNIALIP AAGIGVRFADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
m233.pep	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
g233	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
m233.pep	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
g233	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
g233	ARLIEQAGNA AEGGILAVPVADTLKRAESQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq  
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGCA TCGGGGCGCG  
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG  
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTTG  
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC  
 201 GGCATTTCCT CAGGTTCTGGG TGTGGAAGAA CGGCCGACAG ACCCGCGCCG  
 251 AAACGTGTCG CAACGGTGTG GCAAAATTGT TGGAAACCGG TTTGGCGGCG  
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC  
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG  
 401 GGATTTTGGC AATTCCCGTT GCCGATACGC TCAAGTGC GCACGGTGGG  
 451 AACATTAGTG CAACCGTCGA GCGGACGAGC CTTTGGCAGG CGCAAACGCC  
 501 GCAGCTTTTC CGCGCCGGGC TGCTGCACCG CGCATTGGCT GCGGAAACT  
 551 TGGACGGCAT TACCGATGAA GCGTCCGCGG TGGAAAAATT GGGCATCCCG  
 601 CCTTGCTGGG TGCAGGGCGA CGCGCGCAAT TTGAACTGA CGCAGCCGCA  
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1  MKRKNIALIP AAGIGAREFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFP QVRVWKNNGGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAI PV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDVAV*
```

m233/a233 99.3% identity in 152 aa overlap

```

      10      20      30      40      50      60
m233.pep  MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
          |||
a233      MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
          10      20      30      40      50      60

      70      80      90     100     110     120
m233.pep  FADKVQTAFPQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
          |||
a233      FADKVQTAFPQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
          70      80      90     100     110     120

      130     140     150
m233.pep  TRLIEQAGNA AEGGILAIPIADTLKCADGGNI
          |||
a233      TRLIEQAGNA AEGGILAI PVADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA
          130     140     150     160     170     180

a233      AENLDGITDEASAVEKLGIRPLL VQGDARN LKLTQPQDAYIVRLLLDVAVX
          190     200     210     220     230
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1  atgaaaaccg tttccgccgc catcgctttt gccgccgctg ccgtttcact
51  gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat caccgtgttc gcaccccgat ttccgtcgga
151 acattcgaca accgtccag cttccaaaaa ggcattttct ccgacagtga
201 agaccgtctg ggcagccagg caaaaacccat cctggtaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaatccg gcatttccgg caaagcgag aacctgaaag gcgagatta
351 tgcgttacc ggcgatgtaa cgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggtcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctattc
501 cacacagggc gcgggcgaat acgcactttc caaccgcgaa atcatcggtt
551 tcggcgccac ttccgggtac gatgcgactt tgaacggcaa agtttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaacgg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1  MKTVSAAIAF AAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
51  TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRNFV LNRTNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSNRE IIGFGGTSY DATLNGKVLVD
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1  ...GGCGCGGGCG AATACGCACT TTCCAACCGT GAAATCATCG GTTTCGGCGG
51  CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTGA GACTTGGCAA
101 TCCGCGAAGC .GTCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

m234.pep (partial)  
 1 ..GAGEYALSNR EIIGFGGTSG YDATLNGKVL DLAIKAVNS LVQAVDNGAW  
 51 QPNR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng)  
 from *N. gonorrhoeae*:

m234/g234

						10	20	30
m234.pep						GAGEYALSNREIIGFGGTSGYDATLNGKVL		
g234	LGRGKSQIAYAKVALNIVNVNTSEIVYSTQGAGEYALSNREIIGFGGTSGYDATLNGKVL							
	140	150	160	170	180	190		

		40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX		
	:		
g234	DLAIREAVDNLVQAVDNGAWQSNRX		
	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)  
 1 AACCGCACCT ATTTGAACGC ATTAAAACAG GAATCCGGCA TTTCCGGCAA  
 51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG  
 101 AATTCGGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTTTGGGT  
 151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA  
 201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GGCGAATACG  
 251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCACTTC CGGCTACGAT  
 301 GCGACTTTGA ACGGCAAAGT TTTAGACTTG GCAATCCGCG AAGCCGTCAA  
 351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)  
 1 NRTYLNALKQ ESGISGAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG  
 51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD  
 101 ATLNGKVLDL AIREAVNSLV QAVDNGAWQP NR\*

m234/a234 100.0% identity in 54 aa overlap

						10	20
30							
m234.pep	GAGEYALSNREIIGFGGTSGYDATLNGKVL						
a234	LGRGKSQIAYAKVALNIVNVNTSEIVYSAQGAAGEYALSNREIIGFGGTSGYDATLNGKVL						
	50	60	70	80	90	100	

	40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX	
a234	DLAIREAVNSLVQAVDNGAWQPNRX	
	110	130

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq

536

```

1  atgaaacctt tgattttagg gcttgccgcc gtgttggttc tgtctgcctg
51  ccaagttcga aaagctcccc acctcgacta cacgtcattc aaagaaagca
101 aaccggcttc aattttggtg gttccgccgc tgaacgagtc gcctgatgtc
151 aacggcactt gggggatgct ggcttcgacc gccgcgccga tttccgaagc
201 cggctattac gtctttcccg ccgcagtcgt ggaggaaacc ttcaaagaaa
251 acggcttgac caatgccgcc gatattcacg ccgtccggcc ggaaaaactg
301 catcaaattt tcggcaatga tgcggttttg tacattacgg ttaccgaata
351 cggcacttca tatcaaattt tagacagcgt gacgaccgta tccgccaaag
401 cacggctggt cgattcccg caggggaaag agttgtggtc ggggttcggcc
451 agcatccgcg aaggcagcaa caacagcaac agcggcctgt tgggggcttt
501 ggtcggcgca gtggtcaatc agattgccaa cagcctgacc gaccgcggtt
551 atcaggtttc caaaaccgcc gcatacaacc tactgtcgcc ctattcccg
601 aacggtatct tgaaaggtcc gagattcgtc gaagagcagc ccaataaa

```

This corresponds to the amino acid sequence <SEQ ID 870; ORF 235.ng>:

g235.pep

```

1  MKPLILGLAA VLALSACQVR KAPDLDTYSF KESKPASILV VPPLNESPDV
51  NGTWGMLAST AAPISEAGYY VFPAAVVEET FKENGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVGA VVNQIANSLT DRGYQVSKTA AYNLLSPYSR
201 NGILKGPRFV EEQPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 871>:

m235.seq

```

1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCG CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAAACTG
301 CATCAGATT TCGGCAATGA TCGGTTTGT TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC CAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCGTT GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 872; ORF 235>:

m235.pep

```

1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQENGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng)

from *N. gonorrhoeae*:

m235/g235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST					
g235	MKPLILGLAAVLALSACQVRKAPDLDTYSFKESKPASILVVPPLNESPDVNGTWGMLAST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYYVFPAAVVEETFKQENGLTNAADIHAVRPEKLHQIFGNDAVLVITVTEYGTS					
g235	AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLVITVTEYGTS					
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||
          130      140      150      160      170      180

          190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||
g235      DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPKX
          |||
          190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTTCGACTA CACGTCATT C AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TGCGGTTTGG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

          10      20      30      40      50      60
m235.pep  MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          |||
a235      MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          |||
          10      20      30      40      50      60

          70      80      90      100     110     120
m235.pep  AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
          |||
a235      AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
          |||
          70      80      90      100     110     120

          130     140     150     160     170     180
m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||
a235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||
          130     140     150     160     170     180

          190     200     210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||
a235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq

```

1 ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51 CGGTTTCATA ACCTGCAACC GCGCCACAT CGCGGTGTA ATGCCAGCAG
101 CGTTCGCATT TTTCGCCGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTTCGGCGC GGTAATTTCTG
251 GCTTCGCCCT GCAAggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTTACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAgTTC GGCTTCGGCT TTTTCGTTGA TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGTCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGGCGGGC GCGGCTGTCTG
551 GCTTTGTGTG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGAAGG
651 CATAGCGCGG ATAGTAACCG CTGCCAAAC GCTCTTGcAG CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCACC ATATCCGCTT GTTGCACGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAAacag AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTTCGGTAA CGCGTTTGAG GATTTCTTTG
851 GAAatcgCCA ATtcgcgct gTAATCGGTG GATGCCGCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCGT TATAGACTTC CTGCGGCGCG ACGACGTTGC
951 CGATGGATTT CGACATTTTG CGGCCGTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TGC CGCTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1 MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAFAFFAV AGFGGNGKFI
51 TDFHFCFRHQ QGKAQFFAQS IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGLLRAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNV FHEVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAO
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1 ..TTGCACGGAC GAACCGACGG TTTTGTCCGGC GCGCAAAGGC TCGATGGCGG
51 CGGTTACCGC TTCGCGGGCT TCGCGGATG CCGTCCATTT TTTCACCAGT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCTCTTCGC CGCCGCCGwT GayGTCCAC GCTTCTTCG
201 CGGTGAAGCA CAAATCGGT GCAATCAAGA GAACCAACT GCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTCGGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACAATG TCTTTTACGG CAAAGTGGAa kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG AACTCTTGC AGCTGACGTG CCAATACCAC
451 GCGGTAGCGG TCGATTTCa CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTTG AGGATTTCTT TGGAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCGC CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCCTTC GCCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1 ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGFGFFV DGRELVPME
51 EDAVXFAAAX DVPRPFAGEA QNRCNQENQT ACDVIQGS LC AAACMAVCFG
101 GVEAVFQDVE VERTQVFRAE RNXFYQKVE XITRIVIACQ TLLQLTCQYH
151 GVAVDFFHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQO
251 LFIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng)

from *N. gonorrhoeae*:

m236/g236

539

					10	20	30
m236.pep					LHGR	TDGFVGAQRLDGGGYRFAGFADCRPF	
g236	FRHQQGKAQFFAQSIQIAGHFFRRGNFGFRLQGR	TDSFVGAQRLDGGGYCFARFADCRPF					
	60	70	80	90	100	110	
m236.pep		40	50	60	70	80	90
	FHQFGFGFFVDGRELVPSMEEDAVXFAAAXDVP	PRFFAGEAQNRCNQENQTACDVIQGS	LC				
g236	FHQFGFGFFVDGRELVPSMEEDAVXFAAADDP	PRFFAGEAQNRCNQENQAARDVVQGLR					
	120	130	140	150	160	170	
m236.pep		100	110	120	130	140	150
	AAACMAVCFGGVEAVFQDVEVERTQVFR	ERNXVFGKVE	XITRIV	IACQTL	LQLTCQYH		
g236	AAAGAAVGGFVEAVFQDVEVERAQVFR	ERNNVFHGEVEGIARIVTACQTL	LQPPRQYQ				
	180	190	200	210	220	230	
m236.pep		160	170	180	190	200	210
	GVAVDFHHIRLLHGIFNRIKVAQVGKQKAQ	GIADTAVAFGYAFEDFFGNRQFAAVIGR	CR				
g236	GVAVDFHHIRLLHGIFNRIKVAQIGKQEAQ	GIADAFAVAFGNAFEDFFGNRQFAAVIGG	CR				
	240	250	260	270	280	290	
m236.pep		220	230	240	250	259	
	PQAQDVCAEFVINLLRCNDVADGFRHFAFA	VNDNETMGQQLFIR	RATHX				
g236	PQAQDVRAEFVIDFLRRDDVADGFRHFAA	VLNVHETVGQQLFIR	CASHG				
	300	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

```

a236.seq
1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCTGCACAG CGTTTGCAGA
51  CGGTTTCATG GCCTGCAACC GCGCCACAT CGCGGGTGTG GTGCCAGCAG
101 CGTTCGCATT TTTCACCATC ACTGGCTTTA GCGGCAACGG CAAGTTCGCT
151 GCCTACTTTC ACTTCTGCTT TAGACACCAG CAAAGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATT CTTCGCGCGC GGTAATTTCTG
251 GCTTCGGCTT GCAAGGACGA ACCGACGGTT TTGTCGGCGC GCAAAGGCTC
301 GATGGCGGCG GTTACCGCTT CGCGGGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAAGTC GGCTTCGGCT TTTTCGTTGA TGGTCGGGAA CTCGTGCCAA
401 GTATGGAAA GCACGCTGTC TTCTGCGCCG CCGCCGATGA TGTCCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGCGG GTTTGCGCGC TCGGCGGGC GCGGCTGTCG
551 GCTTTGGTGG TATAGAGGCG GTCTTTCAGG ATATCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACCATTTT TTTCACGGCA AAGTGGGAAG
651 CATAACGCGG ATAAAAATCA CCGGCAACGC GTTCTTGCAG CCGCCTTGCC
701 AACACCAAGG CATAGCGGTC GATTTCACC ATATCCGCCT GTTGCACGGC
751 ATCTTCAATA GGATTGAAGT CGCTCAAGTT GGCAAACAAA AAGCTCAAGG
801 TATTGCGGAT ACGGCGGTAG CTTTCGGTTA CGCGCTTGA GATTTCTTTG
851 GAAATCGCCA ATTCGCGGCT GTAATCGGTG GATGCCGCC ACAGGCGCAG
901 GATGTCCGCG CCGAACTCGT TATACACTTC TTGCGGCGCG ACGACGTTGC
951 CGATGGATT CGACATTTG CGCCCGTTTT GATCCACCAC GAAACCATGG
1001 GTCAGCAGCT GTTGTACGG CGCGGACCC ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

```

a236.pep
1  MARFAFSADI LCTAFADGFM ACNRAHIAGV VPAAFAFFTI TGFSGNGKFA
51  AYFHF CFRHQ QSKAQFFAQSIQIAGHFFRR GNFGFGLQGR TDGFVGAQRL
101 DGGGYRFAGF ADCRPFFHQF GFGFFVDGRE LVPSMEKHAV FCAAADDVPR
151 FFAGEAQNRC NQENQAARDV VQGLLRAAAG AAVGFGGIEA VFQDIEVERA
201 QVFRAERNHF FHGKVEGTR IKITGNAFLQ PPCQHOGIAV DFHHIRLLHG
251 IFNRIEVAQV GKQKAQGIAD TAVAFGYALE DFFGNRQFAA VIGGCRPQQA
301 DVRAELVIHF LRRDDVADGF RHFAPVLIHH ETMGQQLFVR RATH*

```



540

m236/a236 81.0% identity in 258 aa overlap

					10	20	30
m236.pep					LHGRTDGFVGAQRLDGGGYRFAGFADCRPF		
a236	FRHQQSKAQFFAQSIQIAGHFFRRGNFGFLQGR	TDGFVGAQRLDGGGYRFAGFADCRPF					
	60	70	80	90	100	110	
m236.pep		40	50	60	70	80	90
		FHQFGFGFFVDGRELVP	SMEEDAVXFAAAXDVP	PRFFAGEAQNRCNQEN	TACDV	IQGSLC	
a236		FHQFGFGFFVDGRELVP	SMEKHAVFCAAADDV	PRFFAGEAQNRCNQEN	QAARDV	VQGGLR	
	120	130	140	150	160	170	
m236.pep		100	110	120	130	140	150
		AAACMAVCFGVEAVFQD	VEVERTQVFRAERNXV	FYGVK	EXITRIV	IACQTL	LQTCQYH
a236		AAAGAAVGFGGIEAVFQD	IEVERAQVFRAERNH	FFHGK	VEGITRI	KITNAFL	QPPCQHQ
	180	190	200	210	220	230	
m236.pep		160	170	180	190	200	210
		GVAVDFHHIRLLHGIEN	RIKVAQVGKQKAQGI	ADTAVAFGYAFED	FFGNRQ	FAAVIG	RGR
a236		GIAVDFHHIRLLHGIEN	RIEVAQVGKQKAQGI	ADTAVAFGYALE	FFGNRQ	FAAVIG	GGR
	240	250	260	270	280	290	
m236.pep		220	230	240	250	259	
		PQAQDVCAEFVINLLRC	NDVADGFRHFFAFV	DNETMGQQLF	FIRRATHX		
a236		PQAQDVRAELVIHFLR	DDVADGFRHFAPVLI	HETMGQQLF	VRATHX		
	300	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

g237.seq

```

1  atgcgggaca aggttggcgg taatatcgca ctccccgccc cacgaatatt
51  cgattctaac atcggaagc tgcggaaaaa ctttaagcat atcttgccgg
101 acaagctcgg tcatacgcg aggattgtcg ataaattcgt tacccttacc
151 gccgaaaagc agcctgccgt ccgcgctgag gcggtataaa tccaaaatat
201 ggcggttgct gcatactgcc atattgttgc ggataagccc ttttgtgcgc
251 gcgccaagg gttcggtggc aataataaag gtgctgacgg caatcgctt
301 gcgttccaaa ggccggaata tcgggttcaa accgacataa gtattgacgg
351 catagaccac atttttacac tcgacgctgc cttcgggcgt gtaaacacgc
401 caaccgtttt gatacgggtc gatgcgcgtc atcggggatt gctcgaaaat
451 ctgcgcgcgc gcttcggcag cggcgctggc aacacccaac gtgtaattga
501 gcggatgaag atgcccggac aagggatcga actgtgcgcc ttggtacata
551 tcgctgtcaa gctgctgtt caactcggct ttatcccaaa gttgataatg
601 actcgaccgc taatgcccgt ggcgctgttc atgccactgc tgcaactctt
651 cccaatgctg cggacggacg gcaaccgtgg cataaccgcg ctgccaatcg
701 caatcgatgg catgtttgcg gacgcgttcg tccaccagtt cgaccgcctg
751 caaagactgt tgccaaaacc attgcgcctg ctccaagcgc acctgttttt
801 caatttcccc cataccgcag gcgtagtcgc tgataacctg cccgccactc
851 ctgccggacg cgcggaagcc gatacgtgcg gcttccaaaa cgacggcttc
901 atgtccgtgt tccgccagcg gcaatgcggt acacaaaccg ctcaaaccgc
951 cgccgataat gcaggtttcg gctttcagac ggcattggag tttcggataa
1001 acagtatgcg gattaaccga actaaaataa taagaaggca gatattcttg
1051 aaaatcaggg cgaatcattg tgtttgcttt atcggtataa ttttcggacg
1101 gaatgataca gactgtcggg ccatatcgtc caaacagaaa atcggttga

```

This corresponds to the amino acid sequence &lt;SEQ ID 882; ORF 237.ng&gt;:

g237.pep

```

1  MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51  AEKQPAVRAE AVIIQNMAVV AYCHIVADKP FCARAQGFGG NNGADGNRL

```

541

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN  
 151 LRAGFGSGAG NTQORVIERMK MPQGQIELCA LVHIAVKLLF QLGFIPKLIM  
 201 TRTVMPPLGVF MPLQLQFPML RTDGNRGITA LPIDIDGMFA DAFVHQFDRL  
 251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTCGFQNDGF  
 301 MSVFRQRQCG TQTAQTAADN AGFGFQTALE FRINSMRINR TKIIRRRQIFL  
 351 KIRANHCVCF IGYIFGRNDT DCRAISSXQK IG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m237.seq

1 ATGCGGGACA AGGTTGGCGG TAATGTGCGA CTCCCCGCCC CACGAATATT  
 51 CGATTTTGGAC ATCGGCAAGC TCGGGAAGAA CTTTAAGCAT ATCTTGGCGG  
 101 ACAAGCTCGG TCATaCGCTC AGGATTGTCG ATAAACTCGT TATCCTTACC  
 151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT  
 201 GCGGTTTGTG GCATACTGCC ATATTGTTAC GGATAAGCCC TTTTGGCGCG  
 251 GCCCCCAAGG GTTCGGTCGC AATAATAAAG GTGCTGACAG CAATCGCCTT  
 301 GCGTTCCTAA GGCCGGAATA TCGGGTTCAG ACCTGCATAA GTATTGACAG  
 351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTCCGGCGT GTAAACCAGC  
 401 CAACCGTTT GATGCGGTTG GATGCACGTC ATCGGGGATT GCTCGAAAAT  
 451 CTGCGCACCG GCTTCGCGAG CGGCACGAGC GATGCCCAA GTGTAAGTGA  
 501 GCGGATGACG GTGTCCGAT AAGGGGTCGA ATTGTGCCCC TTGGTACATA  
 551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG  
 601 ACTCGCACCG TAATGCCGTT GGGCGTGTTC ATGCCACTGC TGCAACTCTT  
 651 CCCAATGCTG CGGACGGACG GCAACCGTGG CATAACCGCG CTGCCAATCA  
 701 CAATCGACGG CATGTTTTCG GACGCGTTCG TCCACCAGTT CGACCGCCTG  
 751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT  
 801 CAATTTCCCC CATAACCGAG nCGTAATCGC TGATAACCTG CCCGCCACTC  
 851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC  
 901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCCAATCCGC  
 951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTtCGGATAA  
 1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG  
 1051 AAAATCAGGG CGAATCATTG TGTTCGCTTT ATCAGGTGTA TTTTCGGACG  
 1101 GAATGATACA GGCTGTGCGG CCATATCGTC CAwACAGAAA ATCGGTTGA

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m237.pep

1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGH TL RIVDKLVILT  
 51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPGGFGR NNGGADSNRL  
 101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN  
 151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFIPKLIM  
 201 TRTVMPPLGVF MPLQLQFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL  
 251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRAET DTRGFQHNRF  
 301 MSLLRQGQCS AOTTQSAADD TGIGFQTALK FRINSMRINR TEIIRRRQIFL  
 351 KIRANHCVCF IRCIFGRNDT GCRAISSXQK IG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m237/g237

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGH	TLRIVDKLVILTAEKQSAVRAE				
g237	MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGH	TRIVDKFVILTAEKQPAVRAE				
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMAVVAYCHIVTDKPF	CARPGGFGRNNGGADSNRLAFQRPEYRVQTCISIDSIDH				
g237	AVIIQNMAVVAYCHIVADKPF	CARAQGGGNNKGADGNRLAFQRPEYRVQTDISIDGIDH				
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGT	SDAQSVSERMQVSGXGVELCP				

[illegible]

a237.seq

1	ATGCGGGACA	AGGTTGGCGG	TAATGTGCBA	CTCCCCGCC	CACGAATATT
51	CGATTTTGAC	ATCGGCAAGC	TGCGGAAAAA	CTTTAAGCAT	ATCTTGGCGG
101	ACAAGCTCCG	TCATACGCG	GGGATTTGTC	ATAAACTCTA	TTCCTTACC
151	GCCGAAAAGC	AGCTTCCGCT	CCGCGCTGAG	CGGTAATAGT	TCCAAATAT
201	GACGGTTGTC	GCATACTGCC	ATATTGTTGC	GGATAAGCCC	TTTTGCAGCG
251	GCGCCCAAGG	GTTCTGTGGC	AATAATAAAG	GTGCTGACAG	CAATCGCCTT
301	GCGCTCCAAA	GGCTTGAATA	TCGGATTCAA	ACCGGCATAA	GTATTGACGG
351	CGTACACCA	ATTTTGTGAT	TCGACGCTGC	CTTCGGGGGT	GTAACCACG
401	CAACCGTTTT	GATAAGGTTT	ATGCGGTATC	ATCGGAGAAT	GCTCAAAAT
451	CTTCGTACCA	GCTTCGGCAG	CGGCGCGGGC	GATGCCAAC	GTGTAATTGA
501	GCGGATGGAG	ATGCCCGGAC	AAGGGATCGA	ACTGTGCGCC	TTGGTACATA
551	TCGCTGTCAA	GCTGCTGCTT	CAGTTTCAGT	TTATCCCGA	GTTGATAATG
601	AGTTGCACCG	TAATATTTTT	GGGCGTGCTC	ATGCCATTGT	TGCAATCTTT
651	CCCAATGCTG	CGAACGGATG	GCAACCGTGG	CATAACCGCG	TCGCCAATCG
701	CAATCAATGG	CATGTTTTCG	GACGCGTTTC	TCCACCAGTT	CGACCGCCTG
751	CAAGAGCTGT	TGCCAAAAACC	ATTGCGCTTG	CTCCAAACCG	ACCTGTTTTT
801	CAATTTCTCT	CATACCGCAG	GCGTAATCGC	TGATAAAGCT	CCCGCCACTC
851	CGTCCCGACG	CGCCGAAACC	GATGCGCGCG	GCTTCCAACA	CACCGCTTTC
901	ATGTCCCTGC	TCCGCCAAGG	GCAATGCAGT	GCACAAACCA	CTCAATCCGC
951	CGCGGATGAT	ACAGGTATCG	GTTTTCAGAC	GGCATTGAAG	TTTCGGATAA
1001	ACAGTATGAG	GATTAACCGA	ACTGAAATAA	TAAGAAGGCA	GATATTTCTG
1051	AAATCAGGG	CGAATCATTT	TGTTTGCTTT	ATCGGGTATA	TTTTCGGACG
1101	GAATGATACA	GCGTGTCTGAG	CGTATTCGTC	CAACACAGAA	ATCGGGTTGA

a237.pep

1	MRDKVGGNVA	LPAPRIFDFD	IGKLRKNFKH	ILADKLGHTR	GIVDKLVILT
51	AEKQSAVRAE	AVIIQNMTVV	AYCHIVADKP	FCTRAQGFQG	NNKGADSNRL
101	ALQRLEYRIQ	TGISIDGVHQ	IFAFDAAGFG	VNQPTVLIRF	NAYHGRMLKN
151	LRTSFGSGAG	DQARVIERME	MFGQGIELCA	LHVIAVKLLQ	QSFVIPLEIM
201	SCTVIFLGLV	MPLLQFFPML	RTDGNRGITA	LPIAINGMFA	DAFVHQDFRL
251	QRLLPKPLRL	LQTDLEFNFL	HTAGVIADNL	PATFSRRAET	DTRGFQHNRF
301	MSLLRGQCS	QOTQSAADD	TIGIGFTALK	FRINSMRINR	TEIIRRQIFL
351	KIRANHCVCV	IGYIFGRNDT	GCRAISSKOK	IG*	

m237/a237 85.6% identity in 382 aa overlap

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEQSAVRAE					
a237	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTRGIVDKLVILTAEQSAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMAVVAYCHIVTDKPFPCARPQGFRNNKGADSNRLAFQRPYRVQTCISIDSIDH					
a237	AVIIQNMTVVAYCHIVADKPFCTRAQGFQGNKGADSNRLALQRLYRIQTGISIDGVHQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDARHGRLLNLRGFGSGTSDAQSVSERMQVSGXGVELCP					
a237	IFAFDAAFGGVNQPTVLIREFNAYHGRMLKNLRTSFGSGAGDAQRVIERMEMPGQGIELCA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m237.pep	LVHIAVKLLFQLGFI PKLIMTRTVMPLGVFMPLLQLFPMRLTDGNRGITALPITIDGMEA					
a237	LVHIAVKLLQLFSVIPPELIMSCTVIFLGVLMPLQLFFPMRLTDGNRGITALPIAINGMEA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m237.pep	DAFVHQFDRLQRLLPKPLRLQLADLFFNFPHXTAXVIADNLPATPSRRAETDTRGFQHNRF					
a237	DAFVHQFDRLQRLLPKPLRLQLADLFFNFLHTAGVIADNLPATPSRRAETDTRGFQHNRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m237.pep	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRROIFLKIRANHCVCFF					
a237	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRROIFLKIRANHCVCFF					
	310	320	330	340	350	360
	370	380				
m237.pep	IRCIIFGRNDTGCRAISSXQKIGX					
a237	IGYIFGRNDTGCRAISSKQKIGX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctgttgccag cggcaatata
51  gatgctgcat atccccatta gtcatgcgaa cggtttggat gcccgtttgc
101 gcgatgatat gcaggcaaaa cactacgaac cgggtggcaa ataccatctg
151 tttggtaatg ctgcggcgag tgtaaaaaat cgggtttgcg ccgtccaaac
201 atttgatgca actgcggtcg gcccataact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtccgtt cgataatcat gattcaaaaa gcacttctga
351 tttcagcggc ggcgtagacg gcggttttac cgtttaccaa cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacgggcc tcaaggcggc
451 ggttatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaaaaa agataaacac tgttccgcaa gccccttttt
551 cagaccgctg gctaaaagaa aatgccggtg ccgcttcagg ttttctcagc
601 cgtgcggatg aagcaggaaa actgatattg gaaaacgacc ccgataaaaa
651 ttggcgggct aaccgtatgg atgatattcg cggcatcgtc caagggtcgg
701 ttaatccttt tttacgggt tttcaagggg tagggattgg ggcaattaca
751 gacagtgcgg taagcccgtg cacagataca gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtcc ggaagcacia cttgccgccg

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544

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851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgcccttgcc gtagcagagg ccgcaggtag gggtttggcg ggtaaaaaag
1001 tagaacttaa cccgaccaa tgggattggg ttaaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcgga aggaaaagct aatgctgcaa
1151 cctatcctaa gttgggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atgggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacaatt
1401 tgcaactaca ggtattcaag caaatTTTga aacttTact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1 MNLPIQKFMM LLAAAIISMLH IPISHANGLD ARLRDDMQAK HYPEPGGKYHL
51 FGNARGSVKN RVCAVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGTs TKTKINTVPO APFSDRWLKE NAGAASGFLS
201 RADEAGKLIW ENDPDKNWRA NRMDDIRGIV QGAVNPFLTG FQGVGIGAIT
251 DSAVSPVTDI AAQQTLOGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGINS
301 ARQWADAHFN ITATAQTALA VAEAAGTVWR GKVELNPTK WDWVKNTRYK
351 KPAARHMQTV DGEMAGGNRP PKSITSEGKA NAATYPKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYT IDSNEKRNI KNGHLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGGTTTGA AGGTGTTATC GGTATGAAA CCCATTTTTC AGGGCAGGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAA GCACTTCTGA
351 TTTCAGCGGC GGTGTAGACG GCGGTTTAC TGTTTACCAA CTTTCATCGAA
401 CAGGGTCCGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCAGGAG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACCTCA ACAAAAACAA AGACTAATAT TGTCCTCAA GCCCATTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTTG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTTAGGAA AATTAAGTCC GGAAGCACAA CTTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGCGG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCCAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAaaaaaag
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TAAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAAATCTT TACCAAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCGTGATA
1251 AGTTAAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACATTTTT AGAATCCATG ATAATTCACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAATTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTACAAC AACAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYPEPGGKYHL
51 FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

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151 DYPPFGGARD IYSYYVKGTS TKTKTNIVPQ APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDVRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQOTLQGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS
301 AKQWADAHFN ITATAQTALS AAEAAGTVWR GKKVELNPTK WDWVKNTGYK
351 KPAARHMQTL DGEMAGGNKP IKSLPNSAAE KRKQNF EKFN SNWSSASFDS
401 VHKTLPNAP GILSPDKVKT RYTSLDGKIT IIKDNENNYF RIHDNSRKQY
451 LDSNGNAVKT GNLQGGKQAKD YLQQQTHIRN LDK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 238 shows 86.0% identity over a 401 aa overlap with a predicted ORF (ORF 238.ng) from *N. gonorrhoeae*:

m238/g238

m238.pep	10	20	30	40	50	60
	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
g238	MNLPIQKFMMLLAAISM LHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
m238.pep	70	80	90	100	110	120
	RVYAVQTFDATAVSPVLPITHERTGFEVIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG					
g238	RVCVAVQTFDATAVGPILPITHERTGFEVIGYETHFSGHGHEVHSPFDNHSDSKSTSDFSG					
	70	80	90	100	110	120
m238.pep	130	140	150	160	170	180
	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYYVKGTS TKTKTNIVPQ					
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGGYPEPQGARDIYSYHIKGTSTKTKINTVPQ					
	130	140	150	160	170	180
m238.pep	190	200	210	220	230	240
	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDDVRGIVQGAVNPFLMG					
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPDKNWRANRMDDIRGIVQGAVNPFLTG					
	190	200	210	220	230	240
m238.pep	250	260	270	280	290	300
	FQGVGIGAITDSAVSPVTD TAAQOTLQGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS					
g238	FQGVGIGAITDSAVSPVTD TAAQOTLQGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS					
	250	260	270	280	290	300
m238.pep	310	320	330	340	350	360
	AKQWADAHFNITATAQTALS AAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL					
g238	ARQWADAHFNITATAQTALAVAEAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTV					
	310	320	330	340	350	360
m238.pep	370	380	390	400	410	420
	DGEMAGGNKPIKSLPNSAAEKRKQNF EKFN SNWSSASFDS VHKTLPNAP GILSPDKVKT					
g238	DGEMAGGNRPKSI - TSEGKANAATYPKLVNQLNEQNLNNIAAQDPRLSLAIHEGKKNFP					
	370	380	390	400	410	
m238.pep	430	440	450	460	470	480
	RYTSLDGKITIIKDNENNYFRIHDNSRKQYLD SNGNAVKTGNLQGGKQAKDY LQQQTHIRN					
g238	IGTATYEEADRLGKIWVGEGARQTS GGGWLSRDGTRQYRPPTEKKSQFATTG IQANFETY					
	420	430	440	450	460	470

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

**m238/a238 91.9% identity in 385 aa overlap**

	10	20	30	40	50	60
m238.pep	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
a238	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
m238.pep	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHHDSSKSTSDFSG	70	80	90	100	110
a238	RVYAVQTFDATAVGPILPITHERTGFEGIGYETHFSGHGHEVHSPFDNHDSKSTSDFSG	70	80	90	100	110
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYYVKGTSTKTKTNIVPQ					
a238	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYYVKGTSTKTKSNIVPR					
	130	140	150	160	170	180
m238.pep	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMD DVGIVQGAVNPFLMG	190	200	210	220	230
a238	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMD DVGIVQGAVNPFLMG	190	200	210	220	230
	250	260	270	280	290	300
m238.pep	FQGVGIGAITDSAVSPVTD TAAQQT LQGINDLGKLSPEAQLAAASLLODSAFAVKDGIN S					

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|||||
a238      FQGVGIGAITDSAVSPVTDAAQQTLOGINHLGNLSPEAQLAAATALQDSFAVKGINS
          250      260      270      280      290      300

          310      320      330      340      350      360
m238.pep  AKQWADAHPNITATAQTALSAEEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMTL
          |||||
a238      ARQWADAHPNITATAQTALAVEAATTWGGKKVELNPTKWDWVKNTGYKTFAVRTMHTL
          310      320      330      340      350      360

          370      380      390      400      410      419
m238.pep  DGEMAGGNKPIKSLP-NSAAEKRRQNFEKFNSNWSSASFDSVHKTLPNAPGILSPDKVK
          |||||
a238      DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1  atgttcacc ataaaggat tgcccgaac cggcggatgg aggttttgtt
51  tttctgccc cgccctgat gcttcgtgat tcgccaacg cgccgtgttc
101 agcctcattt gcgcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctggttttgc tgcatacaca
201 cggaaaaagc ggaaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcattgccg ttcagacggt tttctctgtt attattccgg tatcggaccg
301 gcagtcgctt cgcgcacacg caaaactgcg ctccctcgcc tcgggttggc
351 ggcaatttcc gcttcaccgc gctttaatgc cctgcccacg attttcaggg
401 gcggatcggg caaatccgct tctctgaccg ccgcccagct cggcaggggc
451 tcgtgttgcg aatatTTTTT gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaacgccc gccctcttcc agacggcaca
551 tgacctgcgg caataccgcc cctacttctt caagctcgcg gttataaag
601 atgctgattg cctggaaggt gcgctcgca ggatcctgcc cccgctcgcg
651 agtacggacg ttttgtgcca cgatctgcgc cagcttgcgg gttgtatcga
701 ttggactttc cgcccgttgc gcgacaatgg cgcgcacaat ctggcggcta
751 aaccgctctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1  MFHHKGIARN RRMEVLFFCR RPDRFVIRQT RLLQPHLR II LLQGDFLFFR
51  LVQSCEVEPV LVLLHHNGKS GNAHRKQKE IRFVHCRSDV FLCYYSIGIP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPT IFRGSGKSA SLTAAQLGRG
151 SCCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARTIWR
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1  ATGCTCCACC ATAAAGGTmy kGCCCgAAAC CGGCKGATGG AGGTTTTGTT
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCGCTT CCGCCACACG CAAACCCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCGCCACG ATTTTCAGGG
401 GCAGCTCGGG CAAATCCGCT TCCCTGaCCG CCGCCAGCG CGGCAGGGGC
451 GCGTGTTCGC AATATTTTTT GACAACTGC TTACAATGC GATCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAACGTCG GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTAATTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGACG TTTTGTGCCA CGATCTGCGC CAGCTTGGCG GTTGATCGA
701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT cCGCGGCTa
751 AACCCTCTT cACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:



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m239.pep  
 1 MLHHKGXARN RXMEVLFFCR RPDRFVVRQT RLLQPHLRIT LLQGDFLFFR  
 51 LIQSCEIEPV LVLLHHNGKS GNAHRKQKE IQFVHCHSDV FLCDCSGIGP  
 101 AVRSATRKTAL LALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQRGRG  
 151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSRLIK  
 201 MRTAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIRRL  
 251 NRSSP\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng)  
 from *N. gonorrhoeae*:

m239/g239

m239.pep	10	20	30	40	50	60
	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRITLLQGDFLFFRLIQSCEIEPV					
g239	MFHHKGIARNRMEVLFFCRRPDRFVIRQTRLLQPHLRITLLQGDFLFFRLVQSCEVEPV					
	10	20	30	40	50	60
m239.pep	70	80	90	100	110	120
	LVLLHHNGKSGNAHRKQKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
g239	LVLLHHNGKSGNAHRKQKEIRFVHCRSDVFLCYYSIGIPAVRSATRKTALLALGLAAIS					
	70	80	90	100	110	120
m239.pep	130	140	150	160	170	180
	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
g239	ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
m239.pep	190	200	210	220	230	240
	RRHMTGNTAPTSSSRLIKMRRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
g239	RRHMTGNTAPTSSSRLIKMRRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
m239.pep	250					
	ATMARAIRRLNRSSPX					
g239	ATMARTIWRNLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

a239.seq  
 1 ATGCTCCACC ATAAAGGTAT TGCCCGAAAC CGGCGGATGG AGGTTTGTG  
 51 TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC  
 101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTCCT GTTTTTCGC  
 151 CTTATCCAAA GCTGTGAAGT TGAGCCTGTA CTGGTTTTCG TGCAATCACA  
 201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG  
 251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCGG TATCGGACCG  
 301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC  
 351 GGCAATTTCG GCCTCACCCG GCTTTAATGC CCTGCCCGCG ATTTTCAGGG  
 401 GCGGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCAGCG CGGCAGGGG  
 451 GCGGTGTGCG AATATTTTTC GACAACTGC TTCACAATGC GGTCTTCCAA  
 501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA  
 551 TGACCTGCGG CAATACTGCC CCTACTTCTT CAAGCTCGCG GTTAATAAAG  
 601 ATGCGGATTG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG  
 651 AGTACGGACG TTTGTGCCA CGATCTGCGC CAGCTGCGG GTTGATCGA  
 701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CTGGCGGCTA  
 751 AACCCTCTT CACCATAA

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
  1 MLHHKGIARN RRMEVLFFCR RPDRFVVRQT RLLQPHLR II LLQGDFLFFR
  51 LIQSCEVEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
 101 AVRSATRKTAL LALGLAAIS ASPGFNALPA IFRGGSGKSA SLTAAQRGRG
 151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
 201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIIGLSARC ATMARAIWRL
 251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

	10	20	30	40	50	60
m239.pep	MLHHKGXARNRXMEVLFFCRRPDRFVVRQT	RLLQPHLR	II	LLQGDFLFFR	LIQSCEIEPV	
a239	MLHHKGIARNRRMEVLFFCRRPDRFVVRQT	RLLQPHLR	II	LLQGDFLFFR	LIQSCEVEPV	
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDV	FLCDCSGIGPAVRSATRKTALLALGLAAIS				
a239	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDV	FLCDCSGIGPAVRSATRKTALLALGLAAIS				
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGFNALPTIFRGSSGKSASLTAAQRGRG	ACCEYFLTNCFTMRSSNEWKAMTAKRPPSF				
a239	ASPGFNALPAIFRGSSGKSASLTAAQRGRG	ACCEYFLTNCFTMRSSNEWKAMTAKRPPSF				
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAG	GSCPRSRVRTFCATICASLRVVSIIGLSARC				
a239	RRHMTGNTAPTSSSSRLIKMRIAWKVRVAG	GSCPRSRVRTFCATICASLRVVSIIGLSARC				
	190	200	210	220	230	240
	250					
m239.pep	ATMARAIIRRLNRSSPX					
a239	ATMARAIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
  1 atgatagaag tcatacatatt cttcggcgcc gaaacgcgca gacagtttgc
  51 ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
 101 gggtaaacat gggatatcat gcgcacggga gacggtccga tttataagg
 151 ctgcgtattc agccgttcgt tcaaatcggg ttgcccgcga tccaatgcct
 201 tcgcaatcac gaacggtttg attgccgaac caggttcgat catatcggtt
 251 acggcacggt tgcgcgcgtg ttcgctgtct gcccggccgg gtctgttggg
 301 atcgtaggcg ggcgtatttg ccaaggcgag gatttcccc gtgcgggcgt
 351 ccaaaaccac caccgttcgg gcttttgctt gatggtattc gaccgccttg
 401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
 451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagctgt
 501 ccacaatatt gccctgccgg tcccgcacaa caacttcgcg gccgtcttcg
 551 ccatacaggc tgtcttcaag cgaaagtcc aaaccttcct gacctttgce
 601 gtcaatatcg gtaaatccga tgacgtgtgc aaacagggtg cccatcgggt
 651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
  1 MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
  51 LRIQPFVQIG FARIQCLRNH ERFDCTRFD HIGYGTVAPL FAVCPAGSVG
 101 IVGGRIGQGE DFPRAGIQNH HRSGFCLMVF DRLVQLFIGQ GLNPLIEGKD
 151 DVFAVLRCFI ARGVQAVHNI ALPVPQNNFR AVFAIQAVFK RKFQTFLTFA
```

550

201 VNIGKSDDVC KQVAHRVMAF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

m240.seq

```

1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
151 CGTATTACAG CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 ArACCACCAC CGTTCGGGCT TTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGCTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 902; ORF 240&gt;:

m240.pep

```

1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51 RIQPFVQIGF ARIQCLRNHK RFD CRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIQGED FPRAGIQXHH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFXA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFTFLTFVAV
201 NIGKSDDVCK QVAHRVMAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

m240/g240

	10	20	30	40	50	59
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMG I-AHGRRSDFIRLRIQPFVQIG					
	:     :     :     :     :     :					
g240	MIEVIHFFGAETRRQFACADVGRFLHNAAH IQRGVNMG IIAHGRRSDFIRLRIQPFVQIG					
	10	20	30	40	50	60
	60	70	80	90	100	119
m240.pep	FARIQCLRNH KRFD CRTGFDH IGYGTVAPLF AVCPAGPVGI VGGRIQGED FPRAGIQXH					
	:     :     :     :     :     :					
g240	FARIQCLRNH RFD CRTGFDH IGYGTVAPLF AVCPAGSVGI VGGRIQGED FPRAGIQNH					
	70	80	90	100	110	120
	120	130	140	150	160	179
m240.pep	HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFR					
	:     :     :     :     :     :					
g240	HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVLRCFIARGVQAVHNIALPVPQNNFR					
	130	140	150	160	170	180
	180	190	200	210	220	
m240.pep	AVFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
	:     :     :     :     :     :					
g240	AVFAIQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAF					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 903>:

a240.seq

```

1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
151 CGTATTACAG CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG

```

551

```

251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
  1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
  51 RIQPFVQIGF ARIQCLRNHK RFDCRTGFDH IGYGTVAPLF AVCPAGPVGI
 101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
 151 VFAVFRGFIA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTLTFAV
 201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH	IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF				
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH	IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF				
	10	20	30	40	50	60
m240.pep	ARIQCLRNHHRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXHH					
a240	ARIQCLRNHHRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQNH					
	70	80	90	100	110	120
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFRA					
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFIARGVQAVHNIALPVPQNDFRA					
	130	140	150	160	170	180
m240.pep	VFAMQAVFKRKFTLTFAVNIGKSDDVCKQVAHRVMAFX					
a240	VFAMQAVFKRKFTLTFAVNIGKSDDVCKQVAHRVMAFX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
  1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
  51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
 101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
 151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
 201 CAATACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
 251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
 301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
 351 AACCACCAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
 401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
 451 GTCTTTGCCG TTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
 501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
 551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
 601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCC ATCGGGTAAT
 651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
  1 MPTRPTRAAN PPTPTWLQT AYCPRPYRP PSVQTHPHE PASSTCAAKS

```

```

51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVVMTVR
101 TVDMTVCDFL IGCIAHAFNR SPKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)

```

1  ..CGGCAATCAG TGGTGGTGAT GACCGTGCGG GCCGTGGACA TGACCGTGTG
51  CGATTTCCTC ATCGGATGCA TCGCGCACGC TTTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCGGATCC TGCTCGCCGA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGAACG
351 CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT AACCGCCGTG CAGATACGCA
401 ATCGGTCTTT CGGTTTGTG CAAAAGCTGA TTGTTGGCAT CATACATCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGTCCTTT
501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)

```

1  ..RQSVVVMTVR AVDMTVCDFL IGCIAHAFNC SLKADFHACQ RMVAVHHRLA
51  VGNIGYTIDD NIAGFRIVGF KHHADDFNR EHARIFDQDQ LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

m241/g241

m241.pep				10	20	30
				RQSVVVMTVRAVDMTVCDFLIGCIAHAFNC		
g241	QPTYLLHPSN	KMPSETEQTL	FRRHQIPPSQ	RQSVVVMTVR	IVDMTVCDFL	IGCIAHAFNR
	70	80	90	100	110	120
m241.pep		40	50	60	70	80
		SLKADFHACQ	RMVAVHHRLA	VGNIGYTIDD	NIAGFRIVGF	KHHADDFNR
g241		EHARIFDQDQ	LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV
		130	140	150	160	170
m241.pep		100	110	120	130	140
		LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFV
g241		QKLIVGIIHL	LRIMLTERIV	GRKRHFDRIA	GILTVQRLFH	QRENAVVTAV
		190	200	210	220	230
m241.pep		160	170			
		IMQRNHGIFH	DSHICPFRNS	RLITGAFX		
g241		IMQRNHGIFC	NSHICPFRNS	RLITGAFX		
		250	260			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq

```

1  ATGCCAACAC GTCCAACTCG CGCCGCAAAG CATCCAACCC CGCCAACTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC

```

553

```

251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTGCT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTAATA CAGGCGCATT
801 CTA

```

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

```

a241.pep
1  MPTRPTRA AK HPTPTWLQT AYCPRPYPYR PSVQTHPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVVMTVR
101 TVDMTVCDLF IGCIAHTFNR SLKADFHACQ RMVAVHHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDENR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFEGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241/a241 96.0% identity in 177 aa overlap

```

m241.pep                                10      20      30
                                      RQSVVVMTVRAVDMTVCDFLIGCIAHAFNC
a241                                |||:|||||:|||||:|||||:|
QPTYLLHPSNKMPSMEQTLFRRHQIPPSQSVVVMTVRVTVDMTVCDFLIGCIAHTFNR
      70      80      90      100     110     120

m241.pep                                40      50      60      70      80      90
SLKADFHACQRMVAVHHRLAVGNIGYTIDDNIAGFRIVGFKHHADFDENREHARIFDSTDQ
a241                                |||:|||||:|||||:|||||:|||||:|
SLKADFHACQRMVAVHHRLTVGNIGYTIDDNIAGFRIVGFKHHADFDENREHARIFNTDQ
      130     140     150     160     170     180

m241.pep                                100     110     120     130     140     150
LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFEGFVQKLIVGIIHL
a241                                |||:|||||:|||||:|||||:|||||:|
LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFEGFVQKLIVGIIHL
      190     200     210     220     230     240

m241.pep                                160     170
IMQRNHGIFHDSHICPFRNSRLITGAFX
a241                                |||:|||||:|||||:|||||:|
IMQRNHGILHDSHICPFRNSRLITGAFX
      250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 911>:

```

g241-1.seq
1  ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTC AATCGGTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CCGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTT CTTGCTCTGC CGCCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 ArACCACCAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTAKTGC CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGGCCTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGTTGCCC ATCGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

554

## g241-1.pap

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYP PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPSPC RQSVVMTVR
101 TVDMTVCDFL IGCIAHAFNR SFKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

## m241-1.seq

```

1  ATGCCAACAC GTCCAACCTG CGCTGCAAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCAGC GGGAAAAATC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCGGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CGGATTTCAT TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCGA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCAGCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACACCGG AATTTTTCAC
751 GATAGCCATA TTTGTCCCTT CAGGAACAGC AGATTAAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

## m241-1.pap

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYP PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPSPC RQSVVMTVR
101 AVDMTVCDPL IGCIAHAFNC SLKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVGF KHHADDFNR EHARIFDQDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFC
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pap	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pap	QPTYLLHPSNKMMPSETEQLFRRHQIPSPCRQSVVMTVRVDMTVCDFLIGCIAHAFNC					
g241	QPTYLLHPSNKMMPSETEQLFRRHQIPSPCRQSVVMTVRTVDMTVCDFLIGCIAHAFNR					
	70	80	90	100	110	120
m241-1.pap	SLKADFHACQRMVAVHHRLAVGNIGYTIDNIAAGFRIVGFKHHADDFNREHARIFDQDQ					
g241	SFKADFHACQRMVAVHHRLAVGNIGYTIDNIAAGFRIVRFKHHTDLDFNRERARIFNTDQ					
	130	140	150	160	170	180
m241-1.pap	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFIQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pap	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

## a241-1.seq

```

1  ATGCCAACAC GTCCAACCTG CGCGCAAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```

555

```

101 AAACGCATAC ACCGCATGAA CCGGCTTCTT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAAC AAAATGCCGT CTGAAATGGA ACAAACCCCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTCCTA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1  MPTRPTRAAK HPTPTWLQT AYCPRPYP RP SVQTHTPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPS RQSVVVMTVR
101 TVDMTVCDFL IGCIHTFNR SLKADFHACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDNR EHARIFNTDQ LRILLAERIV GRKRHDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
a241	MPTRPTRAAKHPTPTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENFHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSNKMPSETEQLFRRHQIPPSCRQSVVVMTVRAVDMTVCDFLIGCIAHAFNC					
a241	QPTYLLHPSNKMPSEMEQLFRRHQIPPSCRQSVVVMTVRTVDMTVCDFLIGCIAHTFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQRMVAVHRLAVGNIGYTIDNDNIAGFRIVGFKHHADFDNREHARIFDNDQ					
a241	SLKADFHACQRMVAVHRLTVGNIGYTIDNDNIAGFRIVGFKHHADFDNREHARIFNTDQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
a241	LRILLAERIVGRKRHDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
a241	IMQRNHGILHDSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1  atgatcggcg aacttggtgt ttgttcgtg atcgagcact tcaagcaacg
51  cgctggcgcg atcgccccga aagtcgctgc ccaatttgtc gatttcgtcg
101 agcaggaaca acgggtttct tacgcctgct ttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccg cggatttcgc
201 tttcgctcg cagccgccc aaggccatac ggacatattt ccgccccggt
251 gctttggcga tggattcgcc caaagaggtt ttgccacgc ccggagggccc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt tttggacgg
351 cgaggtattc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtcggc tttggcgatg tctttgctga cgcgggattt
451 tttcttcac ggcagtcga gcagggtgct gatgtagttg cgtacgacgg

```



556

```

501  tggattcggc agacatcggc ggcattcattt tgagtttttt cagttcggac
551  aggcattttt cttccgcttc tttggtcata cccgcctttt tgatgcctgc
601  ctccaaggca tccagttcgc cgttttcgctc ttcttcgccc aattccttgt
651  gtatcgcttt aatctgttcg ttcagataat attcgcgttg ggatttttcc
701  atttggcggt tgacgcgtcc gcgtatgcgt ttttcggcct gcataatgtc
751  gagttcggat tccagctttg ccagcaggaa ttccatccgt ttgccgattt
801  cgggaatctc caaaatctgt tggcggttgc ccagtttcaa ctgcaaatgc
851  gctgcgaccg tatcggttag

```

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

g242.pep

```

1  MIGELVVLV IEHFKQRAGG IAPKVAQFV DFVEQEQRV YACFCHILQN
51  LAGHRADIGT AVPADFAFVA HAAQGHDTIF PPRCFDGF A QRGFAHARRA
101 DQTQNRTEFEL VHTFLDGEVF QNPFFDFFQA VVVGIQHQS FGDVFADAGF
151 FLPRQSEQGV DVVAYDGGFG RHRHHFEFF QFGQAFFFR FGHTRLFDAC
201 LQGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPFADFGNL QNLLALRQFQ LQMRCDRIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

m242.seq

```

1  ATGATCGGCA AACTTGTTGT TTTGTTCCGG ATCGAGCACT TCGAGCAACG
51  CGCTGGCGGG ATCGCCTCGG AAGTCGTAC CCAATTGTG GATTTCGTCG
101 AGCAGGAACA AGGGGTTTTT CACGCCGGCT TTTGCCATAT TCTGCAAAAT
151 CTTACCGGGC ATAGAGCCGA TATAGGTGCG GCGGTGTCCC CTGATTTCGC
201 TTTCTGTCGC CACGCCGCC AAAGCCATGC GGACATATTT CCGCCCCGTT
251 GCTTTGGCGA TGGATTCCGC CAAAGAGGTT TTGCCACGCG CCGGAGGGCC
301 GACCAGGCAC AGAATCGGGC CTTTGAGTTT GTCCATACGT TTTTGGACGG
351 CGAGGTATTC CAAAATCCGT TCTTTGACTT TTTCCAGGCC GTAGTGGTCC
401 GCATCCAGCA CCAGTCCGGC TTTGGCGATG TCTTTGCTGA CGCGGGATT
451 TTTCTTCCAC GGCAGCTCGA GCAAAGTGTC GATGTAGTTG CGTACGACGG
501 TGGATTCCGC AGACATCGGT GGCATCATTT TGAGCTTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCCGCTTC TTTGGTCATA CCCGCCTTTT TGATATCTGC
601 TTCCAAGGCA TCCAGTTCGC CGTTTTCGTC TTCTTCGCCC AGTTCTTTGT
651 GTATCGCTTT AATCTGTTTC TTCAGATAAT ATTCGCGCTG GGATTTTTC
701 ATTTGGCGTT TGACGCTGCC GCGTATGCGT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCCGT TTGCCGATT
801 CGGGAATTTC CAAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAATGC
851 GCTGCGACCG TATCGGTTAG

```

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

m242.pep

```

1  MIGKLVLVLF IEHFEQRAGG IASEVVTQFV DFVEQEQGVF HAGFCHILQN
51  LTGHRADIGA AVSPDFAFVA HAAQSHADIF PPRCFDGF A QRGFAHARRA
101 DQAQNRAREF VHTFLDGEVF QNPFFDFFQA VVVGIQHQS FGDVFADAGF
151 FLPRQLEQSV DVVAYDGGFR RHRWHHFELF QFGQAFFFR FGHTRLFDIC
201 FQGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPFADFGNF QNLLALRQFQ LQMRCDRIG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

m242/g24290.3% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVLVLFIEHFEQRAGGIASEVVTQFVDFVEQEQGVFHAGFCHILQNLTGHRADIGA					
	:          :      :  :          :       :     :					
g242	MIGELVVLVLFIEHFKQRAGGIAPKVAQFVDFVEQEQRVSYACFCHILQNLGHRADIGT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGFQARGFAHARRADQAQNRAREFVHTFLDGEVF					
	:     :     :     :     :     :     :     :     :     :     :					
g242	AVPADFAFVAHAAQGHDTIFPPRCFGDGFQARGFAHARRADQTQNRTEFELVHTFLDGEVF					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m242.pep	QNPFDFFFQAVVVGIIHQSGFGDVADAGFFLPRQLEQSVDDVAYDGGFRRHRWHHFELF					
g242	QNPFDFFFQAVVVGIIHQSGFGDVADAGFFLPRQSEQGVDDVAYDGGFGRHRHRHFEFF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m242.pep	QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS					
g242	QFGQAFFFRFFGHTRLFDACLQGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS					
	190	200	210	220	230	240
	250	260	270	280	290	
m242.pep	AYAFFGLHNVEFGFQLCQEQEFHPFADFGNLFQNLALRQFQLQMRCDRIGX					
g242	AYAFFGLHNVEFGFQLCQEQEFHPFADFGNLFQNLALRQFQLQMRCDRIGX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 921>:

a242.seq	1	ATGATCGGCG	AAC TTGTGT	TTTGCTCGGG	ATCAAGCACT	TCGAGCAACG
	51	CGCTGGCGGG	ATCGCCCCG	AAGTCGCTAN	CCAATTGTG	GATTTCGTCG
	101	AGCAGGAACA	ATGGGTTTT	TACGCCGGCT	TTTGCCATAT	TCTGCAAAAT
	151	CTTACCGGGC	ATGAGGCCGA	TATAGGTGCG	GCGGTGTCCC	CGGATTCGCG
	201	TTTCGTCGCG	CACGCCGCC	AAAGCCATGC	GGACATATT	CCGCCCGGTT
	251	GCTTTGGCGA	TGGATTCCGC	CAAAGAGGTT	TTGCCACGC	CTGGAGGGCC
	301	GACCAGGCAC	AGAATCGGGC	CTTGAGTTT	GTCCATACGT	TTTTGGACGG
	351	CGAGGTATTC	CAAATCCGT	TCTTGACTT	TTTCCAGGCC	GATGTGGTCG
	401	GTATCCAGCA	CCAATCCGGC	TTTGGCGATG	TCTTTGCTGA	CGCGGGATTT
	451	TTTCTTCAC	GGCAGTTCGA	GCAGGGTGTC	GATGTAGTTG	CGTACGACGG
	501	TGGATTCGGC	AGACATCGGC	GGCATCATTT	TGAGCTTTT	CAGTTCGGAC
	551	AGGCATTTT	CTTCCGCTTC	TTTGGTCATA	CCCGCCTTT	TGATATCTGC
	601	TTCCAAGGCA	TCCAGTTCGC	CGTTTTCGTC	TTCTTCGCC	AGTTCTTTGT
	651	GTATCGCTTT	AATCTGTTTC	TTTCAATAAT	ATTCGCGCTG	GGATTTTTC
	701	ATTTGGCGTT	TGACGCGTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
	751	GAGTTCGGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TTGCCGATT
	801	CGGGAATTTC	CAAAATCTGT	TGGCGTTGCG	CCAGTTTCAA	CTGCAATGC
	851	GCTGCGACCG	TATCGGTTAG			

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

a242.pep	1	MIGELVLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQWVF	YAGFCHILQN
	51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHAWRA
	101	DQAQNRAFEF	VHTFLDGEVF	QNPFDFFFQA	VVVGIIHQSG	FGDVADAGF
	151	FLPRQFEQGV	DVVDYDGGFG	RHRHRHFELE	QFGQAFFFRF	FGHTRLFDIC
	201	FQGIQFAVFV	FFAQFFVYRF	NLFVQIIFAL	GFHHLAFDAS	AYAFFGLHNV
	251	EFQFQLCQQE	FHPFADFGNF	QNLALRQFQ	LQMRCDRIG*	

m242/a242 95.2% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVVLFIEHFEQRAGGIASEVVTFQFVDFVEQEQQVFHAGFCHILQNLTGHRADIGA					
a242	MIGELVLLGIKHFEQRAGGIAPEVAXQFVDFVEQEQQVFYAGFCHILQNLTGHRADIGA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGFAQRGFAHARRADQAQNRAFEFVHTFLDGEVF					
a242	AVSPDFAFVAHAAQSHADIFPPRCFGDGFAQRGFAHAWRADQAQNRAFEFVHTFLDGEVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m242.pep	QNPFDFFFQAVVVGIIHQSGFGDVADAGFFLPRQLEQSVDDVAYDGGFRRHRWHHFELF					

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```

a242      QNPFFDFFQAVVVGIQHSGFGDVFADAGFFLPRQFEQGVDDVAYDGGFGRHRRHHFELF
           130      140      150      160      170      180

           190      200      210      220      230      240
m242.pep  QFGQAFFFRFFFGHTRLEFDICFQGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS
           |||||||
a242      QFGQAFFFRFFFGHTRLEFDICFQGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS
           190      200      210      220      230      240

           250      260      270      280      290
m242.pep  AYAFFGLHNVEFGFQLCQQEFHFPADFNGFNLLALRQFQLQMRCDRIGX
           |||||||
a242      AYAFFGLHNVEFGFQLCQQEFHFPADFNGFNLLALRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243.seq
1  ATGGTaatcg tctGGTTGCC cgAGTTaccg CCGATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GCGGAGCCAC
151 ATCCAGCGGT TTTGACGGA ATCCAAGACG GGGGCGAACA GGTCTTCCTC
201 TTCCTGCAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCc tgCCGATGAG CTTTTGTGTT
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51  IQRFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GyGAGTGCGA CGATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGGCGAGG AAGGCGGTGC AGAGGTTGAC GCGGAGCCAC
151 ATCCAGyGGT TTTTACCGA ATCCACACG GGGGCGAAyA GGTCTTCCTC
201 TTCCTGCAA CCCGCCATAT TCAGCATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTGTGTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243.pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

```

m243/g243

           10      20      30      40      50      60
m243.pep  MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g243      MVIVWLPELPPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT
           10      20      30      40      50      60

           70      80      90      100     110
m243.pep  GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```

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70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1 ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51 CATCAGCGCG GCGAGTGCGA CGATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGCGGTGC AGAGTTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCTCT
201 TTCTTGCAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1 MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51 IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSEFL
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIOXFFFTESHT					
a243	MVIVWLPELPPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSISASDSSRITSTISSMVLPMSEFLFSSTTGAVTKSX					
	:					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSTVTLPMSEFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1 atgccgcctg aagccccgcc ggcgggttca gacggcattg ccgctttact
51 tcgatcggtt tatacgcaaa acgcgcttca ggaaataaat cagattatc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcatcgctg atggatattc
251 ggatcgagct tatcgccgcg ttaggattg atttccttga tttgcgtggc
301 atcaaacgcc tctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcatcgaa attaccgctc tgatccaaaa gcgcatttc cagataatcc
401 ttgaccggca acatttccac ggcaaaactt tgtccggcga acttggtcgt
451 atcggaatt tctgctggtt ggcggcgccg caggttttgc tcgtttgcca
501 aagcgcgag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacgggttc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgctgtgtct gttcgtcat atcgatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgccgcg
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1 MPPEARPAGS DGIAALLRSV YTONALQEQI QIIPQTPSGF LPCHRNHSRA
51 QHTVGQGITL LHHTNHGIGF LLTGHLRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQH FH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRQLILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSGYYPKIR
251 TFSRNFQQRQ EISHPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

m244.seq

m244.pcp

M244/G244

		10	20	30	40	50	60
m244 . pep		MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244		MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLPCHRNHSRAQHTVQGQITL					
		10	20	30	40	50	60
		70	80	90	100	110	120
m244 . pep		LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
		:       :   :                             :       :         :					
g244		LHHTNHGIGFLLTGHRLLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLTHFQRIE					
		70	80	90	100	110	120
		130	140	150	160	170	180
m244 . pep		IAALIQRHFQIILDRQHFGKLLSGELVRI RNFLVAAAQVLLVCQSAALLVFQLRFQL					
		:					
g244		ITALIQRHFQIILDRQHFGKLLSGELVRIGNFLVAAAQVLLVCQSAQLVFVQLRFQL					
		130	140	150	160	170	180
		190	200	210	220	230	240
m244 . pep		GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
		:           :					
g244		GNPRLQILISRLGGSFLYTVRISYCLDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
		190	200	210	220	230	240
		250	260	270			
m244 . pep		KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKXYYRRX					
		:                       :     :       :     :					
g244		KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQKPYKRX					
		250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCTT CTTTCATCAG CCCACCACGG
201 TATTGGGTTT CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTCAAAGT CATCTGCACG CCCATTTC
351 GCGCATCGAA ATTGCGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAATTC TGTCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTCCAGCTC GGCAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTGC TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTAACAACAA TTGGAATCA AATCCAGTT ATTACCGCG CAGATAAAGG
751 ACATTTTCAA GAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1  MPSEARQAGS DGIAALLRSV YTONALQEI QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLLVQVS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTONALQEI QIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244	MPSEARQAGSDGIAALLRSVYTONALQEI QIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLLVQSHLHAHFQRIE					
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244.pep	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSA-LLVFQLRFQL					
a244	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	239
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLCLFAHIVSLKTNWKS					
a244	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFT VLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	240	250	260	270		
m244.pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKKXYRRX					
a244	KSSYYPRKIRTFSRNFQQRISNSFSNPLPKKXYRRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1  atgccgcctg aagcccgcc gccgggttca gacggcattg ccgctttact
```

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```

51  tcgatcggtt  tatacgcaaa  acgcgcttca  ggaaataaat  cagattattc
101  cccagacgcc  ttcaggcttc  cttccgtgcc  accgtaacca  tagccgggcy
151  caacacacgg  teggacaggg  tataaccctt  cttcatcaca  ccaaccacgg
201  tattgggttc  ctgctcaact  gccacgcct  gcacgcctg  atggatattc
251  ggatcgagct  tatcgccgc  tttaggattg  attccctga  tttgctggc
301  atcaaacgcc  ttctgcaact  cattcaaat  catctgcaca  cccattttca
351  gcgcacgaa  attaccgctc  tgatccaaaa  gcgccatttc  cagataatcc
401  ttgaccggca  acatttccac  ggcaaaactt  tgccggcgga  acttgtgcgt
451  atcggcaatt  tcctgctggt  ggccggcgcg  caggttttgc  tcgtttgcca
501  aagcgcgag  ttgttctgt  ttcaactgcy  cttccagctc  ggcaatccgc
551  gcctgcaaat  cctcataagc  cggctcgcg  gcagcctgtt  cctgtacacc
601  gtccgcattt  cctactgtct  cgaagggttc  caccgcctcc  acattttcaa
651  ccgctctctc  actgttttgc  tgcgtgtct  gttcgtctat  atcgatcccc
701  tcaaaacaaa  ttggaatca  aaatccggtt  attaccgag  caagataagg
751  acattttcaa  gaaacttcaa  gcaaggcgag  gaaatttcac  atccgcgcgc
801  gaatacccta  ccgcaaaaac  catataaacg  gtaa

```

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

```

g244-1.pep
1  MPPEARPAGS  DGIAALLRSV  YTQNALQEI  QIIPQTSGF  LPCHRNHRSR
51  QHTVGGQITL  LHHTNHGIGF  LLTGHRHLRL  MDIRIELIAR  FRIDFLDLRG
101  IKRLQLIQS  HLHTHFQRIE  ITALIQRHF  QIILDRQHPH  GKLLSGELVR
151  IGNEFLVAAA  QVLLVCQSAQ  LFFVQLRFQL  GNPRLQILIS  RLGGSLFLYT
201  VRISYCLDGF  HRLHIFNRF  TVLLCLFAH  IVSLKTNWKS  KSGYPSKIR
251  TFSRNFQRQ  EISHPPNTL  PQPKYKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

```

m244-1.seq
1  ATGCCGCTCTG  AAGCCCGACA  GCGGGGTTCA  GACGGCATTG  CCGCTTTACT
51  TCGATCGGTT  TATACGCAAA  ACGCGCTTCA  GGAAATAAAT  CAGATTATTC
101  CCCAGACGCC  TTCAGGCTTC  CTCTGCGCC  ACCGTAACCA  TAGCCGGGCG
151  CAACACGCGG  TCGGACAGCG  TATAACCCTT  CTTTCATCACA  CCCACCACGG
201  TATTCGGCTC  CTGTTGCTT  GCCACGCGCT  GCATCGCCTG  ATGGATATTC
251  GGATCGAGCT  TATCGCCGCG  TTTAGGTTG  ATTTCCTTGA  TTTGCGTAGC
301  ATCAAAATGCT  TTCTGCAACT  CGTTCAAAGT  CATCTGCAGC  CCCATTTTCA
351  GCGCATCGAA  ATTGCCGCTC  TGATCCAAA  GCGCCATTTC  CAGATAATCC
401  TTGACCGGCA  GCATTTCCAC  GGCAAACCTC  TGTCCGGCGA  ACTTGTGCGT
451  ATCCGCAATT  TyCTGCTGGT  GGCGGCGCG  CAGGTTTTCG  TCGTTTGCCA
501  AAGCGCGCTG  CTCGTCTTTC  AACTGCGTTT  CCAGCTCGGC  AATCCGCGCC
551  TGCAAAATCCT  CATAAGCCGG  CTCTGCGGCA  GCCTGTTTCT  GCACACCGTC
601  CGCATTTTCT  ACTGTTTCGA  CGTTTCCAC  CGCTCCACA  TTTCAACCG
651  CTTCTTCACT  GTTTGCTGCT  TGTGCTGTT  CGCTCATATC  GTATCCCTTA
701  AAACAAATTG  GAAATCAAAA  TCCAGTTATT  ACCCGCGCAA  GATAAGGACA
751  TTTTCAAGAA  ACTTCAAKCA  AAKCAGAGA  ATTTCAAATT  CATTTTCAAA
801  TCCCTACCG  AAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

```

m244-1.pep
1  MPSEARQAGS  DGIAALLRSV  YTQNALQEI  QIIPQTSGF  LLRHRNHSRA
51  QHAVGQRITL  LHHTNHGIRL  LFACHRLHRL  MDIRIELIAR  FRVDFDLRS
101  IKCFLLVQS  HLHAHFQRIE  IAALIQRHF  QIILDRQHPH  GKLLSGELVR
151  IRNFLVAAA  QVLLVCQSAL  LVFQLRFQLG  NPRLQILISR  LCGSLFLHTV
201  RISYCFDGFH  RLHIFNREFT  VLLCLFAHI  VSLKTNWKSK  SSYYPRKIRT
251  FSRNFXQQR  ISNSFSNPLP  KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEIQIIPQTSGFLLRHRNHSRAQHAVGQRITL					
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEIQIIPQTSGFLPCHRNHRSRAQHTVGGGITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTNHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLLVQSHLHAHFQRIE					
g244-1	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120

563

	130	140	150	160	170	180
m244-1.pep	IAALIQRHFQIILDRQHFGKLLSGELVRIIRNELLVAAQVLLVCQSAALLVFQRLRFQL					
g244-1	ITALIQRHFQIILDRQHFGKLLSGELVRIIRNELLVAAQVLLVCQSAQLFVFQRLRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
g244-1	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTFSRNFKQXQRISNSFSNPLPKKX					
g244-1	KSGYYPSKIRTFSRNFKQREISHPPNTLPQKPKYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

```

1  ATGCCGCTCTG AAGCCCGACA GCGGGGTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCTT CTTATCAGCG CCCACCACGG
201 TATTGGGTTT CTGTTGCGTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGCGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TCAACTGCGC CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTCG TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTAAACAAA TTGGAATCA AAATCCAGTT ATTACCGCGC CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCTA CCGAAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

```

1  MPSEARQAGS DGIAALLRSV YTONALQEQI QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLLQVQS HLHAHFQRIE IAALIQRHF QIILDRQHFG KLLSGELVR
151 IRNELLVAAA QVLLVCQSAQ LLVFQRLFQL GNPRLQILIS RLCSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFKRQ RISNSFSNPL PKK*

```

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTONALQEQIIPQTPSGFLLHHRNHSRAQHAVGQRITL					
a244-1	MPSEARQAGSDGIAALLRSVYTONALQEQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLLQVQSHLHAHFQRIE					
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLLQVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244-1.pep	IAALIQRHFQIILDRQHFGKLLSGELVRIIRNELLVAAQVLLVCQSA-LLVFQRLRFQL					
a244-1	IAALIQRHFQIILDRQHFGKLLSGELVRIIRNELLVAAQVLLVCQSAQLLVFQRLRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	230
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
a244-1	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
	180	190	200	210	220	230
	190	200	210	220	230	240



564

	240	250	260	270
m244-1.pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKKX			
a244-1	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKX			
	250	260	270	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 941>:

```

g246.seq
1  atgtacgggc ggaacggtag tactcaagcg gccgttgect tcgttttcga
51  ccagacacag cgtgcccgtt tcggcaacgg cgaagtttac gccgctcaag
101 ccgacatcgg cagtgtctgta aatatcgcg agggctttgc gggcgaatcc
151 ggtcagttgg tccacgtcgt ctgtaagcgg tgtgccgagg ttttggtgga
201 acagttcgct gacctgttct ttggttttat ggattgcggg catcacgata
251 tgggtcgggt tttcgctgc catttgacg ataaactcgc ccaagtcgct
301 ttccaccgcc ttaatgcctt ttgcttcaag ataatggttc agctcgattt
351 cttcgctgac catggatttg cctttgacca tcagcttgcc gtttttggtt
401 gtgatgatgt cgtggataat ttggcaggct tcggcagggg tttccgcccc
451 gtgtactttc acgccaact tagtcagggt ttcttccaac tgctccagca
501 gcgcgggtaa

```

This corresponds to the amino acid sequence <SEQ ID 942; ORF 246.ng>:

```

g246.pep
1  MYGRNGSTQA AVAFVFDQTQ RARFGNGEVY AAQADIGSAV NIAQGFAGES
51  GQLVHVVCXR CAEVLVEQFA DLFFGFMDCG HHDMMGRFFAC HLDDKLAQVA
101 FHRLNAFCFK IMVQLDFFAD HGFAFDHQLA VFGCDDVVDN LAGFGRGFRP
151 VYFHAQLSQV FFQLLQQRG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 943>:

```

m246.seq (partial)
1  ATGCACGGGC GGTACGGTGG TACTCAAGCG ACCGTTgCTT CGTTTTCCAC
51  CAGACACAGC GTACCTGTTT CAGCAACGGC AAAGTTTACG CCACTCAAAC
101 CGACATCGGC AGTGCTGTAA ATATCGCGCA GTGCTTTACG GGCGAAGCCG
151 GTCAGTTGGT CTACATCGTC TGTACGCGGC GTACCGAGGT TTTGGTGGAA
201 CAGTTCGCTA ACCTGTTCTT TGGTTTTGTG GATAGCAGGC ATCACGATAT
251 GGGTCGGTTT TTCGCCTGCC ATTTGGACGA TGAAGTCGCC CAAGTCGCTT
301 TCTACCGCTT TAATGCyTTT TGCTTCAAGA TAATGrTTCA GCTCGATTTC
351 CTCGCTGACC ATCGATTGTC CTTTGACCAT CAGCTTGCCG TTTTGGCTG
401 TGATGATGTC GTGGATAATT TGGCAGGCTT CGGTCGGGGT TTCTGCCCG...

```

This corresponds to the amino acid sequence <SEQ ID 944; ORF 246>:

```

m246.pep (partial)
1  MHGRYGGTQA TVAFVFHQTQ RTCFSNGKVY ATQTDIGSAV NIAQCFTGEA
51  GQLVYIVCQR RTEVLVEQFA NLFFGFVDSR HHDMMGRFFAC HLDDKLAQVA
101 FYRFNAFCFK IMXQLDFLAD HRFAFDHQLA VFGCDDVVDN LAGFGRGFCP...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 246 shows 80.0% identity over a 150 aa overlap with a predicted ORF (ORF 246.ng)

from *N. gonorrhoeae*:

m246/g246

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQTQRTCFNSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
	:    : : :        : : : : : :					
g246	MYGRNGSTQA AVAFVFDQTQ RARFGNGEVY AAQADIGSAVNIAQGFAGES GQLVHVVCXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDDKLAQVAFYRFNAFCFKIMXQLDFLAD					
	: : : : : : : : :					
g246	CAEVLVEQFADLFFGFMDCGHHDMMGRFFACHLDDKLAQVAFHRLNAFCFKIMVQLDFFAD					

565

	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAFGRGFCP					
g246	HGFAFDHQLAVFGCDDVVDNLAFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246.seq (partial)

```

1  ATGCACGGGC  GGAACGGTGG  TACTCAAGCG  ACCGTTGCCT  TCGTTTTCCT
51  CCAGACACAG  CGTACCTGTT  TCAGCAACGG  CGAAGTTCAC  GCCACTCAAA
101 CCGACATCGG  CAGTGCTGTA  AATATCGCGC  AGTGCTTAC  GGGCGAAGCC
151 GGTCAAGTGG  TCTACGTCGT  CCGTTAACGG  TGTGCCGAGG  TTTTGGTGGA
201 ACAGTTCGCT  AACCTGTTCT  TTGGTTTTAT  GGATTGCGGG  CATCACGATA
251 TGGGTCGGTT  TTTCACCTGC  CATTGGACG  ATGAACGCG  CCAAGTCGCT
301 TTCCACCGCT  TTAATGCCTT  TTGCTTCAAG  ATAATGGTTC  AGCTCGATTT
351 CCTCGCTGAC  CATCGATTG  CCTTTGACCA  TCAGCTTGCC  GTTTTGGCT
401 GTGATGATGT  CGTGGATGAT  TTCGAGGCT  TCGGCCGGTG  TTCCGCCCA
451 GTGTACTTTT  ACGCCCAACT  TGTCAGGTT  TTCTCCAGC  TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246.pep (partial)

```

1  MHGRNGGTQA  TVAFVFHQTO  RTCFSNGEVH  ATQTDIGSAV  NIAQCFTGEA
51  GQLVYVVR*R  CAEVLVEQFA  NLFFGFMDCG  HHDMMGRFFC  HLDDELAQVA
101 FHRENAFCFK  INVQLDFLAD  HRFAFDHQLA  VFGCDDVVDD  FAGFGRCFRP
151 VYFYAQLGQV  FFQLLQQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQTO RTCFSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQTO RTCFSNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHHDMMGRFFCHLDDELAQVAFHRENAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAFGRGFCP					
a246	HRFAFDHQLAVFGCDDVVDDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247.seq

```

1  atgaaacgta  aaatgctaaa  cgtaccaaag  ggcgggttatg  atggtatgaa
51  gggttttacc  attgttgaat  ttctggttgc  gggcctgctc  agtataattg
101 tcctgatagc  ggtcgtatcg  agttacttta  catcccggaa  attaaatgat
151 gtggcaaacg  agcgtcttgc  cattcaacag  gatttgcgga  atgcggcaac
201 attaattgtc  cgcgatgcaa  gaatggcggg  gagcttcggt  tgtttcaata
251 tgtccgagca  tactaaagac  gatattgttg  attcaagtaa  tcaaactcaa
301 tctaaccttg  caaaacccgg  tgccaaacaa  gaaaatcccc  ttttttcctt
351 aaaaaggagc  ggcattggata  aacaactgat  tcccgttgct  gaatccatag
401 atattaaata  tccgggtttt  atccagcgcc  ttaacgcatt  ggttttccaa
451 tacggatatc  atgatcttga  tgcgagtgtc  gagactgttg  tagtcagcag
501 ctgttccaaa  atagcaaaac  cgggtaagaa  aatatctacc  ttgcaagaag
551 caaagagtgc  attacagatt  actaatgatg  ataacaacaa  tggaaatatc

```

This corresponds to the amino acid sequence <SEQ ID 948; ORF 247.ng>:

```

1  MKRKMLNVPK GGYDGMKGFT IVEFLVAGLL SIIVLIAVVS SYFTSRKLND
51  VANERLAIQQ DLRNAATLIV RDARMAGSFG CFNMSEHTKD DIVDSSNQTD
101 SNLAKPGAKQ ENPLFLSKRS GMDKQLIPVA ESIDIKYPGF IQRLNALVFAQ
151 YGIDDLDAAS ETVVVSSCSK IAKPGKKIST LQEAKSALQI TNDDKQNGNI
201 TRQKHVVNAY AVGRFGNNEE SLRFQDLDDK GKWGNPQLLV KVKVRMDVRY
251 IYVSGCPEDE DAGKEEKFYI TNKFDKSKNA VTPAGVEVLL DSGLNAKIAA
301 SSDNSIYAYR INATIRGGNV CANRTL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 949>:

```

1      AATGAGCGTA  AATAGCTAAA  CGTwsyArAA  GGCAGTTATG  ATGGTATGAA
51     AGGTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCCTGCTC  AGTATGATTG
101    TCCTGATGGC  GGTCCGATGC  AGTTACTTCA  CATCCCCGGA  ATTAATATGAT
151    CGGGCAAACG  AGCGCTCTGC  CGCGAACAAC  GATTTGCGGA  ATGCGGCAAC
201    ATTGATTGTC  CGCGATGCGA  GAATGGCAGG  CGCGTTCGGT  TGTTTCAATA
251    TGTCCGAGCA  TCCTGCAACT  GATGTTATTC  CCGATACGAC  GCAACAAAAT
301    TCTCCTTTT  CCTTAAAAAG  GAACGGTATA  GATAAACTTA  TTCCCATAGC
351    GGAATCTTCA  AATATCAATT  ATCAGAATTT  TTTCCAGGTT  GGTAGCGCAT
401    TGATTTTTCA  ATACGGGAATC  GATGATGTTA  ATGCAAGCAC  CGCGCATACC
451    TCGTGCAGCA  GCTGTGCGCG  AATATCGAAA  CCGGGCAAGC  AAATCCCTAC
501    TTTAGAAGAT  GCAAAAAAAG  AATTGAAGAT  TCCGGATCAG  GATAAGGAGC
551    AAAATGGCAA  TATAGCCGCT  CAAAGGTCAT  TGGTCAATGC  TATGCGGGT
601    GGCAGGATTG  CCGATGAGGA  AAGTTGGTTC  CGTTCCAAT  CGATGATAA
651    GGGCAAGTGG  GGTAACTCTC  AGTTGC...

```

This corresponds to the amino acid sequence <SEQ ID 950; ORF 247>:

```

1  XRRKMLNVYXK GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51  AANERLAAQQ DLRNAATLIV RDARMAGGFG CFFNMSEHPAT DVIPTDTQON
101 SPFSLKRNGI DKLIPIAESS NINYQNFFQV GSAILFYQYGI DDVNSTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEESLF RFQLDDKGKW GNQOL....

```

Computer analysis of this amino acid sequence gave the following results:

**Homology with a predicted ORF from *N. gonorrhoeae***

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng)

from *N. gonorrhoeae*:

```

                10      20      30      40      50      60
m247.pep    XRRKMLNVXXGSYDGMKGFTIIEFLVAGLLSMIVLMAVGSSSYFTRSKRLNDAANERLAQQ
              :||| |:||||| |:||||| |:|||: | ||||| |||: ||| |
g247         MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSIIVLIAVVSSYFTRSKRLNDVANERLAIQQ
              10      20      30      40      50      60

                70      80      90            100
m247.pep    DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQNPSFSLKRNR
              ||| ||| ||| ||| |:| ||| |:: | ::| ||| |
g247         DLRNAATLIVRDARMA GSGFCFNMS EHTKDDIVDS NQTQS NLAKPG AKQENPL FSLKRS
              70      80      90      100     110     120

               110     120     130     140     150     160
m247.pep    GIDK-LPIAESSNINYQNFFQVGSALIFQYGIDDVNASTATTVSSCAAISKPGKIPT
              :|:||:|::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

[illegible]

```

a247.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTTTAC  ATTATTGAAT  TTTTGGTTGC  GGGCATGGTC  AGTATGATTG
101 TCCTGATGGC  GGTCCGATCG  AGTTACTTCA  CATCCCGTGA  ATTAATGAT
151 CGGGCAAACG  AGCGTCTTTC  CGCGCAACAG  GATTGCGGA  ATGCGGCAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGCTTCGGT  TGTTTCAATA
251 TGTCGGAGCA  TACTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAATC
301 CAACATGTCC  CTGTAAACC  CGGTGCCAAA  CAAGAAAAAT  CCCTTTTTC
351 TTTAGATGTG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAAATTGA
401 TTCCTATTGC  TGAATCCACA  GATATTAAAT  ATCCGGGTTT  TGCCAGGCT
451 CGTCCGGCAT  TGATTTTCCA  ACTCGGCATC  GATGATCTTG  ATGCGAGTGC
501 TGAGACTGTT  GTAGTCAGCA  GCTGTTCCAA  AATAGCAAAA  CCGGGTAAGA
551 AAATATCTAC  CTGTGCAAGAA  GCAAAGAGTG  CATTACAGAT  TACTAATGAT
601 GATAAACAAA  ATGGAATAT  CACCCGTCAA  AGGCATGTGG  TCAATGCCTA
651 TGCGGTGCGG  AGGATTGCCG  GTGAGGAAGT  TTTGTTCCGC  TTCCAATTGG
701 ATGATAAGGG  CAAGTGGGGT  AATCTCAGT  TGCTCGTGAA  AAAGATTAGA
751 CATATGAAAG  TGCGGTATAT  TATGTTTTCC  GACTGTCTGT  AAGATGACGA
801 TGCCGGCAAA  GAGGAAAAAT  TCAAATATAC  GGGTACATT  GACAGCTCCA
851 CAAATGCTGT  TACGCCCGCC  GGGGTGGAGT  TTTTATTGAG  TANCGGTACT
901 GATACCAAGA  TTGCCGCTTC  TTCAGACAT  CATATTATG  CTTACCGTAT
951 CGATCGGACA  ATACGCGGGG  GAATGTATG  CGCAACACGA  ACACTTTGA

```

a247.pep

1	MRRKMLNVPK	GNYDGMKGFT	IEFLVAGML	SMIVLMAVGS	SYFTSRKLN
51	AAANERLSAQK	DLRNAATLIV	RDARMAGGFG	CFNMSEHTKN	DIIVDPSPKQT
101	QHVPVKPAQK	QENPLFSLEW	ANTNTNNNT	AKLIPIAEST	DIKYPGFAQA
151	RPALIFQYGI	DDLDAEAETV	VVSSCSKIAK	PGKKISTLQE	AKSALQITND
201	DKQNGNITRQ	RHVYVNAVYG	RIAGEEGLFR	FQSLDDKGKWG	NPQLLVKKIR
251	HKMKVRYIYS	DCPEDDDAGK	EEKFYKTGTF	DSSTNAVPTA	GVEVLLSXGT
301	DTKIAASDNN	HIYAYRIDAT	IRGNVCNAR	TL*	

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTTIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAAANERLAAQQ					
		:	:	:	:	:
a247	MRRKMLNVPKGNYDGMKGFTTIEFLVAGMLSMIVLMAVGSSYFTSRKLNDAAANERLSAQQ					
	10	20	30	40	50	60
	70	80	90		100	
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQONSPPFSLK-					
				:		:
a247	DLRNAATLIVRDARMAGGFGCFNMSEHTKNDIIVDPSKQTHVPVKPGAKQENPLFSLEW					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	-----RNGIDKLIPIAESSNINYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAIISK					
	:		:	:	:	
a247	ANTNNTNNNTAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLDASETVVVSSCSKIAK					
	130	140	150	160	170	180

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	170	180	190	200	210	220
m247.pep	PGKQIPTLED	AKKELKIPDQ	KEQNGNIARQ	RHVVNAYAVG	RIADEESLFR	QQLDDKGKW
	:	::  :	: :	:		:
a247	PGKKISTLQ	EAKSALQIT	NDDK-QNGN	ITRQ	RHVVNAYAVG	RIAGEEGLFR
	190	200	210	220	230	
m247.pep	GNPQL					
a247	GNPQLLVKK	IRHMKVRYI	YVSDCPEDD	DAGKEEKFKY	TGTFDSSTNA	VTPAGVEVLLS
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

g247-1.seq (partial) ..

```

1   CCCGGTGCCA AACAGAAAA TCCCTTTT TCCTAAAAA GGAGCGGCAT
51  GGATAAACAA CTGATTCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101 GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151 CTTGATGCGA GTGCTGAGAC TGTGTAGTC AGCAGCTGTT CCAAAATAGC
201 AAAACCGGGT AAGAAAATAT CTACCTTGCA AGAAGCAAAG AGTGCAATTAC
251 AGATTACTAA TGATGATAA CAAAATGGAA ATATCACCCG TCAGAAACAT
301 GTGGTCAATG CCTATGCGGT CGGCAGGTTT GGCAATAATG AGGAAAGTTT
351 GTTCCGCTTC CAATTGGATG ATAAGGGCAA GTGGGGTAAT CCTCAGTTGC
401 TCGTGAAGAA GGTTAAACGT ATGGATGTGC GGTATATTTA TGTTCCGGT
451 TGTCCTGAAG ATGAAGATGC CGGCAAGAG GAAAAATCA GATATACGAA
501 TAAATTCGAC AAATCCAAA ATGCTGTAC GCCTGCCGG GTGGAGGTTT
551 TATTGGTAG CCGCCTTAAT GCCAAGATTG CCGCTTCTC AGACAATAGT
601 ATTTATGCTT ACCGTATCAA TGCACAAAT CGCGGGGAA ATGTATGCGC
651 AAACAGAAC CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

g247-1.pep (partial) ..

```

1   PGAKQENPLF SLKRSMDKQ LIPVAESIDI KYPGFIQRLN ALVFQYGIDD
51  LDASAETVVV SSCSKIAPG KISTLQEA SALQITNDDK QNGNITRQKH
101 VVNAYAVGRF GNNEESLFR QLDDKGKWN PQLLVKKVKR MDVRYIYVSG
151 CPEDEDAGKE EKFRYTNKFD KSKNAVTPAG VEVLLDGLN AKIAASSDNS
201 IYAYRINATI RGGNVCANRT L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

m247-1.seq

```

1   ATGAGACGTA AAATGCTAAA CGTACCAAAA GGCAGTTATG ATGGTATGAA
51  AGGTTTACC ATTATTGAAT TTTTGGTTGC GGGCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCCGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAACAG AGCGTCTTGC CGCGCAACAG GATTGCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTTCAATA
251 TGTCGAGCA TCCTGCAACT GATGTTATC CCGATACGAC GCAACAAAT
301 TCTCCTTTT CCTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTCA ATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTCAGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AGGTTTGTTT CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAACTCTC AGTTGCTCGT GAAAAAGTT AGACATATGA
701 AAGTGCGGTA TATCTATGTT TCCGGCTGTC CTGAAGATGA CGATGCCGGC
751 AAAGAGGAAA CATTCAAATA TACGGATAAA TTCGACAGCG CCCAAAATGC
801 TGTTACGCCC GCCGGGTGG AGGTTTATT GAGTAGCGGT ACTGATACCA
851 AGATTGCCGC TTCTTCAGAC AATCATATT ATGCTTACCG TATCGATGCG
901 ACAATACGCG GGGGAAATGT ATGCGCAAAC AGAACACTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

m247-1.pep

```

1   MRRKMLNVPK GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLN
51  AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPDTTQON
101 SPFSLKRNIGI DKLPIAESS NINYQNFFQV GSALIFYQYI DDVNASTATT
151 VVSSCAAIK PGKQIPTLED AKKELKIPDQ KEQNGNIAR QRVVNAYAV
201 GRIDEDEGLF RFQLDDKGKW GNPQLLVKKV RHMKVRYIYV SGCPEDDDAG
251 KEETFYTKD FDSAQNAVTP AGVEVLLSSG TDTKIAASSD NHIIYAYRIDA
301 TIRGGNVCAN RTL*

```

569

m247-1 / g247-1 72.1% identity in 222 aa overlap

	70	80	90	100	110	120
m247-1.pep	NAATLIVRDARMAGGFGCFNMSEHPATDVIPTDQQNSPFLKRNIGDK-LIPIAESSNI					
				:   :	:   :	:     :
g247-1	PGAKQENPLFSLKRSMDKQLIPVAESIDI					
				10	20	30
	130	140	150	160	170	180
m247-1.pep	NYQNFFQVGSALIFQYIGDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDK					
	:  :  :	:  :  :	:  :  :	:  :  :	:  :  :	:  :  :
g247-1	KYPGFIQRLNALVFQYIGDDLDASAETVVVSSCSKIAKPGKKISTLQEAKSALQITNDDK					
	40	50	60	70	80	90
	190	200	210	220	230	240
m247-1.pep	EQNGNIARQRHVVNAYAVGRIAD-EEGLFRFQLDDKGKGNPQLLVKKVRHMKVRYIYVS					
	:  :	:  :	:  :	:  :	:  :	:  :
g247-1	-QNGNITRQKHVVNAYAVGRFNGNEESLFRFQLDDKGKGNPQLLVKKVRMDVRYIYVS					
	100	110	120	130	140	
	250	260	270	280	290	300
m247-1.pep	GCPEDDDAGKEETFKYTDKFDQAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDAT					
	:  :	:  :	:  :	:  :	:  :	:  :
g247-1	GCPEDDDAGKEEFKRYTNKFDKSKNAVTPAGVEVLLSGLNAKIAASSDNSIYAYRINAT					
	150	160	170	180	190	200
	310					
m247-1.pep	IRGGNVCANRTLX					
	:  :					
g247-1	IRGGNVCANRTLX					
	210	220				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

a247-1.seq (partial)

```

1  AATAATACAG CTAAATTGAT TCCTATTGCT GAATCCACAG ATATTAAATA
51  TCCGGGTTTT GCCCAGGCTC GTCCGGCATT GATTTTCCAA TACGGCATCG
101 ATGATCTTGA TGCGAGTGCT GAGACTGTTG TAGTCAGCAG CTGTTCCAAA
151 ATAGCAAAAC CGGGTAAGAA AATATCTACC TTGCAAGAAG CAAAGAGTGC
201 ATTACAGATT ACTAATGATG ATAAACAAAA TGGAATATC ACCCGTCAAA
251 GGCATGTGGT CAATGCCTAT GCGGTCGGCA GGATTGCCGG TGAGGAAGGT
301 TTGTTCCGCT TCCAATTGGA TGATAAGGCG AAGTGGGGTA ATCCTCAGTT
351 GCTCGTGAAA AAGATTAGAC ATATGAAAGT GCGGTATATC TATGTTCCG
401 ACTGTCCTGA AGATGACGAT GCCGGCAAAG AGGAAAAATT CAAATATACG
451 GGTACATTCG ACAGCTCCAC AAATGCTGTT ACGCCCGCCG GGGTGGAGGT
501 TTTATTGAGT AGCGGTACTG ATACCAAGAT TGCCGCTTCT TCAGACAATC
551 ATATTTATGC TTACCGTATC GATGCGACAA TACGCGGGGG AAATGTATGC
601 GCAAACAGAA CACTTTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 958; ORF 247-1.a&gt;:

a247-1.pep (partial) ..

```

1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLDAEA ETVVVSSCSK
51  IAKPGKIST LQEAKSALQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQLDDKG KWGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEFKYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIYAYRI DATIRGGNVC
201 ANRTL*

```

m247-1 / a247-1 80.6% identity in 206 aa overlap

				10	20	30
a247-1.pep	NNTAKLIPIAESTDIKYPGFAQARPALIFQ					
				:   :	:   :	:     :
m247-1	GFGCFNMSEHPATDVIPTDQQNSPFLKRNIGDKLIPIAESSNINYNQFFQVGSALIFQ					
	80	90	100	110	120	130
	40	50	60	70	80	89
a247-1.pep	YGIDDLDAEAETVVVSSCSKIAKPGKKISTLQEAKSALQITNDDK-QNGNITRQRHVVNA					
	:  :	:  :	:  :	:  :	:  :	:  :
m247-1	YGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVNA					
	140	150	160	170	180	190
	90	100	110	120	130	149
a247-1.pep	YAVGRIAGEEGLFRFQLDDKGKGNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKY					
	:  :	:  :	:  :	:  :	:  :	:  :

```
g248.seq
1  atgcgcaaac agaacacttt gacaggaatc ccgacttctg acggacagag
51  ggggctcgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgcgcccagc tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggctttgcg
201 ggagggcgaa ttccaggttt tggatttggg atatgtctcg gacagtaagg
251 ttacgttttag cgaaaactgt gaaaaaggtc tgtgtaccgc actgtaatgg
301 cggacaataa ataattgtag tgaaggagct ttggcaata tctgtgtgca
351 aggcaagccc gcggttgagg cggtgaaacg ttcttgccct gcaaagtcctg
401 gcaaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aaaggcgctg caggcgctag caaaatgccg cgctatatta tcgaatatatt
501 aggcgtgaag aacggacaaa atgtttatcg ggttactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatccttatg aggcaataat
601 gatgagcaat aa
```

g248.pep

1	MRKQNTLTGI	PTSDGQRGSA	<u>LFIVLMVMIV</u>	<u>VAFVLVTTAAQ</u>	SYNTEQRISA
51	NESDRKLALS	LAEAALREGE	<u>FQVLIDLEYAA</u>	DSKVTFSENC	EKGLCTAVNV
101	RTNNNGSEEA	FGNIVVQGKP	AVEAVKRSCP	AKSGKNSTDL	CIDNKGMEYN
151	KGAAGVSKMP	RYIIEYLGVK	NGQNVYRVTA	KAWGKNANTV	VVLQSYVGNN
201	DEQ*				

```
m248.seq (partial)
1      .GGGTTTGCAC TGTTAATCGT GCTGATGGTG ATxATCGTCG TGGCT.TyWT
51     gWtTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTkCCA
101    ACgAAATCAGa CAGGAaATtG GCTwTGTCTT TGGCCGAGkC GkCtWTGCGG
151    GAAGGCGGAaC TTCAGGTTTT GGAATTGGAA TATGATACCG ACAGTAAGGT
201    TACACTTAgC GAAAActGTG GAAAAGGTCT GTsTGCCGCA GTGAATGTGC
251    GGACAaATAA TGATAATGAa GAGGCTTTTG ACAATATCGT GGTGCAAGGC
301    AAGCCCACCG TTAGGCGCGT GAAGCGTCTT TGCCCTGCAa ATTCTACCGA
351    CCTGTGCATt GACAAGAAAG GGWtGGAATA TAAGAAAGCG ACGAGAAGCG
401    TCac.AAAAt GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGaACCGa
451    GAAaATGTtTt ATCGGGTTAC TGCCaAGGCT TGGGGTAAGA ATGCCAAATAC
501    CGTGGTCTGtC CTTCAATCTT ATGTAAGCAa TAATGATGAG TAA
```

```
m248.pep (partial)
  1  ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISXNESDRKL AXSLAEXXXR
51  EGELQVLdle YDTSKVTfTS ENCGKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS CFANSTDLCI DKKGXeyKKG TRSVTKMPRY IIEYLGvXNG
151 ENVYRVtAKA WGNKNTVVVV LQSYVSNNDE *
```

m248.pep

GFALLIVLMVXIVVAFXXVTAQAQSYNTEQRISXNESDRKLAXS

10 20 30 40

: :

```

g248      MRKQNTLTGIPTSDGQRGSALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS
           10          20          30          40          50          60

           50          60          70          80          90          100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCCKGLXAAVNVRTNND-NEEAFDNIVVQGKP
           |||  |||:||||| : ||||| ||| : |||||: : ||| |||||
g248      LAEAAALREGEFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNNGSEEAFGNIVVQGKP
           70          80          90          100          110          120

           110          120          130          140          150
m248.pep  TVEAVKRSCPA----NSTDLCIDKKGXEYKKGTRSVTKMPRYII EYLGVMXNGENVYRVTA
           : ||||| ||| |||||: || ||:|: |: ||||| ||||| : |||||
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYII EYLGVMXNGQNVYRVTA
           130          140          150          160          170          180

160          170          180
m248.pep  KAWGKNANTVVVLQSYVSNNDEX
           ||||| ||||| |||||: |||
g248      KAWGKNANTVVVLQSYVGNNDBQX
           190          200

```

```

a248.seq
1  ATGCGCAAAC  AGAACACTTT  GACGGGAATC  CCGACTTCTG  ACGGACAGAG
51  GGGGTTTGCA  CTGTTTATCG  TGCTGATGGT  GATGATCGTC  GTGGCTTTTT
101  TGGTGTATAA  TCGCCGCGCA  TCTTACAATA  CCGAGCAGCG  GTTCAGTGCC
151  AACGAATCAG  ACAGGAAATT  GGCTTTGTCT  TTGGCCGAGG  CGGCTTTGCG
201  GGAAGCGCAA  CTTCAAGTTT  TGGATTTCGA  ATATGATACG  GACAGTAAGG
251  TTACATTTAG  CGAAAACGTG  GGAAAAGGTC  TGTGTACCCG  AGTGAATGTG
301  CGGACAAATA  ATGATAATGA  AGAGGCTTTT  GACATATATC  TTGGTGCAAG
351  CAAGCCCAAC  GTTGAGCGCG  TGAAGCGTTC  TTGCACTGCA  AAATCTACAG
401  GCCTGTGCAT  TGACAATAAA  GGGATGGAAT  ATAAGAAAGC  CACGCAAAGC
451  GTCACAAAAA  TGCCACGTTA  TATTATCGAA  TATTTTGGCG  TAAAGCAACG
501  AGAAAATGTT  TATCGGGTTA  CTGCCAAGGC  TTGGGTAAAG  GTAGGCAATA
551  CCGTGGTCGT  CCTTCAATCT  TATGTAAGCA  ATAATGATGA  GTAA

```

a248.pep

1	MRKQNTLTGI	PTSDGQRGFA	LFIVLMVMIV	VAFLVVTAAQ	SYNTEQRISA
51	NESDRKLALS	LAEEALRPE	LQVLDDLEYDT	DSKVTFSENC	GKGLCTAVNV
101	RTNNDNEEAF	DNIVVQKGKT	VEAVKRSCTA	KSTGLCIDNK	GMEYKKGTS
151	VSKMPRYIIE	YLGVKNGENV	YRVTAKAWGK	NANTVVVLQS	YVSNND*

[illegible]



572

|||||  
a248 NANTVVVLQSYVSNNDX  
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq  
1 ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG  
51 GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTTT  
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC  
151 AACGAATCAG ACAGGAAAT GGCCTTGTCT TTGGCCGAGG CGGCTTTGCG  
201 GGAAGGCGAA CTTCAAGTTT TGGATTGGA ATATGATACG GACAGTAAGG  
251 TTACATTTAG CGAAACTGT GGAAGAGGTC TGTGTGCCGC AGTGAATGTG  
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG  
351 CAAGCCACCC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG  
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC  
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG  
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA  
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep  
1 MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFLVVTAQ SYNTEQRISA  
51 NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV  
101 RTNNDNEEAF DNIVVQKPT VEAVKRSCPA NSTDLCDKK GMEYKKGTRS  
151 VSKMPRIIE YLGVKNGENV YRVTAWGWK NANTVVVLQS YVSNND\*

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRG	FALFIVLMVMIVVAFLVV	TAAQSYNTEQRISANES	DRKLALS		
g248	MRKQNTLTGIPTSDGQRG	SALFIVLMVMIVVAFLVV	TAAQSYNTEQRISANES	DRKLALS		
	10	20	30	40	50	60
m248-1.pep	LAEALREGE	LQVLDLEYDTDSKVTFSENC	GKGLCAAVNV	RTNND-NEEAF	DNIVVQKPT	
g248	LAEALREGE	FQVLDLEYAADS	SKVTFSENCEKGLCTAVNV	RTNNGSEAF	GNIVVQKPT	
	70	80	90	100	110	119
m248-1.pep						
g248						
	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA	----NSTDLCDKKGMEYKKG	TRSVSKMPRIIEYLGVKNGENV	YRVTA		
g248	AVEAVKRSCPA	SKGNSTDLCDNKGMEYKKAAGV	VSKMPRIIEYLGVKNGQNV	YRVTA		
	130	140	150	160	170	180
m248-1.pep	180	190				
g248	KAWGKNANTVVVLQSYVSNNDX					
	190	200				

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRG	FALFIVLMVMIVVAFLVV	TAAQSYNTEQRISANES	DRKLALS		
a248	MRKQNTLTGIPTSDGQRG	FALFIVLMVMIVVAFLVV	TAAQSYNTEQRISANES	DRKLALS		
	10	20	30	40	50	60
m248-1.pep	LAEALREGE	LQVLDLEYDTDSKVTFSENC	GKGLCAAVNV	RTNNDNEEAF	DNIVVQKPT	
a248	LAEALREGE	LQVLDLEYDTDSKVTFSENC	GKGLCTAVNV	RTNNDNEEAF	DNIVVQKPT	
	70	80	90	100	110	120
m248-1.pep						
a248						
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDLCD	KKGMEYKKGTRSVSKMPRIIEYLGVKNGENV	YRVTAWGWK			
a248	VEAVKRSCPA	STLCLDNKGMEYKKGTSVSKMPRIIEYLGVKNGENV	YRVTAWGWK			
	130	140	150	160	170	180



```

g249      MKNNNDCLRLKNPQSGMALIEVLVAMLVLTTIGILALLSVQLRTVASVREAEQTIVTSQITQ
              10          20          30          40          50          60

              70          80          90         100         110         120
m249.pep  XLMEGMLMNPPTIDSDSNKKNYNLYMGNHTLTSAVDGDFDAIDAMKTGQLAEAQLKRFSYEL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      NLMEGMLMNPPTIDLDSNKKNYSLSYMGKQTLTSAVDGEFMDLAEKSQAQLAEEOQLKRFSHEL
              70          80          90         100         110         120

              130         140         150         160         170         179
m249.pep  KNALPDAAAIHYAVCKDSSGNAPTLSGN-APSSNCNDKANGDTLIKVLWVNDSAGDSDIS
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      KNALPDVAIHYAVCKDSSGDAPTLSDSGAFSSNCNDKANGDTLIKVLWVNDSAGDSDIS
              130         140         150         160         170         180

180        190        200
m249.pep  RTNLEVSGDNIVTYQARVGGREX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      RTNLEVSGDNIVTYQARVGGREX
              190        200

```

```
a249.seq
1  ATGAAGAATA  ATGATTGCTT  CCGCCTGAAA  AACCCCCAGT  CCGGTATGGC
51  GCTGATAGAA  GTCTTGCTCG  CTATGCTCGT  TCTGACCATC  GGTATTTTGG
101  CACTATTGTC  GTTTCAGTTG  CGGACAGTCG  CTTCCGTCAG  GGAGGCAGAG
151  ACGCAAACCA  TCGTCAGTCA  AATCACGCAA  AACCTGATGG  AAGGAATGTT
201  GATGAATCCG  ACCATTGATT  CGGACAGCAA  CAAGAAAAAC  TATAATCTTT
251  ACATGGGAAA  CCAATCATGCA  CTATCATGTT  TGGATGGCGA  TTTTCAGGTT
301  GATGCCATAA  AAACAAAGAC  GCAGTTGGCA  GAGGCACAAT  TGAAGAGATT
351  TAGTTATGAG  CTGAAAAAATG  CCTTGCCCGA  TCGCGGAGCC  ATCCATTACG
401  CCGTCTGCAA  GGATTGCTGC  GGTGTTGCGC  CGACATTGTC  CGCGCGGAGT
451  ACTTTTCTCT  CAAATTCGCA  TGGTAGTGCA  AATGGGGATA  CTTTGATTAA
501  AGTATTGTGG  GTAAATGATT  CGGCAGGGGA  TTCGGATATC  GCCCGTACGA
551  ATCTTGGAGC  GAACGGCAAC  AATATCGTAT  ATACCTATCA  GGC AAGGGTC
601  GGAGGTGCGG  AATGA
```

a249.pep

1	MKNNDCEFLK	NPQSGMALIE	<u>VLVAMLVLT</u>	<u>GILALLSVQL</u>	RTVASVREAE
51	QTQTSVQITQ	NLMEGMLMNP	TIDSNSKNK	YNLYMGNHHA	LSVVDGDFQV
101	DAIKTKTQLA	EAQLKFSYE	LKNALPDAAA	IHYAVCKDSS	GVAPTLSAGS
151	TFSSNCDCGA	NGDTLIKVLW	VNDSAGSDSI	ARTNLETNGN	NIVYTYQARV
201	GGRE*				

	10	20	30	40	50	60
m249.pep	MKNNDCFR	LKDSQSGMALIEVLV	AMLVLTIGILALLSV	QLRTVXXXXXX	XXXXXXXXXXXX	XXXXXX
	:	:	:	:	:	:
a249	MKNNDCFR	LKNPQSGMALIEVLV	AMLVLTIGILALLSV	QLRTVASVREA	ETQTIVSQITQ	:
	10	20	30	40	50	60
	70	80	90	100	110	119
m249.pep	XLMEGMLN	NPITDSDSNKKNY	LYMGNH-TLSA	VDGDFDAIDAM	KTGQLAE	AQLKRF
	:	:	:	:	:	:
a249	NLMEGMLN	NPITDSDSNKKNY	LYMGNH	HALSVVDGDFQ	VDAIKTKTQ	LAE
	70	80	90	100	110	120
	120	130	140	150	160	170
m249.pep	LKNALPDA	AAIH	AVCKDSSGN	APTLS-GNA	FFSSNCN	KANGDTL
	:	:	:	:	:	:
a249	LKNALPDA	AAIH	AVCKDSSG	VAPTLSAG	STFFSSN	CDGSANG
	130	140	150	160	170	180

```

      180          190          200
m249.pep SRTNLEVSGDNIIVYTYQARVGGREX
           :|:|||::||:|||||
a249     ARTNLETNGNNIIVYTYQARVGGREX
           190          200

```

m249-1.seq

1	ATGAAGAATA	ATGATTGCTT	CCGCGTGAAA	GATTCCCAGT	CCGGTATGGC
51	GCTGATAGAA	GCTCTGGTGT	CTATGCTCGT	TCTGACCATC	GGTATTTTGG
101	CACATATTGC	TGTACAGTTG	CGGACAGTCG	CTTCCGTCAG	GGAGGCGGAG
151	ACACAAACCA	TCGTCAGCCA	AATCACGCAA	AACCTGATGG	AGGGAATGTT
201	GATGAATCCG	ACCATTGATT	CGGACGCAA	CAAGAAAAAC	TATAATCTTT
251	ACATGGGAAA	CCATACATCA	TACAGTGTGG	ATGGCGATT	TGCGATTGAT
301	GCCATGAAAA	CTAAGGGGCA	ATTGGCAGAG	GCACATATCA	AGAGATTTAG
351	TTATGAGCTG	AAAATGGCTT	TGCCGGATGC	GGGACCCATC	CATTACGCCG
401	TCTGCAAGGA	TTGCTCGGGT	AACGCGGCGA	CATTGTCCGG	CAATGCTTTT
451	TCTTCAAATT	GCGACAATAA	GGCAAACGGG	GATACTTTAA	TTAAAGTATT
501	GTGGGTAAAT	GATTTCGGAG	GGGATTCGGA	TATTTCCCGT	ACGAATCTTG
551	AGGTGAGCGG	CGACAATATC	GTATATACTT	ATCAGGCAAG	GTCTGGAGGT
601	CGGGGAATGA				

m249-1.pap

1	MKNNDGFR	LK	DSQSGMALIE	<u>VLVAMLVLT</u>	<u>I</u>	GILALLSVQL	RTVASVREAE
51	TQTIVSQITQ	NLMGMLMNP	TIDSDSNKKN	YNLYMGNHTL		SAVDGDFRID	
101	AMKTKGQLAE	AQLKRFSEYL	KNALPDAAAI	HYAVCKDSSG		NAPTLSGNAF	
151	SSNCDNKANG	DTLIKVLWVN	DSAGDSDISR	TNLEVSGDNI		VYTYQARVGG	
201	RE*						

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLK	DSQSG	MALE	VLVAM	LVLTIG
g249	MKNND	CFRLK	DSQSG	MALE	VLVAM	LVLTIG
	10	20	30	40	50	60
m249-1.pep	NLM	EGMLM	NPTID	SDSN	KKNYN	LYMGN
g249	NLM	EGMLM	NPTID	SDSN	KKNYN	LYMGN
	70	80	90	100	110	120
m249-1.pep	HTLSA	VDGDF	AIDAM	KTKG	QLAEA	QLKRF
g249	HTLSA	VDGDF	AIDAM	KTKG	QLAEA	QLKRF
	70	80	90	100	110	120
m249-1.pep	KNALP	DAAAI	HYAV	CKDSS	GNAPT	LSGN-
g249	KNALP	DAAAI	HYAV	CKDSS	GNAPT	LSGN-
	130	140	150	160	170	179
m249-1.pep	AFSSN	CDNKA	NGDTL	IKVLV	WNVND	SAGDS
g249	AFSSN	CDNKA	NGDTL	IKVLV	WNVND	SAGDS
	130	140	150	160	170	180
m249-1.pep	180	190	200			
g249	180	190	200			

```
a249/ L36117
gi|643582 (L36117) prepilin leader sequence requires cleavage to be active [Pseudomonas
aeruginosa]
>gi|1161222 (L48934) involved in type 4 fimbrial biogenesis; contains pre-pilin like leader
sequence [Pseudomonas aeruginosa]
>gi|1246299 (L76605) reference L36117, L48934 [Pseudomonas aeruginosa] Length = 185
Score = 50.4 bits (118), Expect = 9e-06
Identities = 45/183 (24%), Positives = 84/183 (45%), Gaps = 26/183 (14%)

Query: 13  QSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITONLMEGMLMNPFI 72
           QSG ++IEVLVA+L+++IG+L ++++Q +T+  ++ +  + + NL+E M +P
Sbjct: 12  QSGFSMIEVLVALLISIGVLGMIAMQGKTIQYTADSVERNKAAMLGSLNLESMPASPKA 71

Query: 73  DSDSNKKNNLYLMGNHHALSVDGDFQVDAIKTKTQLAEAAA---QLKRFSYELKNALPDAA 129
```

576

D + M G A + T L +A +L ++ ++KN LP A  
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAKGSAPPTAPSSCTPLPDAIKDRLGCVAEQVKNELPGAG 126  
 Query: 130 AI---HYAVCKDSSGVAPTLASGTFSSNCDGSANGDTL-IKVLWVNDASAGDSDIARTNL 185  
 + Y +C+ S +CDG G L I++ W + A ++  
 Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSMLAIRLAWRGKQGCACVNAADSSA 172  
 Query: 186 ETN 188  
 +T+  
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLK	DSQSG	MALIE	VLVAM	LVLTIG
a249	MKNND	CFRLK	NPQSG	MALIE	VLVAM	LVLTIG
	10	20	30	40	50	60
	70	80	90	100	110	119
m249-1.pep	NLM	EGMLM	NPTID	SDSNK	KNYNL	YMGNH-
a249	NLM	EGMLM	NPTID	SDSNK	KNYNL	YMGNH-
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKN	ALPDAA	AHHY	AVCKD	SSGNAP	TLG-
a249	LKN	ALPDAA	AHHY	AVCKD	SSGVAP	TLG-
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRT	NLEV	SGDN	IVYTY	QARV	GGREX
a249	ART	NLET	NGNN	IVYTY	QARV	GGREX
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1 atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51 aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggtg
101 tgcaggcgcg gcaaaaaggt atgggcccgc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataaccttt atgattaatt
251 cgcggcatat cctgatgggg ggcggcgctt gccacgcaca tgaaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1 MHTASPRDE FIRIKESSP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51 GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRARAV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1 ATGCACACCT TCCCCGCATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51 CGCCTATGCT GATTGGGCTG CTGCCTGGG CATTAATACT CGGTATGCAG
101 GGCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCAGTAT
151 GAACTTCGCC GGCGGCTCCG AGTTTGCCAC GGTCAACCTG TGGGCSGAAC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATTCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAAAAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1 MHTPSPHNEF IRGIKESSP LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51 MNFAGGSEFA TVNLWAEPL ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*
  
```

**Homology with a predicted ORF from *N. gonorrhoeae***

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

```

              10      20      30      40      50      59
m250.pep      MHTSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGSWLEMLLMTSMNFAGGSEF
              ||:::|||||||||||||||||||||||:|||||||:|||||
g250          MHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKGMGRLEMLLMTGMNFAGGSEF
              10      20      30      40      50      60

              60      70      80      90      100     110
m250.pep      ATVNLWAEPLPILLIATVTFMINSRHI LMGGGACAPAPERNTAEKSRTVFYVX
              |||||||:|||||||||||||||||||:|||||
g250          ATVNLWAEPLPILLIATITFMINSRHI LMGGGACHAHERNTAEKSRAVFFV
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 979>:

51	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
101	AAGTTCGCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGTA
151	TGCAGGGTGG	ACAAAAAGGC	ATGAGCTGGC	TGGAATGTT	GTTGATGACC
201	GGTATGAACT	TCGCCGGCGG	CTCCGAGTTT	GCCACGGTCA	ACCTGTGGGC
251	GGAACTCTG	CCGATACTGC	TTATCGCCAC	CGTAACCTTT	ATGATTAATT
301	CTCGGCATAT	CTGATGGGG	G, CGGCAC TT	GCCCCGACC	TGAAAGAAAT
	ACCGCTGAAA	AAAGCCGTGC	CGCCTACTGTT	TTTTATGTGT	GA

This corresponds to the amino acid sequence <SEQ ID 980; ORF 250.a>:

1 MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MSWLEMLLMT  
51 GMNFAGGSEF ATVNLWAEPL PILLIATVTF MINSRHILMG XGTCPAPER  
101 TAEKSARTV FYV\*

**m250/a250** 94.6% identity in 111 aa overlap

```

m250      54.8% identity in 111 aa overlap
          10          20          30          40          50
59
m250.pep  MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLLMTSMNFAGGSEF
          |
||:|||||
a250      MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLLMTGMNFAGGSEF
          10          20          30          40          50
60

          60          70          80          90          100         110
m250.pep  ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRARTVFYVX
          |||||
a250      ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCPAPERNTAEKSRARTVFYVX
          70          80          90          100         110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 981>:

```

51  atgcctgacc caatagggat tcttttcgct gccgtcggg  ttgatttttt
    tgccgttgtt ttgagggggc gttttcaacg aaataggcgc gttggcatgt
101 tgataataat aatcctgatg qcggaggctc gaacaaaac  ggtcgtaacc

```

578

```

151 gaggttgacg ctcaggttgt ggcggatttt ggcggtatcg aaggattttt
201 tgaatgccgc ctgcaagagc ctgtggcttt ccccgtaaata caccggtcg
251 gatatttagt aggaagacgg cttgtcggca ctcgggcggc aatatttgte
301 cgaaccgtcg gcggaacagt gcgtctgctg aaaatgattg tccaaaccga
351 tgccctgccg gtcgtaagag aggcgggcat aatccgcca agtgtcttta
401 tcggcattgg tatagacata ttccaaaccg tagcggtttt tgggtgctgt
451 ctgctcgtaa aacacgcccg taccgtattc cgcgcccacc tccgcaccgt
501 tttcaccgtt ggtaatcagc ccgctgtatt tgcggcgccc cgcgtatttg
551 ccgtagcctc ttatcgatcc gtatttttta tttcatcaa aaaccgcctt
601 ggtcaggaaat gccggaaccg tcatatcgcg cgtgtcgaaa gtttgcgtcg
651 tgcgttcgag tatgccgccc atgtagtgcc gtttgttttc aaaacgaaaa
701 cccggcgga acagccacga ccggctttcg tatga

```

This corresponds to the amino acid sequence <SEQ ID 982; ORF 251.ng>:

g251.pep

```

1  MPDPGILFA AVGVDFFAVV LRGFRQIRGA VGMLIIILM AEVGTKTVVT
51  EVDAQVVADF GGIEGFECRL LQEPVAFPVN HAVGVFVGRR LVGTRAAIFV
101 RTVGGTVRLL KMIVQTDALP VVREAGIIRP SVFIGIGIDI FQTVAAFGVR
151 LVVKHARTVF RAHLRTVFTV GNQPAVFAAA RVFAVASYRS VFFIFIKNRL
201 GQECRNRHIA RVESLLRAFE YAADVVPFVF KTKTRAEQPR PAFV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

m251.seq

```

1  ATGCGTGTCTG CGGTAGTCGT AGCGCAAGCC CGCGCCGACA TCCGCCACC
51  TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTACCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACGACATTTT CCCTGCCTAT GGTGACCCAA TAGGGGCTGG
201 TTCACTGCC GTTGGGGCTG ATTTTTTTGC CGTTGTTTTC AGGGGGCGTG
251 TCTGACGAAT AGGCGCGGTT GGCATGTTGA TAATAATAAT CCTGATGGCG
301 GAGATTAGAG CCAAAGCGGT CAAACCCGAG ATTCACGCTC AGGTTGTGGC
351 GGATTTTGGC GGTATCGAAG GATTTTTTGA ATGCCGCCTG CAAGAGCCTG
401 TGGCTTTCCC CGTAAATCAC GCGATCGGAT TTGTAATAGG AAAACGGCTT
451 GTCGGCACTC GGGCGGCAAT ATTTGTCCGA ACCGTCGGCA GAACAGTGCG
501 TCTGCTGAAA ATGATTATCC AAACCGATGC CCTGCGGTC GTAAGAGAGG
551 CGGGCATAAT CCGCCCAAGT GTCTTTATCG GCATTGGTAT AGACATATTC
601 CAAACCGTAG CGGCTTTTGG TGTGCGTCTC GTCGTAACAC ACGCCCGTAC
651 CGTATTCCGC GCCCACCAGC GCACCGTTTT CGCCGTTGGT AAACAGTCCG
701 CCGTATTTGT GGTGCCCCG GTATTGCCC GTACCGGGCA AAGAACCCGC
751 CTGTTTTTTA TTGTCATCAA AAACCGCCTT GGTGAGGAAT GCCGGAACCG
801 TCATATCGCG CGTGTGAAAA GTTTGTGCG TGTGTTGAG TATGCCGCCG
851 ATGTAGTGCC GCTTATTCTC AAAACGAAAA CCCGGGCGGA ACAGCCACGA
901 CCGGCTTTTC TATGA

```

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.pep

```

1  MRAAVVVAQA RADIRPPAQT DIVPNCRVIA FTVDAARRAV RISIVAQAAD
51  LPRNDISPAY GDPGAGFTA VGADFFAVVL RGRVRRIGAV GMLIIILMA
101 EIRAKAVKPE IHAQVVADFG GIEGFFECRL QEPVAFPVNH AIGFVIGKRL
151 VGTRAAIFVR TVGRTVRLK MIIQTDALPV VREAGIIRPS VFIGIGIDIF
201 QTVAAFGVRL VVKHARTVFR AHQRTVFAVG QSAVFPVVAR VFAVTGQTR
251 LFFICIKNRL GQECRNRHIA RVESLLRVFE YAADVPLIL KTKTRAEQPR
301 PAFV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

```

                                40      50      60      70      80      90
m251.pep      TVDAARRAVRISIVAQAADLPRNDISPAYGDPGAGFTA VGADFFAVVL RGRVRRIGAVG
                                ||||  |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g251           MPDPGILFAAVGVDFFAVVLRGRFRQIRGAVG
                                10      20      30

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 985>:

This corresponds to the amino acid sequence <SEQ ID 986; ORF 251.a>:

**m251/a251 88.5% identity in 304 aa overlap**

```

a251      68.5% identity with a251
              10      20      30      40      50      60
m251.pep  MRAAVVVAQARADIRPPAQTDIVPNCRVIAFTVDAARRAVRISIVAQAADLPRNDISPAY
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      MRAAVVVAQPRADIRPPAQTDIVPNCRVIAFAVDAARRAVRISIVAQAADLPRNHISPAY
              10      20      30      40      50      60

              70      80      90      100     110     120
m251.pep  GDPIGAGETAVGADFFAVVLRGRVRRIGAVGMLIIIIILMAEIRAKAVKPEIHAQVVADFG
          :|||:  ::||:  |  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:

```



```

a251      ADPIGLVLAAVGVGGF----RGRFRRIGAVGMLIIIIILMAEIRVKAVKTEIHAQVADFG
              70              80              90              100             110

              130             140             150             160             170             180
m251.pep  GIEGFFECRLQEPVAFPNHAIGFVIGKRLVGTRAAIFVRTVGRVRLKMIQTDLAPV
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      GIEGFFECRLQEPVAFPNHAGFVVGKRLVGTRAAIFVRTVGRVRLKMIQTDALPV
              120             130             140             150             160             170

              190             200             210             220             230             240
m251.pep  VREAGIIRPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFAHQRTVFVAVGKQSAVFVVAR
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VREAGIIHPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFAHQRTVFVAVGKQTAVFVVAR
              180             190             200             210             220             230

              250             260             270             280             290             300
m251.pep  VFAVTGQRTRLFFCIKNRLGQECRNRIARVESLLRVFEYAADVPLILKTKTRAEQPR
            ||||:|:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VFVAVASYRS-VFSIFIKNRLGQECRNRIARVESLLRVFEYAADVPFVFKTKTRAEQPR
              240             250             260             270             280             290

m251.pep  PAFVX
            |||
a251      SAFVX
            300

```

g253 . req

g253.pcp

```

1 MIDRDRMLRD TLERVAGSF WLWVVVASM FTAGFSGTYL LMDNQGLNFF
51 LVLAVGLGMN TLMLAVWLAT LFLRVKVGRF FSSPATWFRG KGPVNQAVLR
101 LYADQWRQPS VRWKIGATAH SLWLCTLLGM LVSVLLLLLV RQYTFRNWEST
151 LLSNAASVRA VEMLAWLPSK LGFPVPDARA VIEGRNGNT IDARAWSGLL
201 VGSIVCYGIL PRLLAVVCK LLKTSSENGL DLEKTYQAV IRRWNQKITD
251 ADTRRETVSA VSPKIVLNDK PKWALMLETE WQDQWFEGR LAQEWLDKGV

```

m253.seq

Seq	1	ATGATTGACA	GGAACCGTAT	GCTGCGGGAG	ACGTTGGAAC	GTGTGCGTGC
51	GGGGTCGTTT	TGGTTGTGGG	TGGTGGCGGC	GACGTTTGCA	TTTTTTTACCG	
101	GTTTTTCAGT	CACTTATCTT	CTAATGGACA	ATCAGGGTCT	GAATTTCTTT	
151	TTGGTTTTTG	CGGGCGTGTG	GGGCATGAAT	ACCGTGATGC	TGGCAGTATG	
201	TGTGGCAATG	TGTTTCTCGT	GTGTGAAAGT	GGGGCGTTT	TTCAGCAGTC	
251	CGGCGACGTG	GTTTCGGGGC	AAAGACCCTG	TAAATCAGGC	GGTGTGTGGG	
301	CTGTATGCGG	ACGAGTGGCG	GCAACCTTCG	GTACGTTTGA	AAATACGGCG	
351	AACGTCGCAC	AGCCTTGTGC	TCTGCACATG	GCTCGGAATG	CTGGTGTCCG	
401	TATTTGTGCT	GCTTTTGGTG	CGGCAACATA	CGTTCAACTG	GGAAGACACG	
451	CTGTGTGACA	ATGCCGCTTC	GGTACGCGCG	GTGGAAATGT	TGGCATGGCT	
501	GCCGTCGAAA	CTCGGTTTCC	CTGTCCCCGA	TGCGCGGGCG	GTCATCGAAG	
551	GCCGTCTGAA	CGGCAATATT	GCCGATCGCG	GGGCTTGCTC	GGGGCTGGTG	
601	GTCCGCGAGT	TGCGCTGTCT	CGGCATCCCTG	CCGCGCTCTG	TGGCTTGGGT	
651	AGTGTGTAAA	ATCCTTTTGA	AAACAAGCGA	AAACGGATTG	GATTTGGAAA	
701	AGGCCATATA	TCAAGCGGTC	ATCCGCCGCT	GGCAGAACAA	AATCACCAGT	
751	GCGGATACGC	GTCGGGAAAC	CGTGTCCGCC	GTTTCACCGA	AAATCATCTT	
801	GAACGATTCG	CCGAAATGGG	CGGTATGCTT	GGAGACCGAG	TGGCAGGACG	
851	GCGAATGGTT	CGAGGGCAGG	CTGGCGCAGT	AATGGCTTGA	TGAAGGCGTT	
901	GCCACCAATC	GGGAACAGGT	TGCCGCGCTG	GAGACAGAGC	TGAAGCAGAA	
951	ACCGGCGCAA	CTGCTTATCG	GCGTGCGCGC	CCAAACTGTG	CCGGACCGCG	
1001	GCGTGTTCG	GCAGATGTTC	CGACTCTCGG	AAGCGGCGCA	GGGCGGGCGG	
1051	GTGCTGCACG	TTTGGGCGCA	ACAGGGGCTT	TCAGACGACC	TTTCGGAAAA	
1101	GCTGGAACAT	TGGCGTACCG	CGCTGBCCTA	ATGCGGCGCG	GCTTGCGCTT	
1151	AGCCTGCACG	GGCGGCGCAG	GAAGGGCGTT	TGAAAGACCA	ATAA	

m253.pep

```

1  MIDRNRMLRE TLERVRAGSF WLWVVAATFA FFTGFSVTYL LMDNQGLNFF
101  LVLAGVLGMN TLMLAVWLAM LFLRVKVGRF FSSPATWFRG KDPVNQAVLR
151  LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSULLLLLV RQYTFNWEST
201  LLSNAASVRA VEMLAWLP SK LGFPVPDARA VIEGRNLNGNI ADARAWSGLL
251  VGSIACYGIL PRL LAWVCK ILLKTSLENG DLEKPYQAV IRRWQNKITD
301  ADTRRETQVSA VSPKILNDA PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
351  ATNREQVAAL ETELKQPKAQ LILIGVRAQTV PDRGVLRQIV RLSEAAQGGGA
VQLLAEQGL SDDLSEKLEH WRNALAECGA AWLEPDRAAQ EGRLKDQ*

```

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

m253/q253

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLEVRAGSFWLVVVAATFAFFTGFVSVTYLLMDNQGLNFFLVLAVGLGMN					
	:       :                     : :   :					
g253	MIDRDRLRDLTLEVRAGSFWLVVVASMMFTAGFSGTYLMDNQGLNFFLVLAVGLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFLRVKVGRRFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
	:					
g253	TLMLAVWLATLFLRVKVGRRFSSPATWFRGKGPNQAVLRRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLNLCTLLGMLVSVLLLLLVRQYTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
g253	SLNLCTLLGMLVSVLLLLLVRQYTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
	130	140	150	160	170	180

582

	190	200	210	220	230	240
m253 . pep	VIEGR	LNGNIADAR	AWSGLLVGS	IACYGILP	RLLA	WVCKILLKTS
	VIEGR	LNGNIADAR	AWSGLLVGS	IACYGILP	RLLA	WVCKILLKTS
g253	VIEGR	LNGNIADAR	AWSGLLVGS	IACYGILP	RLLA	WVCKILLKTS
	190	200	210	220	230	240
	250	260	270	280	290	300
m253 . pep	IRR	WQNKITD	ADTRRET	VS	AVSPKII	LNDA
	IRR	WQNKITD	ADTRRET	VS	AVSPKII	LNDA
g253	IRR	WQNKITD	ADTRRET	VS	AVSPKII	LNDA
	250	260	270	280	290	300
	310	320	330	340	350	360
m253 . pep	ATN	REQVA	ALET	ELKQK	PAQLL	IGVRA
	ATN	REQVA	ALET	ELKQK	PAQLL	IGVRA
g253	AAN	REQVA	ALET	ELKQK	PAQLL	IGVRA
	310	320	330	340	350	360
	370	380	390			
m253 . pep	SDD	LSEK	LEHWR	NALAE	CGAAW	LEPDRA
	SDD	LSEK	LEHWR	NALAE	CGAAW	LEPDRA
g253	SDD	LSEK	LEHWR	NALAE	CGAAW	LEPDRA
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

```

a253.seq
1  ATGATCGACA  GGAACCGTAT  GCTGCGGGAG  ACGTTGGAAC  GTGTGCGTGC
51  GGGGTCGTTT  TGGTTGTGGG  TGGCGGCGGC  GACGTTTGCG  TTTTTCACCG
101  GTTTTTCAGT  TACTTATCTT  CTAATGGACA  ATCAGGCTCT  GAATTTCTTT
151  TTGGTTTGGG  CGGGCGTGTT  GGGCATGAAT  ACGCTGATGC  TGGCAGTATG
201  GTTGGCAATG  TTGTTCTGCG  CCGTGAAAGT  GGGGCGTTTT  TTCAGCAGTC
251  CGGCGACGTG  GTTTCGGGGC  AAAGACCCCTG  TCAATCAGGC  GGTGTGCGCG
301  CTGTATGCGG  ACGAGTGGCG  GCAACCTTCG  GTACGTTGGA  AAATAGGCGC
351  AACGTCGCAC  AGCCTGTGGC  TCTGCACGCT  GCTCGGAATG  CTGGTTCGGG
401  TATTGTTGCT  GCTTTTGGTG  CGGCAATATA  CGTTCAACTG  GGAAGCACG
451  CTGTTGGGCG  ATTCGTCTTC  GGTACGGCTG  GTGGAAATGT  TGGCATGGCT
501  GCCTGCGAAA  CTGGGTTTTC  CCGTGCCTGA  TGCGCGGGCG  GTCATCGAAG
551  GTCGTCTGAA  CGGCAATATT  GCCGATGCGC  GGGCTTGCTC  GGGGCTGCTG
601  GTCGGCAGTA  TCGCCTGCTA  CGGCATCCTG  CCGCGCCTCT  TGGCTTGGGC
651  GGTATGCAAA  ATCCTTTTGA  AAACAAGCGA  AAACGGCTTG  GATTTGGAAA
701  AGCCCTATTA  TCAGGCGGTC  ATCCGCCGCT  GGCAGAACAA  AATCACCAGT
751  GCGGATACGC  GTCGGGAAAC  CGTGTCGCC  GTTTCGCCGA  AAATCGTCTT
801  GAACGATGCG  CCGAAATGGG  CGGTCATGCT  GGAGACCGAA  TGGCAGGACG
851  GCGAATGGTT  CGAGGCGAGG  CTGGCGCAGG  AATGGCTGGA  TAAGGGCGTT
901  GCCGCCAATC  GGGAACAGGT  TGCCGCGCTG  GAGACAGAGC  TGAAGCAGAA
951  ACCGGCGCAA  CTGCTTATCG  GCGTGCGCGC  CCAACTGTG  CCCGACCGCG
1001  GCGTGTTGCG  GCAGATCGTC  CGACTTTCGG  AAGCGGCGCA  GGGCGGCGCG
1051  GTGGTGCAGC  TTTTGGCGGA  ACAGGGGCTT  TCAGACGACC  TTTTCGGAAA
1101  GCTGGAACAT  TGGCGTAACG  CGCTGACCGA  ATGCGGCGCG  GCGTGGCTGG
1151  AACCCGACAG  AGCGGCGCAG  GAAGCCGCTC  TGAAAACCAA  CGACCGCACT
1201  TGA

```

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

```

a253. pep
1  MIDRNRMLRE  TLERVRAGSF  WLWVAATFA  FFTGFSVTYL  LMDNQGLNFF
51  LVLAVGLGMN  TLMLAVLAM  LFLRVKGRF  FSSPATWFRG  KDPVNQAVLR
101  LYADEWRQPS  VRWKIGATSH  SLWLCTLLGM  LVSLLLLLLV  RQYTFNWEST
151  LLGDSSSVRL  VEMLAWLPAK  LGFPVPDARA  VIEGR LNGNI  ADARAWSGLL
201  VGS IACYGIL  PRLLA WAVCK  ILLKTS ENGL  DLEKPY YQAV  IRRWQNKITD
251  ADTRRET VSA  VSPKIVL NDA  PKWAVMLE TE  WQDGEWF EGR  LAQEWLDKGV
301  AANREQVAAL  ETELKQKPAQ  LLIGVRAQTV  PDRGVLRQIV  RLSEAAQGGA
351  VVQLLAEQGL  SDDLSEKLEH  WRNALTECGA  AWLEPDRAAQ  EGRLKTNDR
401  *

```

583

m253/a253 97.2% identity in 395 aa overlap

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLEVRAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFVLVLAGVIGMN					
a253	MIDRNRMLRETLEVRAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFVLVLAGVIGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFRLVKVGRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMLFRLVKVGRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLSNAASVRAVELMAWLP SKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLGDSSSVRLVEMLAWLP AKLGFPVPDARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m253.pep	VIEGRNLNGNIADARAWSGLLVGSIA CYGILPRLLAWVCKILLKTS ENGLDLEKPYQAV					
a253	VIEGRNLNGNIADARAWSGLLVGSIA CYGILPRLLAWVCKILLKTS ENGLDLEKPYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253.pep	IRRWQNKITDADTRRET VSAVSPKIILNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253	IRRWQNKITDADTRRET VSAVSPKIVLNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253.pep	ATNREQVA ALETELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
a253	AANREQVA ALETELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGR LKQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGR LKTNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcaggtttga tgetgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg tttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcactggttt ctttgagaaa cgggccgggc
301 tggacgggat tttcactgtc ctggctgctg gcggctgcag gaatcgaca
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggctcttg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aacccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence &lt;SEQ ID 994; ORF 254.ng&gt;:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```

51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG  
 101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIAIYVMGW MVLAVMKSLT  
 151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF  
 201 VSVYGYVI\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

m254.seq (partial)  
 1 ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTGA GTTCCTGGCT  
 51 GTACCACGGA ATTGCAGCCG GAAAACGTAA AAGCATTGTG AAAAAACCG  
 101 ACCACTGCAT GATTATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA  
 151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG  
 201 GCTGCTGGCG GCTGCAGGAA TCGCACAAGA ACTCACCATC GGACGGAAAA  
 251 GCGAAAAACG TCTGCTGTCT ATTGTGATT ATGTCGTCAT GGGTTGGATG  
 301 GTCTTGGCGG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT  
 351 GGCTTGGCTG GCGGCAGGCG GTATGCTGTA CAGTGTGGC ATTACTGGT  
 401 TTGTAACGA TGAAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTT  
 451 GTATTGGGCG GCAGCATCAC CCAATTTGTC AGCGTGACG GTTACGTAAT  
 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

m254.pep (partial)  
 1 ..VSVYGISLLL LYLSSWLYHG IAAGKLKSI LKKTDHCMYI VLIAGSYTPFA  
 51 LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLLS IYIYVMGWM  
 101 VLAVMKSLTA SLPSAGLAWL AAGGMLYSVG IYWFVNDEKI RHGHGIWHLF  
 151 VLGGSITQFV SVYGYVI\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng)

from *N. gonorrhoeae*:

m254/g254

				10	20	30
m254.pep				VSVYGISLLL	LYLSSWLYHG	IAAGKLKSI
g254	HLSGLILAAAGLMLMLLKTIGHGDGYRIFSVSVYGISLLL	LYLSSSLYHG	IAAGKLKSI			
	20	30	40	50	60	70
		40	50	60	70	80
m254.pep		KKTDHCMYI	VLIAGSYTPF	ALVSLRNGPGW	TVFSLSWLLA	AAAGIAQELT
g254		KKTDHCMYI	VLIAGSYTPF	ALVSLRNGPGW	TVFSLSWLLA	AAAGIAQELT
	80	90	100	110	120	130
	100	110	120	130	140	150
m254.pep		IYIYVMGWM	MVLAVMKSLT	ASLPSAGLAW	LAAGGMLYSV	GIYWFVNDEK
g254		IAIYIVMGWM	MVLAVMKSLT	ASLPPAGLAW	LAAGGMLYSV	GIYWFVNDEK
	140	150	160	170	180	190
	160					
m254.pep		VLGGSITQFV	SVYGYVIX			
g254		VLGGSITQFV	SVYGYVIX			
	200					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

a254.seq  
 1 ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTGTA GCGGTTTGAT  
 51 TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG  
 101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT  
 151 CTGCTCTATT TGAGTTCCTC GCTGTACCAC GGAATTGCAG CCGGAAAACG  
 201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTAT GTGCTGATTG  
 251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGCGCGGGC

585

This corresponds to the amino acid sequence <SEQ ID 998; ORF 254.a>:

1 MYTGERFNTY SHLSGLILAA AGLALMLLKT<sup>+</sup>IGHGDGYRIF SVSVYGISLL  
51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMIIY VLIAGSYTPF ALVSLRNGPG  
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIATYIVMGW MVLAVMKSLT  
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRRGHGIVHL FVLGGSITQF  
201 VSVYGYVI\*

**m254/a254** 97.6% identity in 167 aa overlap

```

30                                     10                                     20
m254.pep
VSVYGISLLLLYLSSWLYHGIAAGKLKSIL
|||||
a254
HLSGLILAAAGLALMLLKTIGHG DGYRIFSVSVYGISLLLLYLSSSLYHGIAAGKLKSIL
20 30 40 50 60 70 80
90
m254.pep
KKTDH CMIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
|||||
a254
KKTDH CMIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
80 90 100 110 120 130 140
150
m254.pep
IVIYVVMGWMVLAVMKS LTASLP SAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF
|:|:|
a254
IAIYIVMGWMVLAVMKS LTASLP SAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF
140 150 160 170 180
190
m254.pep
VLGGSITQFVSVYGYVIX
|
a254
VLGGSITQFVSVYGYVIX
200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

This corresponds to the amino acid sequence <SEQ ID 1000; ORF 255.ng>:

g255.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1001>:

m255.seq

This corresponds to the amino acid sequence <SEQ ID 1002; ORF 255>:

m255.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

m255/g255

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGFDFGIEAVKNRFAQADRD	I				
	:	:	:	:	:	:
g255	MVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGFDFGIEAVENGFAQTGDG	D				
	:	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m255.pep	GCFFDMQLRADGIQGFAHAVHI	VFQLGNL	AMVGGKKRILGNVFAAFK	PDFF	FFADLGNVGGD	
	:	:	:	:	:	:
g255	GGFFDMQFRADGIQGF	AHTVHI	VFQFGDL	AMVGGKKRILGNVFAAFK	PDFF	FFADLGNVGGD
	:	:	:	:	:	:
	70	80	90	100	110	120
	130	140	150	160	170	180
m255.pep	FRAEFFFQPF	FGNGSGSNAGGGFTGGAP	AAAAVVARAVFVPIGIVGV	GAEGAAGGDVA	VVF	
	:	:	:	:	:	:
g255	FRAEFFFQPF	FGNGSGGNAGCGFAGGT	PAAAPVVARVTFVPIGIVGV	SGAEGAAGGDVA	VVF	
	:	:	:	:	:	:

130            140            150            160            170            180

189

```
a255.3eq
1 GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG TGTTTCGCTGC
51 CGCTGTCGCT TACGCTGTCA AAACCTGCGC CGATTTCAC GCCTTTGACG
101 GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GCGCGTCGAA
151 TACGGGTTTCG CCAAGCCGA CGGGACGTT GCGCGCTTCA ATATGCACTT
201 TCGCGCCGAC GGAATCCAAG GATTTCGC CA GCTGTCCAT ATAGTTTTCT
251 AGCTCGGCAA TTTGGCTATG GTTTGCGCGA AAAAAGGAT TTTGGGAAT
301 GTGTPFCGAG CCTTCAAAAC GGATTTCCTT TTCGCCGACT TGGGTAACGT
351 AGGCGGTGAT TTCCGTGCCG AATTTTTCTT TCAACCATTT TTTGGCAACG
401 GCTCCGCGCG CAACGCGGGC GCGCGTTTCG CGGGCGGAAC TCCTGCGGCC
451 GCCCGGGTAG TCGCGCGTGC CGTATTTTGT CCAATAGGTA TAGTCGGCGT
501 GCCCGGGCGG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551 TCGGTATTGC GGATTAA
```

a255.pep

1	VVGQ <b>EALRGE</b>	FVAVFAAALR	YAVKTCADFH	AFDGVDAHHG	VGDFGIEAVE
51	YGFAAQADGDV	GGFNMQRLDR	GIQGF <del>AH</del> AVH	IVFQLGNLAM	VGGKKRILGN
101	VFAAFKPDDF	FADLGNVGGD	FRAEFFFQPF	FGNGSGGNAG	GGFAGGTAA
151	APVVARAVFV	PIGIVGVAGA	EAGGDVAUVF	<u>AALVGIAD*</u>	

		10	20	30	40	50	60
m255.pep	VVGQ	EALRGQFVAVFAA	ALRYAVKTCADFHAFD	GVDAAHHRV	GDFGIEAVKNR	FAQADRD	I
a255	VVGQ	EALRGFEFVAVFAA	ALRYAVKTCADFHAFD	GVDAAHHRV	GDFGIEAVEY	GFAQADGD	IV
		10	20	30	40	50	60
		70	80	90	100	110	120
m255.pep	GC	FDMQLRADGIQGFA	HAVHIVFQLGNL	AMVGGKKRILGN	VFAAFKPD	EFFADLGNV	GGD
a255	GG	FNMQLRADGIQGFA	HAVHIVFQLGNL	AMVGGKKRILGN	VFAAFKPD	EFFADLGNV	GGD
		70	80	90	100	110	120
		130	140	150	160	170	180
m255.pep	FR	AEFFQPF	FGNGSGSNAGGGFT	GGAPAAA	AVVARAVFV	PIGIVGVAGAE	AGGDVAVVF
a255	FR	AEFFQPF	FGNGSGGNAGGGF	AGGTAA	APVVARAVFV	PIGIVGVAGAE	AGGDVAVVF
		130	140	150	160	170	180
		189					
m255.pep	AAL	VGIADXX					
a255	AAL	VGIADXX					

g256.beq

```
1 atgctcgcgg tacgcaatcg gggttggcac ggcgcagtcg tccatttcg
51 cagctgcggc ggcgtagcga acaccgcccc ggtgttctac cacttgggtg
101 ataccgcgga aatcgccctt gctttggaca cgcctacgcg cgyttaccgt
151 gaaatatacg ccgtcggcgt atcgctgggc ggcaacgcgc cggcaaaata
201 tttggggcgaa cagggcaaaa aggcattgcc gcacgcctcg gccgcgcat
251 cggccccctt tgatcacagc gcggcaggca gccgcttcga cagcggcatc
301 acqcgctgct tctacacqcg ctacttcctc cgcaactgta tacccaagc
```



588

```

351 acgttcgctc caagggtttc agacggcatt tgccgcaggg tgcaaaacac
401 tgggcgagtt tgacgaccgt ttcaccgcac cgctgcacgg ctttgccgac
451 cggcagcact actaccgcca aacttcctgc aaaccgctgc tcaaacacgt
501 tgccaaaccg ctgctcctgc tcaatgccgc caacgacccc ttcctgcccgc
551 ccgaagccct gccccgtgca gacgaagcgt ccgaagccgt taccctgttc
601 caacctgcac acggcgggca cgcgggcttt gtcagcagca ccggcggcag
651 gctgcacctg caatggctgc cgcagaccgt cctgtcctat tttgacagct
701 tccgcacaaa caggcggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1006; ORF 256.ng>:

```

g256.pep
1  MLAVRNRGWH GAVVHFRSCG GVANTAPVIFY HLGDTAEIAF ALDTLTARYR
51  EIYAVGVSLG GNAPAKYLGE QGKKALPHAS AAVSAPVDAE AAGSRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAANDP FLPPEALPRA DEASEAVTLF
201 QPAHGGHAGF VSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1007>:

```

m256.seq
1  ATGCTTGCGG TACGCGATCG GGGTTGGCAC GCGGTAGTCG TCCATTTCCG
51  CAGCTGCGGC GGCATTGCCA ACACCGCTCC GGTGTTCTAC CA.CTtGGCG
101 ATACCGCCGA AATCGCCTTT ACTTTGGACA CGTTCGCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCAAAA AGGCATTGCC GCAAGCCGCT GCCGTTCATCT
251 CCGCCCCCGT CGATGCAGAG GCGCGAGGCA GACGCTTCGA CAGCGGCATC
301 ACGCGGCTGC TCTACACGCG CTACTTCCTC CGCACCTGA TACCCAAAGC
351 AAAATCGCTC CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGC TTCACCGCAC CGCTGCACGG CTTTGCCGAC
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCCCT GCCCGCGCA GACGAAGTAT CCGAAGCCGT TACCTGTTC
601 CAGCCGGCAT ATGGTGGTCA TGTGGGCTTT GTCAGCAGCA CCGCGGCGAG
651 GCTGCACCTG CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1008; ORF 256>:

```

m256.pep
1  MLAVRDRGWH GVVVHFRSCG GIANTAPVIFY XLGDTAEIAF TLDTFAARYR
51  EIYAVGVSLG GNALAKYLGE QGKKALPQAA AVISAPVDAE AAGRRFDSGI
101 TRLLYTRYFL RTLIPKAKSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPAYGHHVGF VSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

m256/g256

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVVHFRSCGGIANTAPVIFYHLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	:     :     :     :     :     :     :     :     :					
g256	MLAVRNRGWHGAVVHFRSCGGVANTAPVIFYHLGDTAEIAFALDTLTARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGKKALPQAAAVISAPVDAEAAAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	:     :     :     :     :     :     :     :					
g256	GNAPAKYLGEQGKKALPHASAAVSAPVDAEAAAGSRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHYYRQTSCKPLLKHVAKPLLLLNNAVNDP					
	:     :     :     :     :     :     :     :					
g256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHYYRQTSCKPLLKHVAKPLLLLNNAANDP					

589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	:     :     :     :     :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

```
a256.seq
1  ATGCTCGCGG TACGCGATCG GGGTTGGAAC GCGTAGTCG TCCATTTCGG
51  CAGCTGCGGC GCGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACGCGCGA AATTGCCTTT ACTTTGGACA CGCTCGCCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGCGGAAA ACGCGCTGCC GCAAGCCGCC GCCGTCACTC
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG TACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACCGCCA AACTCCTGCG AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCGCGCA GACGAAGTGT CCGAAGCCGT TACCCTGTTT
601 CAGCCGACAC ACGGTGGTCA TGTCGGCTTT GTCGCGAGCA CCGCGCGCAG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCTAT TTCGACAGCT
701 TCCGCACAAA CAGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

```
a256.pep
1  MLAVDRGWN GVVVHFRSCG GVANTAPVFY HLGDTAEIAF TLDTLAARYR
51  EIYAVGVSLG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVG FVSTGGRLHL QWLPQTVLSY FDSFRTNRR*
```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVDRGWHGVVHFRSCGGIANTAPVFYXLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	:     :     :     :     :					
a256	MLAVDRGWNQGVVHFRSCGGVANTAPVFYHLGDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGGKALPQAAVISAPVDAEAAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	:     :     :     :     :					
a256	GNALAKYLGEQGENALPQAAVISAPVDAEAAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCPKLLKHVAKPLLLLNAVNDP					
	:     :     :     :     :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCPKLLKHVAKPLLLLNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	:     :     :     :     :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

```
g256-1.seq
1  ATGATTTTGA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAT TCCTGCAACA CCGCGACCC GCATACCGCC
```

590

```

101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CCAAAACCGC CTACGACTTT
151 TCAGCAGGCG GCATTTCCGCC CGATGCGCCG CTGGTCGTGC TGTTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTGCAACTG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GCGCGAGTCG TCCATTTCCG CAGCTGCGGC
301 GCGGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGTG ATACGCGCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACCGC GCGTTACCGT GAAATATACG
401 CCGTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCCTCG GCCGCCGTAT CCGCCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAAACAGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCCTGCCGC CCGAAGCCCT
801 GCCCCGTGCA GACGAAGCGT CCGAAGCCGT TACCTGTTC CAACCTGCAC
851 ACGCGGGGCA CGCCGGCTTT GTCAGCAGCA CCGCGGCGAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCTAT TTTGACAGT TCCGCACAAA
951 CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVRNRGWH GAVVHFRSCG
101 GVANTAPVYF HLGDTAEIAF ALDTLTARYR EYAVGVSLG GNAPAKYLGE
151 QGKRALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIFKARSL
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGFD RHDYYRQTSC KELLKHVAKP
251 LLLNNAANDP FLPPEALPRA DEASEAVTLF QPAHGGHAGF VSTGGRLHL
301 QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCCAGCGCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAGTCGCG CTACGACTTT
151 TCAGACGGCA TTTCCGCCGA TGCGCCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGCAGCC ATTACGCGGT CGAAGTATG CTTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTTCCGCAG CTGCGCGGGC
301 ATTGCCAACA CCGCTCCGGT GTTCTACACG TTGGGCGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACAGT TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAAATATTT GGGCGAACAG
451 TGCAGAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCCCCTCGA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAG CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGCG ACCCTGATAC CCAAAGCAAA ATCGCTCCAA
601 GGTTTTCAGA CGGCATTGCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGCTTC ACCGCACCGC TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTTAC CTTGTTCCAG CCGGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCGAGCT GCACCTGCAA
901 TGGCTGCCGC AGACCGTCCT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVDRGWHG VVHFRSCGG
101 IANTAPVYFH LGDTAEIAFT LDTFAARYR EYAVGVSLGG NALAKYLGEQ
151 GKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPKAKSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFD RHDYYRQTSC PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGHHVGFV SSTGGRLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

```

          10      20      30      40      50      59
m256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
          |||||
g256-1      MILTPPDTPFFLRNGNADTIAAKFLQHPAPAYRRELLPDSTGKTKTAYDFSAGGISPDAP
          10      20      30      40      50      60

          60      70      80      90     100     110     119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVDRGWHGVVHFRSCGGIANTAPVYHFGDTAEIAF

```

591

```

g256-1  |||||:|||||:|||||:|||||:|||||:|||||:
        LVVLFHGLEGSSRSYAVELMLAVRNRGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
        70      80      90      100     110     120

m256-1.pep 120      130      140      150      160      170      179
        TLDTFAARYREIYAVGVSLGGNALAKYLGEQGGKALPQAAVISAPVDAEAGRRFDSGI
g256-1      :|||:|||||:|||||:|||||:|||||:|||||:
        ALDTLTARYREIYAVGVSLGGNAPAKYLGEQGGKALPHASAAVSAPVDAEAGSRFDSGI
        130      140      150      160      170      180

m256-1.pep 180      190      200      210      220      230      239
        TRLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRETAPLHGFADRHDYYRQTSC
g256-1      :|||||:|||||:|||||:|||||:|||||:|||||:
        TRLLYTRYFLRTLIPKARSQGFQTAFAAGCKTLGEFDDRETAPLHGFADRHDYYRQTSC
        190      200      210      220      230      240

m256-1.pep 240      250      260      270      280      290      299
        KPILLKHVAKPLLLLNAVNDFLPPEALPRADEVSEAVTLFQPAYGGHVGVFSSTGGRLHL
g256-1      :|||||:|||||:|||||:|||||:|||||:|||||:
        KPILLKHVAKPLLLLNAANDPFLPPEALPRADEASEAVTLFQPAHGGHAGFVSSSTGGRLHL
        250      260      270      280      290      300

m256-1.pep 300      310      319
        QWLPQTVLSYFDSFRTNRRX
g256-1      :|||||:
        QWLPQTVLSYFDSFRTNRRX
        310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```

a256-1..seq
1  ATGATTTTGA CACCGCCGGA CACACCCCTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAT TCCTGCAACG CTCGCCACCT GCATACCGCC
101 GCGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAACCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TCGCCGCTG GTCTGCTGT TTCACGGTTT
201 GGAGGGCGGC AGTGGCAGCC ATTACGCGGT CGAACTGATG CTCGCGGTAC
251 GCGATCGGGG TTGGAACGGC GTAGTCGTCC ATTTCCGCAG CTGCGGGCGC
301 GTAGCGAACA CCGCCCCGGT GTTCTACCA TGGGCGGATA CCGCCGAAAT
351 TGCCTTTACT TTGGACACGC TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAATATTT GGGCGAACAG
451 GCGCAAAACG CGCTGCCGCA AGCCGCCGCC GTCATCTCCG CACCCGTCGA
501 TGCAGAGGCG GCAGGCAACC GCTTCGACAG CGGCATCACA CGGCTGCTCT
551 ACAGCGCCTA CTTCCTCCGC ACACTGATAC CAAAGCAGC GTCGCTCCAA
601 GGTTTTCAGA CGGCATTGCG CGCAGGGTGC AAAAACAATG GCGAGTTTGA
651 CGACCGTTTC ACCGCACCGC TGCACGGCTT TGCCGATCGG CACGACTACT
701 ACCGCCAATC TTCTTGCAAA CCGCTGCTCA AACACGTTGC CAACCGCTG
751 TCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCGCTGCC
801 CCGCGCAGAC GAAGTGTCAG AAGCCGTTAC CCTGTTCAG CCGACACAG
851 GTGGTCATGT CGGCTTTGTC GGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGTTGCCGC AGACCGTCCT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```

a256-1..pep
1  MILTPPDTPF FLRNGNADTI AAKFLQRSAP AYRRELLPDS TGKTKTAYDF
51  SDGISPDAPL VVLFHGLEGG SGSHYAVELM LAVDRGWNG VVHFRSCGG
101 VANTAPVFYH LGDTAEIAFT LDTLAARYRE IYAVGVSLGG NALAKYLGEQ
151 GENALPQAAA VISAPVDAEA AGNRFDSGIT RLLYTRYFLR TLIPKARSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDFP LPPEALPRAD EVSEAVTLFQ PTHGGHVGVFV GSTGGRLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

          10      20      30      40      50      60
a256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRSAPAYRRELLPDSTGKTKTAYDFSDGISPDAPL
          |||||:|||||:|||||:|||||:|||||:|||||:
m256-1      MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFSDGISPDAPL
          10      20      30      40      50      60

          70      80      90      100     110     120
a256-1.pep VVLFHGLEGGSGSHYAVELMLAVDRGWNGVVHFRSCGGVANTAPVFYHLGDTAEIAFT
          :|||||:|||||:|||||:|||||:|||||:|||||:
m256-1      VVLFHGLEGSSRSYAVELMLAVDRGWNGVVHFRSCGGIANTAPVFYHLGDTAEIAFT

```

592

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
m256-1	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAVISAPVDAEAAGNRFDSGIT					
	130	140	150	160	170	180
a256-1.pep	190	200	210	220	230	240
m256-1	RLLYTRYFLRTLIPKARSLQGFQTAFAGCKTLGEFDDRFTAPLHGFAADRHYYRQTSCK					
	190	200	210	220	230	240
a256-1.pep	250	260	270	280	290	300
m256-1	PLLKHVAKPLLLNAVNDFLPPEALPRADEVSEAVTLFQPTHGGHVGFGSTGGRLHLQ					
	250	260	270	280	290	300
a256-1.pep	310	319				
m256-1	WLPQTVLSYFDSFRTNRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

```

g257.seq
1   atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcggcgggtt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgcg atgaaaatgt gtttttctgg
151 aaaggtgtcg cgctgggttc cggcgcgagg ctgcgcctgt tcggcggtgga
201 cgacagacag gcggcggatt tggccaataa ggttttggcg gaagtggcgc
251 gtttgaaaaa aatgttcagc cttaccgtg aagacagcct gatcagccgt
301 ctgaaccgcg acggttatct gacttcgcct ccggcggatt ttttggaaact
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

```

g257.pep
1   MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMF5 LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIFTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

```

m257.seq
1   ATGGGCAGGC ATTTCGGGCG .CAGCGTTT CTGACGGTTG CCGCCGTTGC
51  GGCGGGGAC. GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGGAT GAAAAACGCA ATGAAAATGT GTTTTCTGG
151 AAAGGTGTCT CACTGGGTTC CGGTGCGGA. CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA ATGTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTTATCT GACTTCGCCG TCGGCGGATT TTTTGGAAC
351 GkTGAGCCTG GCCGCATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

```

m257.pep
1   MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNMD EKRNVFFW
51  KGVALGSGAX LRLFGVDDR AADLVNKLVA EVARLEKLF5 LYREDSLISR
101 LNRDGYLTSP SADFLELXSL AAIFTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

10 20 30 40 50 60

593

```

m257.pep  MGRHFGRRFLTVAAVAAGTAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAD
          |||||:||||:||||:|:|||||:|||||:|||||:|||||:|||||:|||||:
g257      MGRHFGRRRFLTAAAVAVAGAAVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVGALGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRRAADLVNKKVLAEEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257      LRLFGVDDRQAADLVNKKVLAEEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTXX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

## a257.seq

```

. 1 ATGGGCAGGC ATTCGGGCG CAGGCGTTTT TTGACAGTTG CCGCCGTTGC
  51 GCGGCGGGC GCGGCGGTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
 101 ATGAAAAACG CAATAAAGAT GAAAAACGCA ATGAAAATGT GTTTTTCTGG
 151 AAAGGTGTCG CACTGGGTTC CGGTGCGGAG CTCCGTCTGT TCGGTGTGGA
 201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
 251 GTTTGGAAAA AATGTTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGT
 301 CTGAACCGTG ACGGTTATTT GACTTCGCCG CCGGCGGATT TTTTGGAACT
 351 GTTGAGCCTG GCCGTGATAT TCACGCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

## a257.pep

```

1 MGRHFGRRRF LTVAAVAAG AAVSFLPNPF AADDEKRNKD EKRNVFFW
51 KGVGALGSGAE LRLFGVDDRR AADLVNKKVLA EVARLEKMFSL YREDSLISRL
101 LNRDGYLTSP PADFLELLSL AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGXQRFLTVAAVAAGXAASFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a257      MGRHFGRRRFLTVAAVAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAE
          10      20      30      40      50
60

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRRAADLVNKKVLAEEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
          ||
a257      LRLFGVDDRRRAADLVNKKVLAEEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110
120

m257.pep  AAIFTXX
          |:|
a257      AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

```

g258.seq
1  atgcgccgct tcctaccgat cgcagccata tgcgccgtcg tcctgtgtga
51  cggattgacg gcggcgaccg gcagaccag ttcgctggcg gattatttct
101 ggtggatagt ctcggtcagc gcaatgctgc tgctggtgtt gtccgccgtt
151 ttggcacgtt atgtcatatt gctgttgaaa gacaggcgca acggcggtt
201 cggttcgtag attgccaaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttctcg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggccgcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccgcgagcg gttttgccca
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccga aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgaa agcataggcg gcgtattgta
651 cgcgcaggga tgggtgtcgg caggtacgca caacgggcgc gattacgcgc
701 tgtttcttcg ccagccgatt ccgaaaatg tggcacagga tgcggttctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgagttaca gcaaaaaagg
801 tttgcagacc tttttctg taacctgtct gattgcctcg ctgctgtcga
851 ttttcttgc gctgtaatg gcaactgtatt ttgccgcgg tttcgtcgaa
901 cccattctgt cgttgccga gggcgcaaag gcggtggcgc aggggtgattt
951 cagccagacg cgcccgtat tgcgcaacga cgagttcgga cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcg ggaagccgcc cgtcactacc tcgagtgcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctctacccc ctctctgtt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctccctctt ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

```

g258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVLSAV
51  LARYVILLK DRRNGVFGSQ IAKRLSGMFT LVAVLPLGLFL FGISAQFTNG
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVFPVQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKGLQT FFLVTLIAS LLSIFLALVM ALYFARRFVE
301 PILSLAEGAK AVAQGDFSQT RPVLNDEFG RLTKLFNMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVDLG LTTGVVVSYP LSCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

```

m258.seq
1  ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCTG TCCTGTGTGA
51  CGGACTGACG GCGGCAACCG GCAGACCAG TTCGCTGGCG GATTATTCTT
101 GGTGGATTGT TCGGTTTCTG GCAATGCTGC TGCTGTTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTCCGAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTCTCTG TTCGGCGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTG AGCAAGTCCG CATTGAATTT GCGGCGAGAC AACGCCCTCG
401 GCAACGCCGT CCCCCTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGTGCT GGAACATTAC GCCGCGAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAGCT CGATCAGCCG TTCCAGGTA AGGCGCGTTG GAAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTGGAAG AGCATAGGCG GCGTATTGTA
651 CGCGCAGGCG TGGCTGTCTG CGGTTACGCA CAACGGGCGC GATTACGCTT
701 TGTTTTCCG TCAGCCGTT CCCAAAGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGCGGAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTCTCTG CAACCTGCT GATTGCTCG CTGCTGTGGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCCGCGG TTTGCTCGAA
901 CCCGTCCTAT CGCTTGCCGA GGGGCGAAG GCGGTGGCGC AAGGCGATT
951 CAGCCAGACG CGCCCGTGT TCGCAACGA CGAGTTCGGA CGCTTGACCA

```

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

1	MRRFLPIAAI	CAVVLLYGLT	AATGSTSSLA	DYFWWIVAFS	AMLLLVLSAV
51	LARYVILLKL	DRRDGVFGSQ	IAKRLSGMFT	LVAVLPGVFL	FGVSAQPFNG
101	TINSWFGNDT	HEALERSLNL	SKSALNLAAD	NALGNAPVPQ	IDLIGASLEP
151	GDMGRVLEHY	AGSGFAQLAL	YNAASGKIEK	SINPHKLDQP	FPKGARWEKI
201	QRAGSRVDEE	SIGGVLYAQG	WLSAGTHNGR	DYALFFRQPV	PKGVAEDAVL
251	IEKARAKYAE	LSYSKKGLQT	FLLATLLIAS	LYSIFLLALVM	ALGYFARRFVE
301	PVLSLAEAGK	AVAQGDFSQT	RPVLRNDEFG	RLTKLFNHMT	EQLSIAKEAD
351	ERNRRREEAA	RHYLECVLEG	LTTGVVVFE	QGCLKTFNKA	AEQILGNPLT
401	PLWGSSRHGW	HGVSAQQSLL	AEVFAAIGA	AGTDKPVHVH	YAAPDDAKIL
451	LGKATVLPED	NGNGVVMVID	DITVLIHAQK	EAAWGEVAKR	LAHEIRNPLT
501	PIQLSAERXA	XLGGKKLDEQ	DAQILTRSTD	TIVKQVAALK	EMVEAFRNYA
551	RSPSLKLENO	DLNALIGDVL	ALYEAGPCRF	AADLPANR*	

### Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

	10	20	30	40	50	60
m258.pep	MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAMPLLLVLSAVLARYVILLLK					
	:           :           :           :					
g258	MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVSFSAMPLLLVLSAVLARYVILLLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLPGVSAQFINGTINSWFGNDTHEALERSINL					
	:           :           :           :					
g258	DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLPGISAQFINGTINSWFGNDTHEALERSINL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m258.pep	SKSALNLAADNALGNVAVPVQIDLIGAASLPGDMGRVLEHYAGSGFAQLALYNAASGKIEK					
	:         :           :         :           :					
g258	SKSALDLAADNAVSNVAVPVQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m258.pep	SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV					
	:       :       :       :       :       :       :					
g258	SINPHQFDQPLPDKHWEQIQQTGSVRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI					
	190	200	210	220	230	240



	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAELSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE					
	:: :                     :					
g258	PENVAQDAVLIEKARAKYAELSYSKKGLQTFFLVTLLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDfsQTRPVLrNDEFGRLTKLFNHMTQELSLIAKEADERNRRREEAA					
	:                     :					
g258	PILSLAEGAKAVAQGDfsQTRPVLrNDEFGRLTKLFNHMTQELSLIAKEADERNRRREEAA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVFDEQGCLKTFNKAAEQILGMPLTPLWGSSRHGWHGVSAQQSLL					
	:       : :					
g258	RHYLECVLDGLTTGVVVSYP LSCCR TAVFSTCHSSPLSYFX					
	370	380	390	400		

```

a258.seq
1 ATGCGCCGCTT TTCTACCGAT CGCAGCCATA TGCGCCGTCG TCCTGTGTGA
51 CGGATGACG GCGGCCAACG GCAGACCAGG TTCGTTGGCG GATTATTCTT
101 GTGGGATTGT TGCCTTCAGC GCAAATGCTGC TGCTGTGTGTT GTCCCGCGCT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGCA ATTGCCAAAC GCCTTTCCGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTTTCTG TTCGGCGTTT CCGCACAGTT TATCAACGGC
301 ACGATAATT CGTGTTTCGG CAACGATAAC CACGAGCGCG TTGAACGCAC
351 CCTCAATTGG AGCAAGTCCG CATTGAATCT GCGCGCAGAC AACGCCCTTG
401 GCAACGCCAT CCCCCTGCGC ATAGACCTCA TCGGCGCGCG TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGCGCAGG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAACGGGCAA AACTGAAAAA AGCATCAACC
551 CGCACAAAGT CGATCAGCCG TTTCCAGSTA AGCGCGCTTG GGAAAAAATC
601 CAACAGCGCG GTTCCGTCAG GGATTTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CAGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGCGC TCGCAGAGGA TGCCGCTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTTCCTGG CAACCTTGCT GATTGCCTCG CTGCTGTGCA
851 TTTTCTTGC ACTGTGTCAT GCATGTATT TCGCCCGCGG TTTCTGTGAA
901 CCGCTCCAT CGTGTGCCGA GGGGCGGAAG CGGGTGCGCG AAGGCGATT
951 CAGCCAGACG CGCCCCGTGT TGCGCAACGA CGAGTTCGGA CGCTTGACCA
1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGACATTATC TCGAATGCGT
1101 GTTGGAGGGG TGCACACCGG CGGTGTTGTT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACCTT CAACAAAGCG GCGGAACAGA TTTTGGGGAT GCCGCTTACC
1201 CCCCTTGFGG GCAGCAGCGC GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTCCGCCCAT CGGCGCGGCG CAGGTTACGG
1301 ACAAACCGTT CCATGTGAAA TATGCGCGCC CGGACGATGC CAAAATCTCT
1351 CTGGGCAAGG CAACCGTCTT GCCCGAAGAC AACGGCAACG GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CCGCAAAAAA GAAGCGCGCT
1451 GGGGCGAAGT GGCAAAACGG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCAGC TTCTTGCCGA ACGGTTGCGG TGGAAATTGG CGGGGAAGCT
1551 GGACGAGCAG GACGCGCAAA TCCTGACACG TTCGACCGAC ACCATCATCA
1601 AACAAAGTGG GGCATTAAAA GAAATGGTCG AGGCATTCCG CAATTACCGC
1651 CGTTCCCTT CGCTCAAAAT GGAATACGAG GATTTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATTGTACG AAGCTGCTCC GTGCCGGTTT CGGCGGGAAC
1751 TTGCCGGCGA ACCGCTGATG ATGGCGGCGG ATACGACCGC CATGCGGCAG
1801 GTGCTGCACA ATATTTTCAA AAATGCCGCC GAAGCGGCGG AAGAAGCCGA
1851 TGTGCCCCGA GTCAGGGTAA AATCGGAAGC GGGCGAGGAC GGACGGATTG
1901 TCTGCACAGT TTGCACAAC GGC AAGGGGT TCGCGCAGGA ATAGTGTGAC
1951 AATGCCTTCG AGCCGTATGT AACGGACAAA CCGGCTGGAA CGGGATTGGG
2001 ACTGCCCGTG GTGAAAAAAA TCATTGAAGA ACACGGCGCG CGCATCAGCC
2051 TGAGCAATCA GGATGCGGGC GCGCGTGTG TCAGAATCAT CTTGCCAAAA
2101 ACGGTAGAAA CTTATGCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```
a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLOT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAAQSSL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLEDE DAQILTRSTD TIIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIFFKNA EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIIEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*
```

m258/a258 99.0% identity in 584 aa overlap

```

10      20      30      40      50      60
m258.pep MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAV LARYVILLLK
|||||
a258     MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAV LARYVILLLK
10      20      30      40      50      60

70      80      90      100     110     120
m258.pep DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
|||||
a258     DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
70      80      90      100     110     120

130     140     150     160     170     180
m258.pep SKSALNLAADNALGNAIPVQIDLIGAASLPGDMGRVLEHYAGSGFAQLALYNAASGKIEK
|||||
a258     SKSALNLAADNALGNAIPVQIDLIGAASLPGDMGRVLEHYAGSGFAQLALYNAASGKIEK
130     140     150     160     170     180

190     200     210     220     230     240
m258.pep SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
|||||
a258     SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
190     200     210     220     230     240

250     260     270     280     290     300
m258.pep PKGVAEDAVLIEKARAKYAE LSYSKKGLOTFFLATLLIASLLSIFLALVMALYFARRFVE
|||||
a258     PKGVAEDAVLIEKARAKYAE LSYSKKGLOTFFLATLLIASLLSIFLALVMALYFARRFVE
250     260     270     280     290     300

310     320     330     340     350     360
m258.pep PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMTEQLSIAKEADERNRRREEAA
|||||
a258     PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMTEQLSIAKEADERNRRREEAA
310     320     330     340     350     360

370     380     390     400     410     420
m258.pep RHYLECVLEGLTTGVVVFDEQGCLKTFNKAAEQILGMPLTPLWGSSRHGW HGVSAAQSSL
|||||
a258     RHYLECVLEGLTTGVVVFDEQGCLKTFNKAAEQILGMPLTPLWGSSRHGW HGVSAAQSSL
370     380     390     400     410     420

430     440     450     460     470     480
m258.pep AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGGVVMVIDDITVLIHAQK
|||||
a258     AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGGVVMVIDDITVLIHAQK
```

598

	430	440	450	460	470	480
m258.pep	490	500	510	520	530	540
	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDEQDAQILTRSTDTIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDEQDAQILTRSTDTIIKQVAALK					
	490	500	510	520	530	540
m258.pep	550	560	570	580	589	
	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNIKFNAEEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

g259.seq

```

1  atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaatctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgccgtc
151 gcgctggtgt ggcctggcgtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatatacc
251 ccgtcctgca cgttcttttg caacacttgg aacacaagcc gcaaatgtc
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccg acgacgaaga cgcgcgcacg attgccgcg
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgccctg
451 ggcgaaacct atggcgcgct gtccgccgat attttcgagt tgcggcgcg
501 tttggaaagg cgcgcgttca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcggtga gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

g259.pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKILKLT AEYKHLRRC LPFGNGVGFG
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

m259.seq (partial)

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGTTT TTTGACCGC GCAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCC ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACKGACGC GGTGCGCTCG
451 GCGGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTGCGmGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGGmGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

m259.pep (partial)

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS

```

599

151 GETYGRVFAD IFELSALEG RAFKGLKLT AEYKXHLRRC LPFGNGVGVG  
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSALEGRAFKGLKLT					
g259	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALERRAFKGLKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRC LPFGNGVG VGR TQSGVAGDF KNIR					
g259	AEYKXHLRRC LPFGNGVG FGRAQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

1 ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT  
51 TTGATTTTC TTGCGCGTT TTTGACCGC GCAAATCTGG TTCAATCAGA  
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGCCGCGATT GTCCGCGGTC  
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCTAA  
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC  
251 CCGTCTGTCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC  
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT  
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG  
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTGCGCTCG  
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTGCGCGGC  
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA  
551 AAAA.CATCT TCGGCGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG  
601 CGCGCTCAAT CAGGCGTTGC AGGAGATTTC AAAAACATCG GAAAAGTCCA  
651 A

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

1 MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSVA  
51 ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML  
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTD AVAS  
151 GETYGRVFAD IFELSALEG RAFKGLKLT AEYKXHLRRC LPFGNGVGVG  
201 RAQSGVAGDF KNIGKVQ

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					

600

	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
a259	SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVVFADIFELSALEGRAFKGMLKLT					
a259	VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVVFADIFELSALEGRAFKGMLKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRLPFGNGVGVGRVTSQSGVAGDFKNIR					
a259	AEYKXHLRRLPFGNGVGVGRAQSGVAGDFKNIGKVQ					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCGATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGTGCGTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGGCGCGT GTTCGCCGAT ATTTTCGAGT TGTCGCGCGC
501 TTTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCGATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGCGCGTT CAAAGGCCAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTCTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGCGCGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTTCG AAACGGCGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTTC AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQLQEIS KTSEKSKRIF Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

```

      10      20      30      40      50      60
g259-1.pep  MMHSAVSQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV
            |||
m259-1      MMHSAVSQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV
            10      20      30      40      50      60

      70      80      90     100     110     120
g259-1.pep  SVRSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE
            |::|
m259-1      SARSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE
            70      80      90     100     110     120

      130     140     150     160     169 ...
g259-1.pep  VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVFADIFELSAALE
            |||
m259-1      VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVFADIFELSAALEGRAFGMLKLT
            130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

```

a259-1.seq
1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTGACCGC GCAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTC TGTCCGCATT GTCGCGCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTCGTG TCGGCGCGTT CAAAGGCTAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATAACAC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAATGCTC
301 GCGCTGTGCG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCC ACGACGAAGA CGCGCGCACG ATTGCCCGCG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTGCGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG CCGGAATATA
551 AAAACATCTT CGCGCATGCC TGCCGTTCCG AAACGGCGTT GGAGTTGGGC
601 GCGCTCAATC AGGCGTTGCA GGAGATTTC AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

```

a259-1.pep
1  MMHSAVSQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSVA
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDASVA
151 GETYGRVFAD IFELSAALEG RAFKGLKLT AEYKNIFGDA CRSETALELG
201 ALNQLQEIS KTSEKSKRIF Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

```

      10      20      30      40      50      60
a259-1.pep  MMHSAVSQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV
            |||
m259-1      MMHSAVSQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV
            10      20      30      40      50      60

      70      80      90     100     110     120
a259-1.pep  SARSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE
            |||
m259-1      SARSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE
            70      80      90     100     110     120

      130     140     150     160     170     180
a259-1.pep  VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVFADIFELSAALEGRAFGMLKLT
            |||
m259-1      VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVFADIFELSAALEGRAFGMLKLT
            130     140     150     160     170     180

      190     200     210     220
a259-1.pep  AEYKNIFGDACRSETALELGALNQLQEISKTSKSKRIFYX
            |||
m259-1      AEYKNIFGDACRSETALELGALNQLQEISKTSKSKRIFYX
            190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

602

```

1  atgggtgcgg gtgtagtatt cgttgctctt cagccgttct tcagcctgtt
51  tcgagcgttg ttcgagggcg gagtcggtat agtcgagggg gcgcacgatg
101 ccgctgaatg cgacttcttg tccgaggaat ttaccctgat ccggatcggg
151 gatgttttta ttgattcggg aggtcagata acggcccggg tctttcaggc
201 ctttggtgta aaccctggcg cctttggtgt acagcagcct gccttcggg
251 cccgagagca ggcgcggcgc ggcagcgggt tctttgcggg aaacgatttg
301 cgggtgctgc ataaagacgc ggtagaagtt gacatcgatg gcgggaatac
351 cgtatccgga cacttcctta tccggactga ttttgacgac ggggatgccg
401 tctgtctgtt ccaagccgag gcgcgggtcg ccgccaacgt agcgcaacac
451 caatacctgg cccggataaa tcaggtcggg attgtggatt tgatcccggt
501 tcgcgcccc caggggggga ccattgccac gggctgtaca ggtatttgcc
551 cgaaataccc cacaggggtg cgccctgttt ga

```

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

g260.pep

```

1  MGAGVVFVVF QPFSLFRAL FEGGVGIVEG AHDAECDL S EEFTRIRIG
51  DVFIDSVGQI TARFFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVLHKDAVEV DIDGGNTVSG HFLIRTFDD GDAVCLFQAE ARFAANVAQH
151 QYLARINQVG IVDLIPVRAP QGGTIATGCT GICPKYPTGC RPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1043>:

m260.seq

```

1  ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGwCA sGCGCGGyGC GGCAGCGGTT TCTTTCGGG AAACGATTTG
301 CCGATGCCCG ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGACTCA TTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTTC CCGTCAACGT GGCGCAACAC
451 CAATACCTGG TCCGATAAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTyCCA CAG

```

This corresponds to the amino acid sequence <SEQ ID 1044; ORF 260>:

m260.pep

```

1  MGAGMVVFVVF RPFSSLFRL FEDRVGIVEG AHDAECDL PEEFTRIRIG
51  DVFIDSVGVQ AARLFQAFGV NPGAFGVQQP AFRARXXARX GSGFFAGNDL
101 RMPHKDAVEV DIDGGNTVSG HFLIRTFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVRINQVG IVDLIPVRVP Q

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFSSLFRLFEDRVGIVEGAHDAECDLPEEFTRIRIGDVFIDSVGVQV					
	:     :					
g260	MGAGVVFVVFQPFSSLFRLFEGGVGIVEGAHDAECDLSEEFTRIRIGDVFIDSVGQI					
	10	20	30	40	50	60
m260.pep	70	80	90	100	110	120
	AARLFQAFGVNPGAFGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
	:   :					
g260	TARFFQAFGVNPGAFGVQQPAFRAREQARRGSGFFAGNDLRVLHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
m260.pep	130	140	150	160	170	
	HFLIRTFDDGDAVCLFQAEARFAVNVAQHQLVRINQVGIVDLIPVRVPQ					
g260	HFLIRTFDDGDAVCLFQAEARFAANVAQHQLARINQVGIVDLIPVRAPQGGTIATGCT					
	130	140	150	160	170	180

603

g260            GICPKYPTGCRPV  
                 190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

```
a260.seq
1  ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGGCGC GGCAGCGGTT TCTTTGCGGG AACGATTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTCT CCGTCAACGT GCGGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC. CCATTGCCAC GGGCTGTACA GGTATTTGCC
551 CGAAATGCCC CACAGGGTGT CGCCCTGTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

```
a260.pep
1  MGAGMVVFVF RPFSSLFRAL FEDRVGIVEG AHDAAECDL PEEFTRIRIG
51  DVFIDSVGVQ AARLFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*
```

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFSSLFRALFEDRVGIVEGAHDAAECDLPEEFTRIRIGDVFIDSVGVQV					
a260	MGAGMVVFVFRPFSSLFRALFEDRVGIVEGAHDAAECDLPEEFTRIRIGDVFIDSVGVQV					
	10	20	30	40	50	60
m260.pep	AARLFQAFGVNPGAFGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
a260	AARLFQAFGVNPGAFGVQQPAFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAFGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
a260	AARLFQAFGVNPGAFGVQQPAFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQLVLRINQVGIVDLIPVRVPQ					
a260	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQLVQINQVGIVDLIPVRVPPQAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

```
g261.seq
1  atggagcttg ggcatacgt attccttggtg ctttgcgcgc gttcagacgg
51  cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctccgggcatt cgcggcagcc gccgacgata ccctttagtc aggtgtgggt
151 ctggttcgcgg atgtagtcca acacgcccac ttcgtccgcc aacgcccacg
201 tttgcgcctt ggtcaggtac atcagcggcg tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcacg gatttgacga acacgccgcg
301 gcagtcggga tagcccgaaa aatcgggttc gcacacgcc cgcgatgatg
351 gccggatacc ctgccctttg gcaaaaatgg cggcgtaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgccgttgt cggcggtttc
451 gatggcggcg gtttcgatgg cggcggtttc gtccatcagg gcgttgtgag
501 taatctgcgc catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcctgcgcga tccactctgc gcgttcacgc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggctt ggacgttttc gcgcccgtag gtttggattg
```



604

651 cctgaatcag gcaggtggtc gaatcctgac cgcccagaaa gatgaccaag  
701 gcttttttgggt ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep

1 MELGHIVFLV LCARSDGLFT FQTFRQPAFA QDTARAFAAA ADDTLVAGVG  
51 LFADVVOHAH FVRQRPRRL GQVHQRRVDL KIVVHRQIKG NVHGFDEHAA  
101 AVGIARKIGF AHARDDVPDT LPFGKNGGVK QEKRVTPVHK GIGNAVVGGF  
151 DGGGFDGGGF VHQGVVRNLP HQAQIEYGLT DTQILRDPLC AFQLDGMALP  
201 VSEGDLDFV APVGLDCLNQ AGGRILTARE DDQGFLV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq

1 ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG  
51 CCTTTTACT TTCCAGATAT TCCGCCAGCC cGcGTTTCGCG CAAGATACAG  
101 CTCGGGCATT CGCGgCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT  
151 TTGCTCGCGG ATATAGTCCA GCACGCCCAT TTCGTCCGCC AACGCCCACG  
201 TTTGCGCCTT GGTGAGATAC ATCAGCGGCG TGTGGATTTG AAAATCATAG  
251 TCCATCGCCA AATTAAGGGT AACGTTTCATC GATTTGACAA ACACGTCGCG  
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCCG GCGATGATGT  
351 GCGGTATCCC CTGCCCTTTG GCGTAAATCG CCGCATAGAG CAGGAAAAGC  
401 gCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTTT CGGCAGTTTC  
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA  
501 GgCTcAAGTC GAGTACGGTT TGTTCGACG CCAATCCTG CGCAATCCAG  
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT  
601 GGCTTGGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG  
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTG TTGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep

1 MELGHIVFLM VCACSDGLFT FOIFRQPAFA QDTARAFAAA ADDAVIAGVG  
51 LLADIVQHAH FVRQRPRRL GQIHQRRVDL KIIVHRQIKG NVHRFDKHVA  
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF  
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFOLD GMALPVLESN  
201 GLDVFPVGL DCLNQAGGRI LTARKDDQGL LV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng)

from *N. gonorrhoeae*:

m261/g261

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
	::					
g261	MELGHIVFLVLCARSDGLFTFQTFRQPAFAQDTARAFAAAADDTLVAGVGLFADVVOHAH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA AVGIAGEVGF AHARDDVPYP					
g261	FVRQRPRRLGQVHQRRVDLKIVVHRQIKGNVHGFDEHAA AVGIARKIGFAHARDDVPDT					
	70	80	90	100	110	120
	130	140	150	160	170	
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGV----VHQGIVRNLPHQAVEYGLF					
	::        :          :					
g261	LPFGKNGGVKQEKRVTPVHKGIGNAVVGGFDGGGFDGGGFVHQGVVRNLPHQAQIEYGLT					
	130	140	150	160	170	180
	180	190	200	210	220	230
m261.pep	DAQILRNPAAGTFQLDGMALPVLESNGLDVFPVGLDCLNQAGGRILTARKDDQGLLVX					
	:     :  :            :					
g261	DTQILRDPLCAFQLDGMALPVSEGDLDFVFPVGLDCLNQAGGRILTAREDDQGFLVX					
	190	200	210	220	230	

605

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCCTTATG GTTTGCGCGT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCCAAG
201 TTTGCGCCTT GGTCAAGATC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTGCGA ACGCCGTTT CCGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGT TGTGACGCG CCAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAGATGA CCAAGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPSLRL GQIHQRRVDL KIIVHRQIKG NVHGFDKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
	10	20	30	40	50	60
m261.pep	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA	AVGIAGEVGF	FAHARDDVPYP			
a261	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVT	AVGIAGEVGF	FAHARDDVPYP			
	70	80	90	100	110	120
m261.pep	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA	AVGIAGEVGF	FAHARDDVPYP			
a261	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVT	AVGIAGEVGF	FAHARDDVPYP			
	70	80	90	100	110	120
m261.pep	LPFGVNRGIEQEKRAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV	EYGLFDAQIL				
a261	LPFGVNRGIEQEKRAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV	EYGLFDAQIL				
	130	140	150	160	170	180
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgcaa
51  accgcgcta gagcggtac ccaaaaacaa cggctttatc cccaacctca
101 tcggcgatt ggcaaacgcc cccgaagctt tggcgttta ccaagaagtc
151 ggcaagctca acgcccgaac cagcctgacc gccggcgaag tcgaagtgat
201 ccgcatcatc gccgtccgca ccaaccaatg cagctctcgc gtggcagggc
251 acaccaaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgcccgcg ctttggcggc aggtaaatct gacgatgcca aactcggcgc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

q263.ppt

```

1 MARLTVHTLE TAPEAAKPRV EAVPKNNGFI PNLIGVLANA PEALAFYQEV
51 GKLNAAANSLT AGEVEVIRII AVR TNQCSFC VAGHTKLATL KKL LSEQSLN
101 AARALAAAGKS DDAKL GALAA FTQAVMAKKG AVSDELNAF LEAGYNRQQA
151 VEVVMGVALA TLCNYANNLA QTEINPKLOA YA*

```

m263.seq (partial)

```

seq      (partial)
1      .. CACGACGAGCGC AATTTGACGA TGCCAAACTC GGC GCGCTCG CCGCCTTCAC
51      CCAAGCCGTA ATGGCGAAAA AAGCGCGGT ATCCGACGAG GAACTCAAAG
101     CATTTTTCGA TGCGGGCTAC AATCCAGCAGC AGCCAGTCTGA AGTCGTGATG
151     GGCCT .AsyC TgGCAACCTT GCACCACTAC GTCAACAACC TCGGACAAAC
201     CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

```

m263.pep (partial)

```

1 pep      (partial)
1  .. CGACGACGGG AATTTGACGA TGCCAAACTC GGC GCGCTCG CCGCCTTCAC
51  CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101 CATTTTTCGA TCGGGGTAC AACGACGAG AGCGAGTCGA AGTCGTGATG
151 GGCAT.AsyC TgCCAACCTT GTGCAACTAC GTTCAACAAC TCGACAACAAC
201 CGAAGTCAAC CCCGAATTGC AGGCTTACGC CTGA

```

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m263/q263

m263.pep  
g263

QCSFCVAGHTKLATLKKLLSEQSLNAARALAAAGKSDDAKLGALAAFTQAVMAKKGAVSDD

80 90 100 110 120 130

m263.pep  
g263

ELKAFFDAGYNQQQAVEVVMGVXLATLCNVVNNLGQTENPELQAYAX  
ELNAFLEAGYNRQQQAVEVVMGVALATLCNYANNLAQTEINPKLQAYAX

140 150 160 170 180

a263.seq

```

seq
1  ATGGCAGCTT TAACCGTACA CACCCTCGAA ACCGCCCCCG AAGCCGCCAA
51  AGCGCGCGTC GAGGCGGTAC TTCAAACAA CGGCTTTATC CCCAACCTTA
101 TCGGCGTATT ATCAAACGCC CCGGAAGCCT TGGCGTTTAT CCAAGAGTCT
151 GGCAGCTTCA ACGCCGCCAA CAGCCTAATG GCCGCGGAAG TCGAAGTAAT
201 CCAGATTACT GCCGCCCGCA CCAACCAATC CGGCTTCTGC TGGCAGGGC
251 ACACCAAATC GCACAACCTG AAAAAACTCC TTTCGAACA ATCCGTCAA
301 GCCGCGCGCG CTTTGCGCGC AGGCGAATTT GACGATGCTA AACTCGCGCG
351 GCTCGCGCGC TTTACCCAAG CCGTAATGGC AAAAAAGGCC GCGGTATCCG
401 ACGAGGAATC CAAAGCATTT TTGTGATCGG GCTACAACCA CGCAGAGGCA
451 TCGCAAGTCG TGATGGCGCT AGCCTTGGCA ACTTTGTGCA ATCAGCTCAA
501 CAACCTCGGA CAAACGGAAT TCAACCCCGA ATTGCAGGCT TACGCTGA

```

a263.pep

```

1 MARLTVHTE TAPEAAKARV EAVLQNNQFI PNLIGVLSNA PEALAFYQEV
51 GKLNAAANSLT AGEVEVIQII AARTNQCGFC VAGHTKLATL KKLLESEQSVK
101 AARALAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQQA
151 VEVVMGVALA TLCNYVNNLG QTEINPELQA YA*

```

607

m263/a263 97.4% identity in 77 aa overlap

					10	20	30
m263.pep					AAGEFDDAKLGALAAFTQAVMAKKGAVSDE		
a263	QCGFCVAGHTKLATLKKLLSEQSVKAAARALAAAGEFDDAKLGALAAFTQAVMAKKGAVSDE						
	80	90	100	110	120	130	
		40	50	60	70		
m263.pep	ELKAFFDAGYNQQQAVEVVMGXLLATLCNYVNNLGQTEINPELQAYAX						
a263	ELKAFFDAGYNQQQAVEVVMGVALATLCNYVNNLGQTEINPELQAYAX						
	140	150	160	170	180		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

g264.seq

```

1   ttgactttaa cccgaaaaac ccttttcctc ctcaccgccc cggttcggcac
51  acaactccctt cagacggcat ccgcccacgc agtgggtcaag ccggaaaaaac
101 tgcacgcctc cgccaaccgc agctacaaag tcgccgaatt cacgcaaacc
151 ggcaacgcct cgtggtacgg cggcagggtt caccggcgca aaacttcggg
201 cggagaccgc tacgatatga acgcctttac cgccgcccac aaaaccctgc
251 ccatccccag ccatgtgcgc gtaaccaaca caaaaaacgg caaaagcgtc
301 atcgtccgcg tcaacgaccg cggccccttc caccgcaacc gcatcatcga
351 cgtatccaaa gccgcgcgcg aaaaattggg ctttgtcagc caagggacgg
401 cacacgtcaa aatcgaacaa atcgtcccgg gccaatccgc accggttgcc
451 gaaaacaaag acatctttat cgacttgaaa tctttcggtc cggaacacga
501 agcacaagcc tatctgaacc aagccgcccc aaatttcgcc gcttcgtcat
551 caagcccgaa cctctcgggt gaaaaacgcc gttacgaata cgttgtcaaa
601 atgggcccgt ttgcctcgca ggaacgcgcc gccgaagccg aagcgcaggc
651 acgcggtatg gttcgggccc tactgacctc cggttga

```

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

g264.pep

```

1   LTLTRKTLFL LTAAFGTHSL QTASADAVVK PEKLHASANR SYKVAEFTQT
51  GNASWYGGRF HGRKTSGGDR YDMNAFTA AH KTLPIPSHVR VTNTKNGKSV
101 IVRVNDRGPF HGNRIIDVSK AAAQKLGFSV QGTAHVKIEQ IVPQGSAPVA
151 ENKDIFIDLK SFGTEHEAQA YLNQAAQNFA ASSSSPNLSV EKRRYEYVVK
201 MGPFAEQERA AEAEQAQARG MRAVLTSQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

m264.seq

```

1   TTGACTTTAA CCCGAAAAAC CCTTTTCCTT CTCACCGCCG CATTCCGGCAG
51  ACACTCCCTT CAGACGGCAT CCGCCGACGC AGTGGTCAAG GCAGAAAAAC
101 TGCACGCCTC CGCCAACCGC AGCTACAAAG TCGCCGGAAG ACGCTACACG
151 CCGAAAAACC AAGTCGCCGA ATTCACGCAA ACCGGCAACG CCTCGTGGTA
201 CGGCGGCAGG TTTCACGGGC GCAAAACTTC CGGCGGAGAA CGATACGATA
251 TGAACGCCTT TACCGCCGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAATTT GGGCTTTGTC AACCAAGGGA CGGCACACGT CAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACCAGTT GCCGAAAACA AAGACATCTT
501 TATCGACTTG AAATCTTTCG GTACGGAACA CGAAGCACAA GCCTATCTGA
551 ACCAAGCCGC CCAAACTTC GCCGTTTCGT CATCGGGTAC GAACCTCTCG
601 GTTGAAAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTTACCTC
651 GCAGGAACGC GCCGCCGAG CCGAAGCTCA GCGCGCGCGT ATGTTCCGGG
701 CGGTATTGAC CGCCGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264.pep

```

1   LTLTRKTLFL LTAAFGTHSL QTASADAVVK AEKLHASANR SYKVAGKRYT
51  PKNQVAEFTQ TGNASWYGGF FHGRKTSGGF RYDMNAFTA HKTLPISYV
101 RVNTKNGKS VIVRVNDRGP FHGNRIIDVS KAAQKLGFSV NQGTAVKIE
151 QIVPQGSAPV AENKDIFIDL KSFGTEHEAQ AYLNQAAQNFA AVSSSGTNLS
201 VEKRRYEYVV KMGPFSQER AAEAEQAQARG MRAVLTSQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHGRKTSGGDRYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGTEHEAQ					
g264	FHGNRIIDVSKAAQKLG FVSQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGTEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAEQA QARGMVRVAVLTAGX					
g264	AYLNQAAQNFAASSSSPNLSVEKRRYEYVVKMGPFASQERAAEAEQA QARGMVRVAVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

1	TTGACTTTAA	CCCAGAAAAC	CCTTTTCCTC	CTCACCGCCG	CATTTCGGCAT
51	ACATTCCTTT	CAGACGGCAT	CCGCCGACGC	AGTGTCAGG	GCAGAAAAC
101	TGCACGCCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGAAA	ACGCTACACG
151	CCGAAAAC	AAGTCGCCGA	ATTACGCAA	ACCGGCAACG	CCTCGTGGTA
201	CGGCGGCAGG	TTTCACGGGC	GCAAACTTC	CGGCGGAGAA	CGATACGATA
251	TGAACGCCTT	TACCGCCGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTCATCGTCC	CGCTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCCG
401	CGCAAAAT	GGGCTTTGTC	AACCAAGGGA	CGGCGCACGT	CAAAATCGAA
451	CAAATCGTCC	CGGCGCAATC	CGCACCGGTT	GCCGAAAACA	AAGACATCTT
501	CATCGACTTG	AAATCTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCGC	CCAAAACCTG	GCTTCATCGG	CATCAAACCC	GAACCTCTCG
601	GTTGAAAAC	GCCGTTACGA	ATACGTCGTC	AAAATGGGAC	CGTTTGCCTC
651	GCAGGAACGC	GCCGCCGAGG	CCGAAGCTCA	GGCGCGCGGT	ATGTTTCGGG
701	CGGTATTAC	CGCCGGTTGA			

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

1	LTLTRKTLFL	LTAAFGIHSF	QTASADAVVR	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTSGGE	RYDMNAFTA	AHKLPIPSYV
101	RVTNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAQKLGFEV	NQGT AHVKIE
151	QIVPGQSAPV	AENKDIFIDL	KSFGTEHEAQ	AYLNQAAQNL	ASSASNPMLS
201	VEKRRYEYV	KMGPFASQER	AAEAEQAQARG	MVRVAVLTAG*	

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m264.pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264.pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDI FIDLKSFGEHEAQ					
a264	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDI FIDLKSFGEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264.pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAQA RGMVRAVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAQA RGMVRAVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```
m265.seq
1  ATGTCGGTGA TTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GCGCGGCTG ATGATTTTGT CTTGTTTGTG GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGGCGGAA
151 ATGCTCAGCA GTGCGGTTGC GCGCGAGGTC AAGAGAAGGT GTTGTATGTT
201 CATAT.TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGGCGGTCA ATACCGCCCG AACCATACCG
301 CGCGCCTGAG CTTCGGCTTC GCGGCGCGT TCCTGCGAGG TAAACGGTCC
351 CATTTTGACG ACGTATTCGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```
m265.pep
1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFI XFVNRGLENV DINKVSNNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265.pep	MSVILPPTRANA AFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGA EMLSSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGA EMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFI XFAFVNRGLENV DINKVSNNRQ PAVNTARTI PRAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNGDINKVSNNRQPEVSTARTI PRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265.pep	TYSX					
g265	TYSX					
	120					

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

```
a265.seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GGGCGGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GCGGCGGGT AAGAGAAGGC GTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... .GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCGAAC CATAACGCGC
301 GCCTGAGCTT CGGCCTCGGC GCGCGTTC TCGAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

```
a265.pep
1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AAPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDVKGAGHP AVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*
```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265.pep	MSVILPPTRANA	AFSAWARLMIL	SCLLCWCAAC	PWSSSPCPS	WWASAGAEM	LSSAVAAEV
a265	MSVILPPTRANA	AFSAWARLMIL	SCLLCWCAAC	PWSSSPCPS	WWASAGAEM	PISAVAAAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFIXFA	VNRGLENDIN	KVSNRQPAV	NTARTIPRAX	ASASAARSCE	VNGPILTT
a265	KRRRLKFI---	FAPAKYLXXCL	KDVKGAGHPA	VNTARTIPRAX	ASASAARSCE	ANGPILTT
	70	80	90	100	110	
m265.pep	TYSX					
a265	TYSX					120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

```
g266.seq
1  agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccacatcg
51  accgcatcca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcctc acgaccagac tggtcggcgt ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgacg gagctggcgg caggtttcgc gctgaccgcc
201 tctcttgccg acatcctcga atcccgtagc ggagcggtag acaatcaggg
251 ttgggagttt tacgccaccg tcgtctgcct gtacctcatt ttcgccttcc
301 cgtgtttcgt gcggcggtat ttttggcaca cgcgcaacag ggaataa
```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

```
g266.pep
1  MQFRRHRRRQ CPNRKPIMTA SMYILLVLAL IFANAPFLT RTLFGVAALKR
51  KHFGHHLIEL AAGFALTASL AYILES RAGA VHNQGWEFYA TVVCLYLIFA
101 FPCFVRRYFW HTRNRE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

```
m266.seq
1  ATGCCGTTCC GCAACGCGtT cAGACGGCAT CGCCGCCGAC AACGCCTAAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGGCAC
101 TCATCTTTGC CAACGCCCCC TTCCTCACGA CCAGACTGTT CGGCGTGGCC
151 rCACTCAAGC GCAAACATT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGCAAGAT
251 CCGTACACGA TCAGGTTTGG GAGTTTATG CCACAGTCGT CTGCTGTAC
301 CTGATTTTGG CGTTTCCATG TTTTGTGTGG CGGTATTTT GGCACACGCG
351 CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng)

from *N. gonorrhoeae*:

m266/g266

	10	20	30	40	50	60
m266.pep	MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH					
g266	MQFRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH					
	10	20	30	40	50	

	70	80	90	100	110	120
m266.pep	MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX					
	:					
g266	LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX					
	60	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTG CTGCTGCCT
101  TGATTTTTC CAACGCCCC TTCCTACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTCGCGCTG ACCGCCGTTT TCGCTACAT CCTCGAATCC CGTGCGGGAG
251  CGGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTGT CTGCCTGTAC
301  CTGATTTTTC CGTTCCCTG TTTCTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLEGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

	10	20	30	40	50	60
m266.pep	MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH					
a266	MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTLKLGIVPLKRKHFGHH					
	10	20	30	40	50	60

	70	80	90	100	110	120
m266.pep	MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE					
	:					
a266	LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE					
	70	80	90	100	110	120

m266.pep	X
a266	X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

g267.seq



This corresponds to the amino acid sequence <SEQ ID 1076; ORF 267.ng>:

1 MQVAFFLAVV FKNMGFHNRI GRAGLFAETA EDALGOVDVV TLGAAGAVFA  
51 FFRFDVDRHC RTHRLAQFTR DAAFLSVRKT ALRVQTAETH GLRRFLPGKI  
101 NCVFAGKKVF ERYAHAFDQF AKQKGFY\*

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	AGTCGGGCAT	GCCTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTAC	CGTCTTCACG
151	TTCTTCCGAT	TCGATGTTAA	TCGCCATTGC	CGGACACACT	GCCTCACACA
201	ACTTACACGC	GATACACCGC	TCTTCGCCCT	TCGGATACCC	CcGCTCGCGG
251	TGCAGACCCG	GGAAACGCAC	GGAATTGCGG	GTTTCTCTCT	CGGGGAAATA
301	AATTGTGTCT	TTGCGGGCGA	AAAAGTTTTT	GAGCGTTACG	CCCATACCTT
351	TTACCAATTG	GCCAAGCAGA	AAGGTTTTTA	CTAA	

1 VQVAFFLAVV FKNMGFHNRI SRACLEAETA EDALGQVDVV TLGAARTVFT  
51 FFRFDVNRHC RTHCLTQLTR DTPLFAVRIP PLRVQTAETH GLRRFLFGEI  
101 NCVFAGEKVF ERYAHTFYQF AKQKGFY\*

from *N. gonorrhoeae*:

		10	20	30	40	50	60
m267.pep		VQVAFFLAVVFKNMGFHNRI	SRACLF	AE	TAEDAL	GQVDVVTLGAARTV	FTFFRFDVNRHC
		:					:
g267		MQVAFFLAVVFKNMGFHNRI	GRAGLF	AE	TAEDAL	GQVDVVTLGAAGAV	FAFFRFDVRHC
		:					:
		10	20	30	40	50	60
		70	80	90	100	110	120
m267.pep		RTHCLTQLTRDTP	PLFAVRI	PPLRVQ	TAETHGLRR	FLFGEINC	VFAGEKV
			: :	:	:	:	:
g267		RTHRLAQFT	RDAAFLSV	RKLTALRV	QTAETHGLRR	FLFGKINC	VFAGKKV
			: :	:	:	:	:
		70	80	90	100	110	120
m267.pep		AKQKG	FYX				
g267		AKQKG	FYX				

seq					
1	GTGCAAGTCG	CCTTTTTTCT	CGCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	GGTCGGGCAG	GCTCTTTCGC	AGAAACCGCA	GAAGATCGAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTGC	CGTCTTCGGC
151	TTCTTCCGAT	TCGATGTTGA	TCGCAGATTG	GGGGCAAACG	GCTTCACACA
201	ATTTACACGC	GATGCAGCGT	TCCTCGCCGT	TTGGATAACG	GC GTTGC GCG
251	TGCAGACCGC	GGAAACGCAC	GGATTGCGGC	GTTTCTCTTT	CGGGAAAAATA
301	AATCGTGTCT	TTGCGGGCAA	AAAGGTTTTT	GACCGTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAAGCAA	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
51  FFRFDVDRHC GANGTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDVV	TLGAARTVFTFF	FRFDVNRHC		
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFAFF	FRFDVDRHC		
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTP	PLFAVRIPPLRVQTAETH	GLRRFLFGEINC	VFAGEKVFERYAHTFYQF		
a267	GANGTQFTRDAAFLAVWIT	ALRVQTAETHGLRRFL	FGKINRVFAGKKVFERYAHTFYQF			
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaattt
101 cctgcggaag cgaagagact aaagagattt tgggtcaaact ggtccgcgac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201 ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggctgaaac
251 gtttgggcat aaccgtcgat gaagtccgaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccagacga
351 tgttgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451 tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaagcaa
501 aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctggtgtc tatggcactg attaaagagc cgttggacaa agcgaaacaa
601 aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgagggg
651 ggcagaagaa gcggcgggcg agggagcatt gggctcggag caggaaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801 ctgcagaaaa acatggaaaa gcggtatgga caagatctgt gccacaatg
851 cgaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901 tgtaaaacgg cagaaaccga agcagcgttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLIGINPFSG KEISCGSEET KEILVKLVDRD
51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTTEKTD
101 SSKLKCEAAL KLDVPDDVVD YAVAAQSIG NSHKKTPDFF EPYYRKEGAY
151 YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201 RNEKLEAAEA TAQEAREAE AAAQEALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKIQASQK TWKSGMDKIC ANNAKAEGET PNGIKVSELA
301 CKTAETEARL EELHNRRKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAAGAGCC GTTGGACAAA GTGAAACAAA GGAACGAAGA
```

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```

51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101 AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTGCGGC
151 AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAACn TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401 AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1  ..MALIKEPLDK VKQRNEELEA AEEAAAEAL GREQEAAVRS EWEERYKLSR
51  XQFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GKTTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

                                10      20
m268.pep                      MALIKEPLDKVKQRNEELEA-----
                                |||:|||:|||:|||:|||:|||:|||:|||
g268      SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQEARE
          160      170      180      190      200      210

                                30      40      50      60      70      80
m268.pep  --EAAAEALGREQEAAVRSWEERYKLSRSQFEQFWKGLPQTQVQNKLPQSQTWKSMD
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      AEEAAAEALGREQEAAVRSWEERYKLSRSEFEQFWKGLPQTQVQNKLPQSQTWKSMD
          220      230      240      250      260      270

                                90      100     110     120     130     140
m268.pep  KICANNAKAEKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      KICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
          280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

```

a268.seq
1  ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTGCGGC
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GGAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

```

a268.pep
1  MALIKEPLDK AKQRNEELEA AEEAAAEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTQVQNKLQA SQKTWKSMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

                                10      20      30      40      50      60
m268.pep  MALIKEPLDKVKQRNEELEAAEEAAAEALGREQEAAVRSWEERYKLSRXQFEQFWKGL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a268      MALIKEPLDKAKQRNEELEAAEEAAAEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

	10	20	30	40	50	60
m268.pep	PQTQVKNKLP	SQKTWKSMDKICANNAKAEGKTPNGIKFSE	LACKTAKEARLEELHNRK			
a268	PQTQVKNKLQASQKTWKSMDKICANNAKAEGETPNGIKFSE	LACKTAETAERLEELHNRK				
	70	80	90	100	110	120
m268.pep	KALIDEMXREADXKELS	KRLX				
a268	KALLDEMAREADKKELP	KRLX				
	130	140				

m268-1.seq

```
1 GTGCAATCCC GATATGATGG TTTGCATAAA TTTAAACATA TATGTTCCGC
51 AGCTATGGCA CTGATTAAAG AGCGTGTGGA CAAAGTGAAG CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 CGCGACGAGG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTCTA AGCCTACAG AARAACTGGA AAAGCGGGAT GGATAAAAATC
301 TGTGCCAACA ATGCGGAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGCGGAAAAC CGAAGCACGC TTGGAGAGAC
401 TGCACAACCG TAAAAAAGCC CTTATCGACG AAATGCCACG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG CTTCTGA
```

m268-1.pep

1	VQSRDGLHK	FKHCSAAMA	LIKEPLDKVK	QRNEELEAAE	EAAAQEALGR
51	EQEAARVSEW	EERYKLSRSE	FEQFWKGLPQ	TVQNKLQASQ	KTWKSGMDKI
101	CANNAKAEGK	TPNGIKFSEL	ACKTAKTEAR	LEELHNKKA	LIDEMAREAD
151	KKELSKRL*				

				10	20	30	
m268-1.pep				VQSR	DGLHKFKHKICS	AAMALIKEPLDKVKQRNE	
				:	:	:	:
g268	KEGAY	YVKTIS	YSVQPT	DDKSK	IFAE	LSQAHDIHPLSELVS	--MALIKEPLDKAKQRNE
	150	160	170	180	190	200	
		40		50	60	70	80
m268-1.pep	ELEAAE	-----	EAAAQ	EALGREQE	AARVSEWEERYK	LSRSEFEQ	FWKGLPQTQVN
	:	:	:	:	:	:	:
g268	KLEAAE	ATAQEAREAE	EAQALGREQE	AARVSEWEERYK	LSRSEFEQ	FWKGLPQTQVN	
	210	220	230	240	250	260	
		90	100	110	120	130	140
m268-1.pep	KLQAS	QKTWKSGMDK	ICANNAKA	EGKTPNGIKF	SELACKTAKTEAR	LEELHNRKKALIDE	
	:	:	:	:	:	:	:
g268	KLQAS	QKTWKSGMDK	ICANNAKA	EGETPNGIKV	SELACKTATETEAR	LEELHNRKKALIDE	
	270	280	290	300	310	320	
		150	159				
m268-1.pep	MAREAD	KKELSKRLX					
	:	:	:	:	:	:	:
g268	MVREED	KKELPKRLX					
	330						

**a268-1.seq**

1	GTGCAATCCC	GATATGATGG	TTTGATAAAA	TTTAAACATA	TATGTTCGCG
51	AGCPATGGCA	CTGATTAAAG	AGCCGTTGGA	CAAAGCGAAA	CAAAGGAACG
101	AAGAACTTGA	AGCGGCAGAA	GAGCGGCGGG	CGCAGGAGCG	ATTGGGTCCG
151	GACGAGGAAG	TCGACGCCGT	ATCCGAATGG	GAGAAGCGCT	ACAAGCTGTC
201	CGCAGCAGCG	TTCGAGCAGT	TCTGGAAGAG	ATTGCCTCAA	ACCGTAGCTA
251	ATAAGCTGCA	AGCCTCACAG	TAACATTTGGA	AAAGCGGGAT	GGATAAAATC
301	TGTGCCCAAC	ATGCGAAAGC	TGAAGGTGAA	ACGCCAAACG	GCATAAAATC
351	CAGCGCAACTG	CGTCGAAAAA	CGGCGGAAAC	CGAAGCACGC	TGGGAAGAGC

616

401 TGCACAACCG TAAAAAGCC CTTCTGACG AAATGGCCAG GGAAGCGGAC  
 451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep  
 1 VQSRDGLHK FKHCSAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR  
 51 EQEVDVRSEW EERYKLSRSE FEQFWKGLPQ TVQNKLOASQ KTWKSGMDKI  
 101 CANNAKAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LLEDEMAREAD  
 151 KKELPKRL\*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHCSAAMALIKEPLDKAKQRNEELEAAEAAAQALGREQEVDRVSEW					
m268-1	VQSRDGLHKFKHCSAAMALIKEPLDKVQRNEELEAAEAAAQALGREQEAARVSEW					
	10	20	30	40	50	60
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEKTPNGIKFSEL					
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEKTPNGIKFSEL					
	70	80	90	100	110	120
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKALLDEMAREADKKELPKRLX					
m268-1	ACKTAETEARLEELHNRKKALLDEMAREADKKELSKRLX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq  
 1 atggtttggc gtgtgaattg cgcggcaacg gcggcgctga ttttttcgtc  
 51 cagcccttgg atttgggagg tggtgtgggt gtggtcgagg tcggcttttt  
 101 cctgcaaac ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttggcg  
 151 gtttcgccgt gggactttat ccggaacacg gcttcgccca aggtgtcggc  
 201 ggctttgatg cacagtttta aaaccagggc tttggggcgg ttttctgcgc  
 251 cggcgttgcc cattttgctg tccaatcgcg gggttaaaaa accggtgtcg  
 301 ttttaagtcgc cgtccgtcca agtcgatacg agcgcgcttc tttgccttcc  
 351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep  
 1 MVWRVNCAAT AALIFSSSPW IWAUVVWWSR SAFSCKPCAS LDASSAPALA  
 51 VSPWDFIRNT ASPKVSAALM HSFKTRALGR FSAPPVAILL SNRGVKKPLS  
 101 FKSPSVQVDT SALLCLSLRS S\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq  
 1 ATGGTTTGGC GTGTGAATTG CGCGCAACG GCGGTGCTGA TTTTTCGTC  
 51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGTCTCGG TCGGCTTTGT  
 101 CTTGCAACC TTGCGCCaCG TGCCCGCGTC CAGCGCCTGC GTTGATGGTT  
 151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTCGGCGGC  
 201 TTTGATGCAC AGTTTAAAA CCAGGGCTTT GGGGCGGTTT TCGTCGCCGC  
 251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TAAAAAGCC GTTGTCGTTT  
 301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGCTTCTCT GCCTTTCGTT  
 351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep  
 1 MVWRVNCAAT AVLIFSSSPW IWAUVVWWSR SALSCKPCAT CPRPAPALMV  
 51 SPWDFIQNTA SPKVSAALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF  
 101 KFSSVQVDT SALLCLSLRS \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng)

from *N. gonorrhoeae*:

```

m269.pep  MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT  59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g269       MVWRVNCAATAALIFSSSPWIWAVVWVWSRSFSCPCASLDASSAPALAVSPWDFIRNT  60

m269.pep  ASPKVSAAALMHSEKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTSAALLCLSLRS  119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g269       ASPKVSAAALMHSEKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDTSAALLCLSLRS  120

m269.pep  SX  121
          ||
g269      SX  122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269.seq
1  ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCCAGCT CCAGCGCGCC GCGGTTGACG
151 GTTTCGCCGT GGGACTTTAT CCAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTAA AAACCAAGGC TTTGGGCGCG TTTTCGTTCG
251 CGCGTGTGCG CATTTTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTTGTCT
301 TTTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1096; ORF 269.a&gt;:

```

a269.pep
1  MVWRVNCAAT AVLIFSSSPW IWAAVWVWAR SALSWRFCAS VPASSAPALT
51 VSPWDFIQNT ASPKVSAAAL HSEKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

m269.pep  10 20 30 40 50 59
MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a269       10 20 30 40 50 60
MVWRVNCAATAVLIFSSSPWIWAAVWVWARSALSWRFCASVPASSAPALTVPWDFIQNT

m269.pep  60 70 80 90 100 110 119
ASPKVSAAALMHSEKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTSAALLCLSLRS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a269       60 70 80 90 100 110 120
ASPKVSAAALMHSEKTRALGRFSSPPVAILLSRGVKKPLSFKFSSVQVDTSAALLCLSLWS

m269.pep  120
          SX
          ||
a269      120
          SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270.seq
1  atgaataaaa accgcaaatt actgcttgcc gcaactgctgc tgactgcctt
51 tgccgccttc aagctcgttt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg aggggtgcac gctgccggac
151 ggaagccgtg tccgcgcgcg cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgcccc cgggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcacg cgctgcccgc tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgccgaa taa

```

This corresponds to the amino acid sequence &lt;SEQ ID 1098; ORF 270.ng&gt;:

g270.pep  
 1 MNKNRKLLLA ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD  
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ  
 101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq  
 1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT  
 51 TGCCGCCGTC AAGCTCGTTT TGTTGCAATG GTGGCAGGCG Ca.CAGCCGC  
 101 AAGCTGTGGC GGCACAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC  
 151 GGAAGCCGCG TCCGCGCCGC CGCGGTTCA ACCAAAAAAC CGTTTGATAT  
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA  
 251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA  
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA  
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTT  
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep  
 1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD  
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ  
 101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng)

from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRKLLLAALLLIAFAAVKLVLLQWWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
g270	MNKNRKLLLAALLLTAFAAFKLVLLQWWQAQQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
	10	20	30	40	50	60
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRI RLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARI RLPVCVEGRR					
	70	80	90	100	110	120
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq  
 1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT  
 51 TGCCGCCGTC AAGCTCGTTT TGTTGCAATG GTGGCAGGCG CAGCAGCCGC  
 101 AAGCTGTGGC GGCACAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC  
 151 GGAAGCCGCG TCCGCGCCGC CGCCGTTTCA ACCAAAAAAC CGTTTGATAT  
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA  
 251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA  
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA  
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTT  
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep  
 1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD  
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ

619

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE \*

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALL	LIAFAA	VLVLLQ	WQAXQP	QAVAAQ
a270	MNKNRKL	LLAALL	LIAFAA	VLVLLQ	WQAXQP	QAVAAQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPF	DIYIEH	APAGTE	QVSISF	SMKNMD	MGFNRY
a270	TKKPF	DIYIEH	APAGTE	QVSISF	SMKNMD	MGFNRY
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADIT	IGSRTF	QTAFTA	EX		
a270	DFTADIT	IGSRTF	QTAFTA	EX		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

```

1  atgttcagtt  cgcgcatggc  gaggatttgg  gcgacggggg  taacgttgtg
51  tatggtcagt  ccgtgtccgg  cggtgacgac  caagcccaaa  tcgccggcga
101  aatgcgcgcc  gttttggatg  cgctcgaaact  gcctgatttg  ttcggcgctg
151  ctttgtgcgt  cggcatatgc  gccggtgtgc  agctcgacaa  cgggcgcgcc
201  gacatcacgg  gcggcttggg  tttgcctgtc  gtcggcatcg  ataaacaagg
251  acacgcgat  gcccgcgctc  gtcaggattt  tggcgaattc  ggcgattttt
301  tcctgttgcg  ccaatacgtc  caaaccgcct  tcggtcgtga  tttcctgccg
351  tttttcaggc  acgatgcaca  cgtcttcagg  catcacttta  agcgcgtttt
401  cgagcatttc  ttccgtcaac  gccatttcaa  gggtcaggcg  cgtgcggtatg
451  gcgtttttga  cggcaaatac  atccgcgtct  ttgatgtggc  ggcggtcttc
501  gcgcaggtgc  atggtaatca  ggtctgcacc  gtgcgtttcg  gcaaccagtg
551  ccgcctccac  ggggctggga  taa

```

This corresponds to the amino acid sequence &lt;SEQ ID 1104; ORF 271.ng&gt;:

g271.pep

```

1  MFSSRMARIW  ATGVTLCMVS  PCPALTTKPK  SPAKCAPFWM  RSNCLICSAW
51  LCASAYAPVC  SSTTGAPTSR  AAWICLSSAS  INKDTRMPAS  VRILANSAIF
101  SCCANTSKPP  SVVISCRFSG  TMHTSSGITL  SAFSSISSVN  AISRFRRVRM
151  AFLTANTSAS  LMWRRSSRRC  MVIRSAPCVS  ATSAASTGLG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

```

1  AwGTTcagTT  CGCGGATGGC  GAGGATTtGG  GCGATGGGGG  TAACGTTtGTG
51  TATGGTcagT  CCGTGTCCGG  CGTTGACGAC  CAAGCCCAAA  TCGCCGGCGA
101  AATGCGCGCC  GTTTTGGATG  CGCTCGAACT  GCCTGATTtG  TTCGGCGTGG
151  CTGCGCGCGT  CGGCATACGC  GCCTGTGTGC  AGCTCGACAA  CGGGCGCGCC
201  GACATCACGG  GCGGCTTGGG  TTTGCCTGTG  GTCGGCATCG  ATAAACAAAG
251  ACACGCGTAT  GCCTGCGTCG  GTCAGGATTt  TGGTGAACCC  GGCgATTtTT
301  TCCTGTTGCG  CCAATACGTC  CAAACCGCCT  TCGGTcGTGA  TTTcCTGACG
351  TTTTcCAGGC  ACgATGCACA  CGTCTTCGGG  CATCACTtTC  AAAGCGTtTT
401  CCAACATTTC  TTCCGTCAAC  GCCATTtCAA  GGTTcAGGCG  CGTGCGGATG
451  GCGTtTTTGA  CGGCAACAC  GTCCGCGTCT  TTgATGTGGC  GGCgGTCTTC
501  GCGCAGGTGC  ATGgTAATCA  AATCCGCACC  GTGCGTtTCG  GCAACcAGTG
551  CCGCCTCCAC  GGGGCTGGGA  TAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1106; ORF 271&gt;:

m271.pep

```

1  XFSSRMARIW  AMGVTLCMVS  PCPALTTKPK  SPAKCAPFWM  RSNCLICSAW
51  LRASAYAPVC  SSTTGAPTSR  AAWICLSSAS  INKDTRMPAS  VRILVNPAIF
101  SCCANTSKPP  SVVISXRFSG  TMHTSSGITF  KAfSNISSVN  AISRFRRVRM
151  AFLTANTSAS  LMWRRSSRRC  MVIKSAPCVS  ATSAASTGLG *

```

Computer analysis of this amino acid sequence gave the following results:



620

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTS KPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANSALFSCCANTS KPPSVVISCRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRSAAPCVS					
g271	TMHTSSGITLSAFSSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRSAAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271.seq

```

1  ATGTTTCAGTT CGCGGATGGC GAGGATTGGG GCGATGGGGG TAACGTTGTG
51  TATGGTCAGT  CCGTGTCCGG CGTTGACGAC CAAGCCCAA TCGCTGGCAA
101 AATGCGCGCC  GTTTTGGATG CGCTCGAACT GCCTGATTTG TTCGCGGTGG
151 CTGCGCGCGT  CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGCGCGGCC
201 GACATCACGG  GCGGCTTGGA TTTGCCTGTC GTCGGCATCG ATAAACAAGG
251 ACACGCGTAT  GCGCGGTCG GTCAGGATT TGGTGAATTC GGCAATTTTG
301 TCTTGTGCG  CCAATACGTC CAAGCCGCCT TCGTCTGTGA TTTCCTGACG
351 TTTTCCGGC  ACGATGCACA CGTCTTCCGG CATCACTTTA AGCGCGTTTT
401 CGAGCATTTT  TTCCGTCAAC GCCATTCAA GGTTCAGGCG CGTGCGGATG
451 GCGTTTTTGA  CAGCAAACAC GTCCGCGTCT TTGATGTGGC GCGGTCTTTC
501 GCGCAGGTGC  ATGGTAATCA GGTCCGCACC GTGCGTTTCG GCAACCAAGT
551 CCGCTCCAC  GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271.pep

```

1  MFSSRMARIW AMGVTLCMVS PCPALTTKPK SLAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNSAIL
101 SCCANTS KPP SVVIS*RFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRSAAPCVS ATSAASTGLG *

```

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTS KPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTS KPPSVVISXRFSG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNISRFRVRMAFLTANTSASLMWRRSSRRRCMVKSAPCVS					
a271	TMHTSSGITLSAFSSISSVNISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1  atgactgcaa aggaagaact gttcgcgatg ctgcgccata tgaacaaaaa
51  caaaggttcc gacctgtttg tgacgacca tttcccgccc gctatgaagc
101 tggacggcaa aatcacccgc atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcacgcacc aacgagtgca atttcgccat cagcctgcgc gacaccagcc
251 gcttccgcgt caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgcccgc
351 ggccttgaag gatgttcgcg tgaaaaaacg cgggctggtt atttttgtcg
401 gcggcaccgg ctccgggcaaa tcgacttcgc tcgcctcgct tatcgactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaa gattccgatcga
501 gtttgtccac gaacacaaaa actgcatcat taccagcgcg gaggtcggcg
551 tggacacgga aaactggatg gcggcggtga aaaatacgct gcgtcaggcg
601 ccggatgtga tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc tttgccgaaa cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctccgaccga tcatcaactt cttccccgag
751 gagcggcgcg aacaattgct gacggatttg tcgtcaacc ttcaggcggt
801 tatttcgcaa cgcctcgctc cgcgagacgg cggcaaggcg aggggtggcg
851 cagtcgaggt gctgctcaat tcgcccctga tttcggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttcgct
1051 ttggcggtac agttgcgcag ccgcagggca caaagtccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1  MTAKEELFAW LRHMNKNKGS DLFVTTTFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNM IQRGATALVF
101 RAITSKIPKF ESLNLPALK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQ EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLGMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDLELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1  ATGACCGCAA AGGAAGAAGT GTTCGCATGG CTGCGCCATA TGAWCCAAAA
51  CAAAGGTTCC GACCTGTTCC TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCCTGAC GGCGGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAAAAACG CGGGCTGTT ATTTTGTTCG
401 GCGGCACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG

```

```

551 TGGATACGGA AACTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCGATGTC TCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTCCCGGAG
751 GAGCGGCGCG AACAAATGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTCGCAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCTGA TTTGGAGTT GATTCACAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTCCCTGCA AGAAGCATTG AAAAAATGCC ATTCCGCACA CGATTTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CAaAGTTyCA GCCCGGATT
1101 GGNACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

```

m272.pep
1  MTAKEELFAW LRHMxQNKGS DLFVTHFPF AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAI IQRGATLVF
101 RTITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQ EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETGHLMA TLHANSTNQA LDRIINFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGDISLQEAL KNADSAHDLR
351 LAVQLRSRRA QXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

	10	20	30	40	50	60
m272.pep	MTAKEELFAWLRHMxQNKGS DLFVTHFPF AMKLDGKITR ITDEPLTAEK CMEIAFSIMS					
g272	MTAKEELFAWLRHMxQNKGS DLFVTHFPF AMKLDGKITR ITDEPLTAEK CMEIAFSIMS					
	10	20	30	40	50	60
m272.pep	70	80	90	100	110	120
g272	70	80	90	100	110	120
	130	140	150	160	170	180
m272.pep	DVALKKRGLVIFVGGTSGSK STSLASLIDY RNENSFGHII TIEDPIEFVH EHKNCIITQR					
g272	DVALKKRGLVIFVGGTSGSK STSLASLIDY RNENSFGHII TIEDPIEFVH EHKNCIITQR					
	130	140	150	160	170	180
m272.pep	190	200	210	220	230	240
g272	190	200	210	220	230	240
	250	260	270	280	290	300
m272.pep	LDRIINFPEERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN					
g272	LDRIINFPEERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN					
	250	260	270	280	290	300
m272.pep	310	320	330	340	350	360
g272	310	320	330	340	350	360
	310	320	330	340	350	360

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m272.pep                    370  
                               QSXSPDLXLLX  
                               || :||| |||  
 g272                        QSSDPDLELLX  
                               370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

a272.seq

```

1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCC TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GGCGGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAACG CGGGCTGGTT ATTTTGTGTC
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTGCGCG
551 TGGATACGGA AACTGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTGG TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCCGAGTT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGCA GGATGCCTTG AAAATGCCG ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTTCCG GTCCCGATT
1101 GGAAGTGCTC TGA
  
```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

a272.pep

```

1  MTAKEELFAW LRHMNKNKGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNAM IQRGATALVF
101 RAITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTGSGK STSLASLIDY
151 RNENSGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RAAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMOF FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDELL *
  
```

m272/a272 97.6% identity in 370 aa overlap

	10	20	30	40	50	60
m272.pep	MTAKEELFAWLRHMNKNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
a272	MTAKEELFAWLRHMNKNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
	10	20	30	40	50	60
m272.pep	AKQAEFFSSTNECNFAISLP DTSRFRVNA MIQRGATALVFRTITSKIPKFESLNLPVVK					
a272	AKQAEFFSSTNECNFAISLP DTSRFRVNA MIQRGATALVFRITSKIPKFESLNLPVVK					
	70	80	90	100	110	120
m272.pep	DVALKKRGLVIFVGGTGSGKSTSLASLIDYRNENSGHII TIEDPIEFVHEHKNCIITQR					
a272	DVALKKRGLVIFVGGTGSGKSTSLASLIDYRNENSGHII TIEDPIEFVHEHKNCIITQR					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
	190	200	210	220	230	240
	250	260	270	280	290	300
m272.pep	LDRIINFFPEERREQLTDL SLN LQAFISQRLVPRDGGKGRVA AVEVLLNSPLISELIHN					
a272	LDRIINFFPEERREQLTDL SLN LQAFISQRLVPRDGGKGRVA AVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272.pep	GNIHEIKEVMKSTTLGMQTFDQHL Y QLYEKGDISLQEALKNADSAHDLRLAVQLRSRRA					
a272	GNIHEIKEVMKSTTLGMQTFDQHL Y QLYEKG E I S L Q D A L K N A D S A H D L R L A V Q L R S R Q A					
	310	320	330	340	350	360
	370					
m272.pep	QSXS PDLXLLX					
	:					
a272	QSSGPDLELLX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

```

g273.seq
1  atgagtccttc aggcgggtatt tatataccccc ccaagccgta ccgcacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattcacccg ttttctgccg gtttctgtgc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcggca gccgcgcccg acattggcat tgtgttcatt
251 gttgttcctt aacggttaaa aaccgcgccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcgggcgc gtgcgcgtga aatcaaggcg
351 gtttgagaag tgtttcnacc gcgcccgcgc tatgtgccga aatattattt
401 gtcgctcacc tgcaaaatcg ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgectg cttttgttt ttcaagcagt
501 tttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

```

g273.pep
1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ QSGKHTDRR QDIGVFEAGT
51  PFTVFLPLV AFEIKDDAGK QRSRARHWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCCR VPLKSRFEK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

```

m273.seq
1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCTCCG TTTCTCTGCC GCTTCTGTGC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT TGTGTTTCATT
251 GTTGTTCTCTT AATGCTTAAA AACC CGCCTG TCCGTGCAAC CGTTTAAAGG
301 CGGCAAATG CAAAATTGTG TTGCGGGCGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTCCCGAC GCGCCGCCCT GTGTGCCGGA GTTATTTGTC
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTACCTGCCT TTTGKTWTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

```

m273.pep
1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ QSGKHADRC QDIGVFKAGT
51  PFFVFLPLLV AFEIKDDAGK QRSRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCCR VPLKSGRFEK CSRRALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSYA *

```

Computer analysis of this amino acid sequence gave the following results:

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/q273

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSR	TAQYNENQENG	GKAHKQ	QSGKHADRC	QDIGVF	KAGTFFPVFLPLL
g273	MSLQAVFIYPPSR	TAQYNENQENG	GKAHKQ	QSGKH	TD	RRQDIGVF
	10	20	30	40	50	60
	70	80	90	100	110	120
m273.pep	AFEIKDDAGK	QGRSRARH	XHC	CVHCCS	LM	LKNP
g273	AFEIKDDAGK	QGRSRARH	WH	CVHCCS	LT	VKNP
	70	80	90	100	110	120
	130	140	150	160	170	
m273.pep	CSRRA-ALCAG	VICRSPAKS	PRTRFAE	FP	HC	PLVSYGVYLP
g273	CFXRARPM	CRNIICRSPAKS	PRTRFAE	FP	RC	PLVSYGVYLP
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

seq					
1	ATGAGTCTTC	AGGCGGTATT	TGTATACCCC	CCAAGCCGTA	C CGCACAAATA
51	CAACGAAAAT	CAGGAAAACG	GCGGTAAAGC	TCATAAACAG	GGACAAAGCG
101	GCAAACACGC	CGACCGCCGT	CAGGATATAG	GCGTATTCCA	GACCGGAACT
151	CCATTACCG	TTTTCTGCC	GCTTTTGTC	GCTTTTGAAA	TAAAGGATGA
201	TGCCGGCAAG	CAGCGCGGCA	GCCGCGCCCC	ACATTAGCAT	AATGTTTATT
251	GTTGTTCTT	AACGTTTAAA	AACCCGCCCG	TCCGTGCAAC	CGTTTTTAAAG
301	AGGCGGTAAA	TCACAAAGTT	TGTTGGCGGA	CGTGCTCTCT	TACAATCAGG
351	GCGGTTTAA	GGGCATGATG	CAC TGCCCCG	TGTGCCGGAT	ATTATTGTGC
401	GCTCACCTGC	AAAATTGCCA	AGAACC GCCT	TTGCGGGATT	TCCACATTGC
451	CCACTTGTTT	CATACGGCGT	TTGCCTGCTT	TTTGT TTTTC	AAGCAGTTTT
501	TTCTTACGCG	TAA			

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

```

1  MSLQAVFVYP  PSRTAQYNEN  QENGGKAHKQ  QSGSKHADRR  QDIGVFQTGT
51  PFTVELPLFV  AFEIKDDAGK  QRGSRARH*H  NVHCCSLTVK  NPPVRATVFK
101 RR*ITKFVGG  RALLQSGREF  GHDALPRVPD  IICRSPAKLP  RTRFAGFPHC
151 PLVSYGVCLL  FVFQAVFSYA  *

```

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKHQGQSGKHADRCQDIGVFKA	AGTFFPVPFLPLL				
a273	MSLQAVFIYPPSRTAQYNENQENGGAHKHQGQSGKHADRRQDIGVFQ	IGTGTFTTVPFLPLFV				
	10	20	30	40	50	60
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRRARHXHC	VMHCCSLMLKNP	PVRATVL-RRQIAKFV	CGRVP	PLKSGRFE	
a273	AFEIKDDAGKQGRSRRARHXH	NVHCCSLTVK	NFPVRATVFKR	XTKFGGR	ALLQSGRFEK	
	70	80	90	100	110	120
	120	130	140	150	160	170
m273.pep	GCSRRALCAGVICRSPAKSP	TRTFAEFPHCPLVSYGV	YLPVFXQAVFSYAX			
a273	GHDALPRV-PDIICRSPAKLP	TRTFAGFPHCPLVSYGV	CLLFVFXQAVFSYAX			
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

g274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCatCGCC AgcgTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGGATG
101 GCAAGCATAT CGACATCCAG CTTATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTCCT CATTCTCCC GATATGAATG CGGCAAAAGT
201 GTTTGTGGGc ggCgagtTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTgt tcaaAACCCT
351 TCCGCCGCC AACCCTGGT ATGTGCGCGT GGAggacgCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AGGCAATGC GGTGCGATTG
451 ACCCCGATGG ACAAACTTTT CAATAATGCA GGAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

g274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLPPA NHWYVRVEDA AGVWRVENKW ITSQGNVAVL
151 TPMDKLFNNA GSK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

m274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAACATAT CGACATCCAG CTTATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTCCCCC GATATGAATG CGGCAAAAGT
201 GTTTGTGGGc GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAAACCCT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGCGATTG
451 ACCCCGATGG ACAAGCTTTT CAATAATACT GAAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

m274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQGNVAVL
151 TPMDKLFNNT ESK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
m274	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g274.pep	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLPPA					
m274	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
g274.pep	NHWYVRVEDA AGVWRVENKW ITSQGNVAVL TPMDKLFN NAGSKX					
m274	NHWYVRVEDA AGVWRVENKW ITSQGNVAVL TPMDKLFN NTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCTCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCGGC GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGGAATAT GAGGCGGTGT TCAAAACCTT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GCGCGCTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTCGATTGG
451 ACCCCGATGG ACAAACCTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQGNVAVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
a274	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
	10	20	30	40	50	60
m274.pep	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
a274	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
m274.pep	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
a274	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
m274.pep	NHWYVRVEDA AGVWRVENKW ITSQGNVAVDL TPMDKLFNNTESKX					
a274	NHWYVRVEDA AGVWRVENKW ITSQGNVAVDL TPMDKLFNNTESKX					
	130	140	150	160		
m274.pep	NHWYVRVEDA AGVWRVENKW ITSQGNVAVDL TPMDKLFNNTESKX					
a274	NHWYVRVEDA AGVWRVENKW ITSQGNVAVDL TPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1  atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tggcgacga tgaatgccgt gcggttttcc atcaggcgtt
101 cgagcgcttg ttggacgagg cgttcggatt cgttgccaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgcgctt ttcaaatgg cgcgggcgat
201 ggcgacgcgt tgcgctgtgc cgccggataa gttgctgccg ttcgatccga
251 tgggctggtg cagtcgagc ggggatgcgt cgatcaggct ttgcagggtg
301 gcggtcttga gggcgacag gacttcggct tcgcccgcgt cgggacggct
351 gtatcgagc ttttcaaaca ggggtgctgc aaacaggaat acgtcttggg
401 agacgagggc gaattgggcg cgcaggcagt cgagttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccggca gacggttcga caaagcgggg
501 cagaagggtg acgacggtg atttccgct gccggaacgt cgcaccaggg
551 cgacgcgttc gccttgcttg atgtcgaggt tgaagtgtc gagggcttgg
601 atgccgtctg aacggtattc gacatcgac ttgcggaagc tgatgcgccc
651 ttcgacacgc tgcgcgcgca gcgtgccttt gtctgttcg ggcgggggtg
701 cgagaaatgc acatacgccg tcggcgcgca ggaacatcgt ctgcataggg
751 atgctgatgt tggcaaggct tttgatggg gcgtacatt gcagcatcgc
801 gacgatgaat gccataaatt cgccgatggt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep



m276.seq

1	ATGATTTTGC	CGTCGTCCAT	CACGATGATG	CGGTCGGCCC	CTTCGATGGT
51	GGTCAGGCGG	TGGGCGACGA	TGATGCCGGT	GCGGTTTTCC	ATCAGGCGTT
101	CGAGCGCCTG	TTGGACGAGG	CGTTCGGATT	CGTTGTCTAA	TGCGCTGGTG
151	GCTTCGTCCA	ATAATAATAT	CGGCGCGTCT	TTCAAATATG	CGCGGGCAAT
201	GGCGACGCGT	TGCCCGTGTG	CGCCGGATAA	TTGCTGCGG	TTGCATCCGA
251	TGGGCTGGTG	CAGTCGCGAG	GGGGAGCTGT	CAATCAGGCT	TTGCAGGTTG
301	GCGGTTTGGA	GGGCGAACAG	GACTTCGGCT	TCGCCCCGCT	CGGGACGGCT
351	GTATCGGACG	TTTTCAAACA	GGGTGTCGTC	AAACAGGAAT	ACGTCTTGGG
401	AGACGAGGGC	GAATTGGGCG	CGCAGGCAT	CGAGTTTGAT	GTCGCGGATG
451	TCGATACCGT	CTATGCAGAT	GTGGCCGCGA	GACGGTTCGA	CAAGCGGGG
501	CAGACAGTTG	ACGACGGTGG	ATTTGCCGCT	GCCGGAACGT	CCGACCAAGG
551	CGACGCGTTC	GCCTTGCTCTG	ATGTCGAGGT	TGAAGTTGTC	GAGGGCTTTG
601	ATGCCGTCTG	AACGGTATTC	GACATCGACG	TTGCGGAAGC	TGATGCGCCC
651	TTCGACACGC	TGCGGTGCGA	GCGTGCCCTT	GTCCTGTTCT	GGCGGGGTGT
701	CGAGAAATGC	ACATACAGCG	TCGGCGGGCA	GGAACATCGT	CTGCATAGGG
751	ATGCTGATGT	TGGCAAGGCT	TTTGATGGGG	GCGTACATTT	GCACATCGC
801	GACGATGAAT	GCCATAAATT	GCCCGATGGT	GGTGTAG	

m276.ppt

```

1  MILPSSITMM RSAPSMVVRW WATMPVVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPS GELSIRLCRL
101 AVWRANRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLSMAS
151 SIPSMQMLPA DGSTKRGSRLL TVDVLPLPER PTRATRSPL MRSLKLSRAL
201 MPSERYLST LRLKMRPSTR CGASVPLSCS GGVSRNAHTP SAARNVICIG
251 MMLLARLTMM AYICISATMM AINSMPVW*

```

Homology with a predicted ORF from *N.gonorrhoeae*

from *N. gonorrhoeae*:

m276/q276

	10	20	30	40	50	60
m276.pep	MILPSSITM	MRSAPSMV	VRWATMM	PVRF	SIRRSSAC	WTRRSDSL
g276	MILPPSMT	MTRSADST	VVRWATMM	PVRF	SIRRSSAC	WTRRSDSL
	10	20	30	40	50	60
m276.pep	70	80	90	100	110	120
g276	FKMARAMA	TRCRCPPD	KLFPDPM	GWCS	PSFG	LSIRLCRL
	70	80	90	100	110	120
m276.pep	130	140	150	160	170	180
g276	FSNRVSS	NRNTSW	ETRANW	ARRQSS	LSMSAM	SIPSMQML
	130	140	150	160	170	180
m276.pep	190	200	210	220	230	240
g276	PTRATR	SPCLMS	RKLKSR	ALMPSE	RYSTST	LRLKLRP
	190	200	210	220	230	240

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	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

```

a276.seq
1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTCAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGGTGTCTG AAACAGGAAT ACGTCTTGGG
401 AGACGAGGCG AAATTGGGCG CGCAGGCAGT CGAGTTGAT GTCGGCGATG
451 TCGATACCGT CTATCGAGAT GTTGCCGCGA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTGT
601 ATGCCGTCCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCCGCC
651 TTCGACACGC TCGGCTGCCA GCGTGCCCTT GTCCTGTTCG GGCGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATTT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG
  
```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

```

a276.pep
1  MILPSSITMM RSAPSMVRR WATMMPVRF IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSILMSAM
151 SIPSMQMLPA DGSTKRGSR TTVDLPLPER PTRATRSPCL MSRLKPSRAL
201 MPSEYSTST LRKLMPSTR CGASVPLSCS GGVSNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*
  
```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVRRWATMMPVRFIRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVRRWATMMPVRFIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSPPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPPDKLLPFDPMGWCSPPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGSRLLTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGSRLLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSNAHTP					
a276	PTRATRSPCLMSRLKPSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

630

250 260 270

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
  1 ..atgggtacacg tcgccgtagc ttacggtatt gccgtccggc gtttttggcc
 51 aaacgaggtc atagacgttt tccacgcctt gcaggtacat cgccaagcgt
101 tcgatgccgt aggtaatttc gccgagtagc ggctgcaat cgataccgcc
151 gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201 cttcccagcc caaaccaccac gcaccgaggg tggggttttc ccagtcgtct
251 tcgacaaagc ggatgtcgtg gactttggga tcgatgccca attcgcgcag
301 ggagtcgaga tagaggtctt ggatattggc gggggcgggt ttgagggcga
351 cttggaattg gtaatagtgt tgcaggcggg tggggttgtc gccgtagcgg
401 ccgtctttgg ggccggcggt ggggtggacg taggcggcaa accaaggctc
451 ggggcccagc gcgcgcagcc aggtggcggg atgggatgtg ccggcaccga
501 cttccatgtc gaagggttgg atgacggtgc agcctttgtc tgcccagaag
551 gtttgcagtt tgaagatgat ttgttgaag gtaagcatgg cttattgttc
601 gataaaataa aggttttatt ttactgtttc catagccgct tgaatagatt
651 tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
  1 ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
 51 DLLEIGKLG YFHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
101 GVEIEVLDI GGGFEGDLEL VIVLQAVGVV AVAAVFGAAA GLDVGGKPRL
151 GAERAQAGG MGCAGTDFHV EGLDDGAFAV CPEGLQFEDD LLEKGHGLLF
201 DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
  1 ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
 51 TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAC TGG
101 CGCAGCAGCC AGTCGGCATC GCTGTATTTC AAGTTGTAGG TGGATTGCTC
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTCGA
201 GCGTTTTTTC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301 GTCGATGCCG CCGACTTGTT GGAATAGGT AAAGTGGGT ACTTCCATGC
351 CGTTGAGCCA GACTTCCCAG CCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451 CAATTCCGCG AGAGAGTCGA GATAGAGGTC TTGGATATTG GCGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGTAATAGT GTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GGCCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGT GGATGACGGT GCAGCCTTTG
701 TCTGCCAGA ATGTTTGCA TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
  1 MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQQPVGI AVFEVVGILL
 51 DFVLVHVAV GDGVAVERFC PNEVVDVFT LQVHRQAFDA VGDFAEYGRA
101 VDAADLLEIG KLG YFHAVEP DFPAQTPRAE GGVFPVVDK ADVVD FGIDA
151 QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAVF GAAAGLDVGG
201 KPRLAGAECQ AGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

g277.pep

10 20 30  
MVHVAVAYGI AVRRFCPNEV IDVFHALQVH

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```

m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVVHVAVGDGVAVERFCPNEVVDVFTLQVH
           30      40      50      60      70      80
g277.pep  RQAFDAVGNFAEYGRAIDTADLLEIGKLGYPHAFEPDFPAQTPTREGGVFPVVFADKADV
           40      50      60      70      80      90
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAFEPDFPAQTPRAEGGVFPVVFADKADV
           90     100     110     120     130     140
g277.pep  DFGIDAQFAQGVEIEVLIDIGGGFEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPRL
           100     110     120     130     140     150
m277      DFGIDAQFAQRVEIEVLIDIGSGLEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPRL
           150     160     170     180     190     200
g277.pep  GAERAQAGGGMGCAGTDFHVEGLDDGAAAFVCPPEGLQFEDDLLEGKHGLL
           160     170     180     190     200
m277      GAECAQAGGGMGCAGTDFHVEGLDDGAAAFVCPPECLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51 TTTCTTCGGC AAGCAGGCGT TTGGCTGCG CTTCGTAGTC GTTGAAGTGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCG AAGTTGTAGG TGATTGTTC
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT GAACTGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCAGTCTGT CTTCGACAAA GCGGATGTCG TGCACTTTGG GGTGATGCC
451 CAATTCGCGC AGGGAGTCGA GATAGAGGTC TTGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGAATAGT GTTGAGGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGGCGGCGG CTGGGTTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGCATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGTT GGATGACGGT GCAGCCTTTG
701 TCTGCCCAGA ATGTTTCAG TTTGAAGATG ATTGTGTTGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DFVLVVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VGDFAEYGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GGVFPVVFDA ADVVHFGVDA
151 QFAQGVIEV LDIGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPRLGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCPPECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

m277.pep  10      20      30      40      50      60
MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLLDFVLVVHVAV
a277      10      20      30      40      50      60
MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLLDFVLVVHVAV

m277.pep  70      80      90      100     110     120
GDGVAVERFC PNEVVDVFTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAFEP
a277      70      80      90      100     110     120
SYCITVQRFC PNEVIDVFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGYFHTVEP

m277.pep  130     140     150     160     170     180

```

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```

m277.pep  DFPAQTPRAEGGVFPVVFDAKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLVLVILQA
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
a277      DFPAQTPRAEGGVFPVVFDAKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLVLVILQA
          130      140      150      160      170      180

          190      200      210      220      230      240
m277.pep  VGVVAVAAVFGAAAGLDVGGKPRLGAECAQAGGGMGCAGTDFHVEGLDDGAAFVCP ECLQ
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
a277      VGVVAVATVFGAAAGLDVGGKPRLGAECAQAGGGMGCAGTDFHVEGLDDGAAFVCP ECLQ
          190      200      210      220      230      240

          250
m277.pep  FEDDLLEGKHGLX
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
a277      FEDDLLEGKHGLX
          250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq (partial)
1  ttgcgtgcaa tcacgcccgg tgcgattttt tcgacagggg cgggtcaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcatcgacga
101 cgcgtccgac caattcgcgt ccgaccggca cttctaaat acggccggta
151 caggtaaccg tgcgccttc ttaatatgt tcgtactcgc ccaacactac
201 ggcaccgacg gagtgcgct ccaggttcat cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcatg catctgaca accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcatttaca gacagatttt cgatcttggc ttaatcaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgta tagtcgtgta
451 caaagcactc agtttgctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep (partial)
1  LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAPK KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSAFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF....

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1  TTGCGCGCAA TCACGCCCGG TCGATTTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GCGCGCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CTTGTCATTG CATCTGACA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTGTCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTG GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1  LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAPK KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPQVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLHLQAD
201 LFVQQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

633

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng)  
from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278 . pep	LRAITPGAIFSTGAVKVVLI	GPLPSIGRPNASTTRPTNSRPTGTSKIRPVQVT	TVSPSLIC			
m278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVT	TVSPSLMC			
	10	20	30	40	50	60
	70	80	90	100	110	120
g278 . pep	SYSNNTTAPTESRSR	FIAPKVLPGNSSIS	PCIASDKP	WMRTIP	SVTEITV	PRVLTSAFT
m278	SYSNNTTAPTESRSR	FIAPKVLPGNSSIS	PCIASDKP	WMRTIP	SVTEITV	PQVRTSAFT
	70	80	90	100	110	120
	130	140	150	160	170	
g278 . pep	DRFSILALIRSLISAGL	SCMKTLLIRHSRVQSTQF	ALYRQIQNLITHFNF			
m278	DRFSILALIKSLISAGL	SCMKTLLIRHSRVQGTQF	ALYRQIQNLITHFNF	YAANQLRFDF		
	130	140	150	160	170	180
	190	200	210			
m278	DRDFQLAVETLIQHL	QLADLFV	QGRIGTVNDGR	FDMVE*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278 . seq

```

1   TTGCGCGCAA TCACGCCCGG TGCATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GCGCGCCGACG GAGTCGCGCT CCAGGTTTCA CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCAATG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278 . pep

```

1   LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLIC SCSPNTTAPT ESRSRFIAP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLRQLAD
201 LFVQGRIGTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278 . pep	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVT	TVSPSLMC			
a278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVT	TVSPSLIC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m278 . pep	SYSNNTTAPTESRSR	FIAPKVLPGNSSIS	PCIASDKP	WMRTIP	SVTEITV	PQVRTSAFT
a278	SCSPNTTAPTESRSR	FIAPKVLPGNSSIS	PCIASDKP	WMRTIP	SVTEITV	PRVRTSAFT
	70	80	90	100	110	120

634

	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLSCMKTLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
a278	DRFSILALIKSLISAGLSCMKTLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
	130	140	150	160	170	180
	190	200	210	220		
m278.pep	DRDFQLAVETLIQHLQLADLFVQGRIGTVNDGRFDMVEX					
a278	DRDFQLAVETLIQHLQLADLFVQGRIGTVNDGRFDMVEX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279.seq

```

1  atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgcg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 cgggcagcgg cagggcgctg ttggctccgg cttctttggc ggcagccatg
151 gtgcgtccga cggcgccggc gttgcctgca atcacgactt gtccggcgga
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcactt tccaaaccca aaatggccgc cattgcgctt
301 acgccttgcg gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcgcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgttt gccgccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279.pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTSS SKPKMAAIAP
101 TPCGTADCIS SARRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

```

1  ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGTTTTCA GGGCTTCGGC
51  AAGTTTGTGCG GCGGCGGTTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGGCAGCGG CAGGGCGCGT TTGGCACC GGCTTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCTGCA ATCAGGATT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACTTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATGCGCCCC
301 ACGCCTTGCG GTACGGCGGA CTGATCAGT TCGGCGCGCA GGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGCGGTGT
401 ATTGCGCGAG GCTGTGTCCG GCAACGCGG CAGGCGTTT GCCGCCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITTCPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRTSLTA SAKFNAPAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m279.pép      ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRSLTA
||| ||||| ||||| ||| : ||||| : ||||| ||||| ||||| ||||| |||||
g279          ITTCPGELKLTASTTSPCADSAQICLTCSSSKPKMAAIAPTPCGTADCISSARRRSLTA
              70          80          90          100          110          120

              130          140          150
m279.pép      SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g279          SAKSNASAATSAVYSPRLCPATAAGVLPPTSIX
              130          140          150

```

```
a279.seq
  1  ATGACNCGA  TTTGCGGCTG  CTTGATTTC  ACGGTTTNN  GGGCTTCGGC
51  GAGTTTGTGC  GCGGCGGGTT  TCATGAGGCT  GCAATGGGA  GGTACNGACA
101  CNGGCGAGCG  CAGGGCGCGT  TTGGCGCCGG  CTCTCTTTGG  GCAACGCATA
151  GCGCGCTCGA  CGGCGCGCGC  ATTGCCTGCA  ATCACGACTT  GTCCGGGCGA
201  GTTGAAGTTG  ACGGCTTCAA  CCACTTCATC  CTGTGCGGAT  TCGGCGCAAA
251  TTTGTTTAC  CTGTTTCATC  TCCAGCCGA  GAATCGCCGC  CATTCGCCCC
301  ACGCCTTGCG  GTACGCGCGA  CTGCATCAGT  TCGGCGCGCA  NGCGCACGAG
351  TTTGACCGCG  TCGGCAAAAT  CCAATGCGCC  GCGGCAACN  AGTGCGGTGT
401  ATTCGCCGAN  GCTGTGTCCG  GCAACGGCGG  CAGCGCTTTT  GCCGCCGCT
451  TCCGAATAG
```

a279.pep

1	MTXICGLIS	TVXRASASLS	AAGFMRLQWE	GTDTGSGRAR	LAPASLAASI
51	ARSTAAALPA	ITTCPEGELK	TASTTSSCAD	SAQICFTCSS	SKPRIAAIAP
101	TPCGTADCIS	SARXRTSLTA	SAKSNAPEAT	SAVYSPXLCP	ATAAGVLPFA
151	SE*				

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	:	:	:	:	:	:
a279	MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTA	STSLWAASQA	LMALTCSSSK	PRIAAIAPT	PCGTADCISS	ARRRSTLTA
	:	:	:	:	:	:
a279	ITTCPGELKLTA	STSSCADSA	QICFTCSSSK	PRIAAIAPT	PCGTADCISS	ARXRSTLTA
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATS	SAVYSPRLCP	ATAAGVLPP	ASKX		
	:	:	:	:	:	:
a279	SAKSNAPAATS	SAVYSPXLCP	ATAAGVLPP	ASEX		
	130	140	150			

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.



1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaaccttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttcggt ttgtaaccag tttcagcatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgtcgga
151 gccaaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 ccgacatcca acgcgccgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgaata tgaccccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccata acgtcgctga aaccctgata aaggccgacg ccgaaggcaa
501 agtttattat caacaacgct tgggcaacta ccaaatgcag cttaaaaaac
551 tgacacagcg cgcaacaagg gcatttaatg ccgtccctgc cgccaaacgc
601 aaagtccctg cggggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtagg cagcgaagcc gagccgtccg
701 ccaaacaagt cgccgccatc atccggcaaa tcaaacgcga aggcatacaa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtt accgcactcg
801 caaagaaacc ggcgtcaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcgcca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTLIA ALLATAATAA PLPVVTSFSI LGDVAQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNLGL LEAADIQRAV KQSKVSYAEA
101 TKGIQPLKAE EGGHHHDHHD HDHHDHDEGH HDHDEYDPH VWNDFVLMDS
151 YAQNVAEETLI KADPEGKVYY QQRILGNQMQ LKKLHSDAQA AFNAVPAAKR
201 KVLTHGDAFS YMGNRYNISF IAPQGSSEA EPSAQVAAI IRQIKREGIK
251 AVFTENIKDT RMVDRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNVE
301 ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAACTCAC CTTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTCAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAGG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAAACTCG TCCTGCTCAA CCGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG AAGGACACCA CCATGACCAC GCGGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCTTA TGCCCCAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGTG CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CCTTTTCCTA TATGGGCAA CATTACCATA TCGAATTCAT
651 CGCCCCGCAA GCGGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTTACC
751 GAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACGCGCCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTLIA ALLTASATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNLGL LEAADVQRAV KQSKVSYTEA
101 TKGIQPLKAE EGGHHHDHHD HDHEGHHHDH GEYDPHVWND PVLMSAYAQN
151 VAKALIKADP EGKVYYQQLR GNYQMLKKL HSDAQAAFNA VPAAKRKVLT

```

637

201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KQVAIIIRQI KREGIKAVFT  
 251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNKALTN  
 301 AMKQ\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng)

from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVTFSFILGDAVKQIGGERVSIQSLVGANQDTHAYHM					
	::					
g280	MKHLKLTLIAALLATAATAAPLPVVTFSFILGDAVKQIGGERVAVQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAEEEGGHHHDH-					
	::					
g280	TSGDIKKIRSAKLVLLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAEEEGGHHHDH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---DHDHEGHHHDHGEYDPHVWNPVLM SAYAQNVAKALIKADPEGKVYYQORLGN YQMQ					
	::					
g280	HDHDHDHEGHHHDHGEYDPHVWNPVLM SDYAQNVAETLIKADPEGKVYYQORLGN YQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAAFNAVPAARKVLTGHDAFSYMGKRYHIEFIAPQGVSEAEPSAKQVAAI					
	::					
g280	LKKLHSDAQAAFNAVPAARKVLTGHDAFSYMGNRYNISFIAPQGVSEAEPSAKQVAAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	::					
g280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNE					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

1	ATGAAACACC	CCAAACTCAC	CCTTATCGCC	GCATTGCTGA	CCACTGCCGC
51	AACTGCCGCC	CCCCTGCCGG	TGTAACCCAG	CTTCAGCATT	TTAGGCGACG
101	TAGCCAAACA	AATCGGCGGA	GAGCGCGTAT	CCATACAAAG	TTTGGTCGGA
151	GCCAAACCAAG	ATACGCACGC	CTATCATATG	ACCAGCGGCG	ACATTAAAAA
201	AATCCGCAGT	GCAAACTCG	TCCTGATTAA	CGGCTTAGGA	CTTGAAGCTG
251	CCGACATCCA	ACGTGCCGTC	AAACAGAGCA	AAGTATCCTA	TGCCGAAGCG
301	ACCAAAGGCA	TCCAACCCCT	CAAAGCCGAA	GAAGAAGGCG	GACACCATCA
351	CGACCACGAT	CATGACCACG	ACCATGACCA	CGAAGGACAC	CACCACGACC
401	ACGGCGAATA	TGACCCCCAC	GTCTGGAACG	ACCCCGTCCT	TATGTCCGCC
451	TATGCCCAAA	ACGTGCCCGA	AGCCCTGATA	AAGGCCGACC	CCGAAGGCAA
501	AGTTTATTAT	CAACAACGCT	TGGGCAACTA	CCAAATGCAG	CTCAAAAAAC
551	TGCACAGTGA	CGCACAAGCC	GCATTTAATG	CCGTCCCTGC	CGCCAAACGC
601	AAAGTCCTGA	CCGGGCACGA	TGCCTTTTCC	TATATGGGCA	AACGTTACCA
651	TATCGAATTC	ATCGCCCCAC	AAGGTGTGAG	CAGCGAAGCC	GAGCCTTCAG
701	CCAAACAAGT	CGCCGCCATC	ATCCGACAAA	TCAAACGCGA	AGGCATCAAA
751	GCCGTATTTA	CCGAAATAT	CAAAGACACC	CGCATGGTTG	ACCGCATCGC

638

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG  
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA  
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep  
 1 MKHPKLTLIA ALLTTAATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG  
 51 ANQDTHAYHM TSGDIKKIRS AKLVLINGLG LEAADIQRAV KQSKVSYAEA  
 101 TKGIQPLKAE EEGGHHHDHD HDHDHDHEGH HHDHGEYDPH VWNDFVLMSA  
 151 YAQNVAEALI KADPEGKVYY QQLGNYQMQ LKKLHSDAQA AFNAVPAAKR  
 201 KVLTGHDASF YMGKRYHIEF IAPQGSSEA EPSAKQVAI IRQIKREGIK  
 251 AVFTENIKDT RMVDRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNK  
 301 ALTNAMKQ\*

m280/a280 96.4% identity in 308 aa overlap

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVTFSISILGDVAQIGGERVSIQSLVGANQDTHAYHM					
a280	MKHPKLTLIAALLTTAATAAPLPVVTFSISILGDVAQIGGERVSIQSLVGANQDTHAYHM					
	10	20	30	40	50	60
m280.pep	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EEGGHHHDHD					
a280	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAE EEGGHHHDHD					
	70	80	90	100	110	120
m280.pep	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EEGGHHHDHD					
a280	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAE EEGGHHHDHD					
	70	80	90	100	110	120
m280.pep	HDH----EGHHHDHGEYDPHVWVNDPVLMSAYAQNVAKALIKADPEGKVYYQQLGNYQMQ					
a280	HDHDHDHEGHHHDHGEYDPHVWVNDPVLMSAYAQNVAEALIKADPEGKVYYQQLGNYQMQ					
	130	140	150	160	170	180
m280.pep	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGSSEA EPSAKQVAI					
a280	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGSSEA EPSAKQVAI					
	180	190	200	210	220	230
m280.pep	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGSSEA EPSAKQVAI					
a280	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGSSEA EPSAKQVAI					
	190	200	210	220	230	240
m280.pep	IRQIKREGIK AVFTENIKDTRMVDRIAKETGNVVSGKLYSDALGNAPADTYIGMYRHNK					
a280	IRQIKREGIK AVFTENIKDTRMVDRIAKETGNVVSGKLYSDALGNAPADTYIGMYRHNK					
	240	250	260	270	280	290
m280.pep	IRQIKREGIK AVFTENIKDTRMVDRIAKETGNVVSGKLYSDALGNAPADTYIGMYRHNK					
a280	IRQIKREGIK AVFTENIKDTRMVDRIAKETGNVVSGKLYSDALGNAPADTYIGMYRHNK					
	250	260	270	280	290	300
m280.pep	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq  
 1 atgcactacg ccctcgcacg cgtcttctgc ctgtccctca gcgcgcgacc  
 51 cgtcggcgta ttcctcgtca tgcgccgat gagcctgata ggcgacgcat  
 101 tgagccacgc cgtcctgccc ggtgccgccc tcggctacat gtttgccggc  
 151 ttgagcctgc ccgctatggg tgtggcgccc tttgccgccc gtatgctgat  
 201 ggcgctgctt gccgactcgc tcagccgctt taccaccctg aaagaagatg  
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgc cgtaatcctc  
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc  
 351 tgtgcttgcc gtcgatattc ccgactgca actcatcgcc gccgtctccg  
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa  
 451 agcatagacc cccttttcct caagtccgct aacggcaaa gcgggctttg

639

501 gcacgtcatt ttcctcatcc tcgtcggtat gaacctcgta tccggcttcc  
 551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt  
 601 accgcccgtt tatgggcaag aaatatgggg acgctcattc tgttgctcgt  
 651 cctcatcgcc ctttttttgcg gtttgatcgg gctgctcatt tcctaccaca  
 701 tcgaaatccc ttccggcccc gccatcatcc tctgttgag cgtcctttat  
 751 ctttttttccg tcatactcgg caaagaaggc ggcatcttgc ccaaatgggt  
 801 caaaaaccac cgccaccaca ccacctga

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

g281.pep

1 MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG  
 51 LSLPAMGVGG FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL  
 101 ISKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSGLTLITL AVIYRPLVLE  
 151 SIDPLFLKSV NGKGGWLWHVI FLVLVVMNLV SGFQALGILM SVGIMMLPAI  
 201 TARLWARNMG TLILLSVLIA LFCGLIGLLI SYHIEIPSGP AIILCCSVLY  
 251 LFSVILGKEG GILPKWFKNH RHHTT\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

m281.seq (partial)

1 ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC  
 51 CGTCGGCGTA TTCCTCGTCA TGCGCCGTAT GAGCCTGATA GGCGACGCAT  
 101 TGAGCCACGC CGTCTGCCCC GGTGCCGCCG TCGGCTACAT GTTTGCCGGC  
 151 TTGAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGAG GCATGCTGAT  
 201 GGCACCTGCT GCCGGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG  
 251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG CGTAGTCCTC  
 301 GTCAGCAAAA ACGGGAGCAG CGTCGATTG CTCCACCTCC TTTTCGGCTC  
 351 TGTACTTGCC GTCGATATC CTGCCCTGCA GCTCATCGCC GCCGTCTCCA  
 401 GCCTCACGCT CATTACCCTT GCCGTCATCT ACCGCCCCGT CGTACTCGAA  
 451 AGCATCGACC CCCTGTTTCT CAAATCCGTC GGCGGCAAG GCGGGCTTTG  
 501 GCACGTCCTC TTTCTCGTCC TGGTCGTCAT GAACCTCGTA TCCGGCTTTC  
 551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TCATGATGCT GCCAGCCATT  
 601 ACCGCCCCGC TGTGGGCGAA GCATATGGGC GCACTCATCC TCCTATCCGT  
 651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA  
 701 TCGAAATCC TTCCGGTCCC GCCATCATCC TCTGTTGCAG CGTCTTTTAT  
 751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CC..

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

m281.pep (partial)

1 MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG  
 51 LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL  
 101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSSLTITL AVIYRPLVLE  
 151 SIDPLFLKSV GKGGLWHVL FLVLVVMNLV SGFQALGILM SVGLMLPAI  
 201 TARLWAKHMG ALILLSVLTA LLCGLSGLLI SYHIEIPSGP AIILCCSVLY  
 251 LFSVILGKEG GILT..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

m281/g281

	10	20	30	40	50	60
m281.pep	MRYALASVFC	LSLSAAPVGV	FLVMRRMSLI	GDALSHAVLP	GAAVGYMFAG	LSLPAMGLGG
	:	:	:	:	:	:
g281	MHYALASVFC	LSLSAAPVGV	FLVMRRMSLI	GDALSHAVLP	GAAVGYMFAG	LSLPAMGVGG
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALL	AGLVSRFTTL	KEDANFAAFY	LSSLAIGVVL	VSKNGSSVDL	LHLLFGSVLA
	:	:	:	:	:	:
g281	FAAGMLMALL	AGLVSRFTTL	KEDANFAAFY	LSSLAIGVIL	ISKNGSSVDL	LHLLFGSVLA
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIA	AVSSLTITL	AVIYRPLVLE	SIDPLFLKSV	GKGGLWHVL	FLVLVVMNLV

```

g281      |||||:::||:|||||
VDIPALQLIAAVSGLTLITLAVIYRPLVLESIDPLFLKSVNGKGGLWHVIFLILVMNLV
          130         140         150         160         170         180

          190         200         210         220         230         240
m281.pep SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTAALLCGLSGLLISYHIEIPSGP
          |||||:::||:|||||
g281      SGFQALGILMSVGIMMLPAITARLWARNMGTLLILLSVLIALFCGLIGLLISYHIEIPSGP
          190         200         210         220         230         240

          250         260
m281.pep AII LCCSVLYLF SVILGKEGGILT
          |||||:::||:|||||
g281      AII LCCSVLYLF SVILGKEGGILPKWFKNHRHHTTX
          250         260         270

```

```

a281.seq
1      ATGCGCTACG  CCTCGCATC  CGTCTTCTGC  CTGTCCCTCA  GTGCCGCACC
51     CGTCGGCGTA  TTCCTCGTCA  TGCGCCGTAT  GAGCCTGATA  GGCAGCGCAT
101    TGAGCCACGC  CGTCTGCCCC  GGTGCCGCCG  TCGGCTACAT  GTTTGCGCCG
151    TTAAGCCTGC  CGCCATGGG  TTTGGGCGCG  GTAGCCGCAG  GTATGCTGAT
201    GGCATCTGTT  CGCGACTCG  TCAGCGCGTT  CACCACTGAT  AAGAAGATG
251    CCAACTTTGC  CGCCTTTTAT  CTCAGCAGCC  TCGCCATCGG  TGTAGTCTCT
301    GTCAGCAAAA  ACGGCAGCAG  CGTCGATTTG  CTCACCTCC  TTTTCGGCTC
351    CGTACTTGCC  GTCGATATT  CTGCCCTGCA  ACTCATCGCC  GCCGATCCA
401    CCTCACACT  GCTTACCOCT  GCGCTCATCT  ACCGCCCGCT  CGTACTCGAA
451    AGCATCGACC  CCTGTTTCT  CAAATCTGTC  GGCGGCAAAG  GCGGGCTTTG
501    GCACGTCCTC  TTTCTCGTCC  TGGTTCGTAT  GAACCTCGTA  TCGGGCTTTC
551    AAGCCCTCGG  CACATCTAG  TCCGTGCGAC  GCACTCATCC  TCCTATCCGT
601    ACCGCCCGCG  TATGGGCGAA  GCACATGGGC  GCACTCATCC  TCCTATCCGT
651    TCTGACAGCC  CTGCTGTGCG  GCTTGAGCGG  ACTGCTCAT  TCCTACCACA
701    TCGAAATTCG  TTCGGTTCCT  GCCATCATCC  TCTGTTGACG  CGCTCTTTAT
751    CTCTTTTCCG  TCATACTCGG  CAAAGAAGGC  GGCATTCTGA  CCAATAGGCT
801    CAAAAACCAC  CGCCACCACA  CCACCTGA

```

a281.pep

1	<u>MRYALASVFC</u>	<u>LSLSAAPGVG</u>	<u>FLVMRRMSLI</u>	<u>GDALSHAVLP</u>	<u>GAAVGYMFG</u>
51	<u>LSLPAMGLGG</u>	<u>VAAGMIMALL</u>	<u>AGLVSRTTL</u>	<u>KEDANFAAFY</u>	<u>LSSLAIGVVL</u>
101	<u>VSKNGSSVDL</u>	<u>LHLLFGSVLA</u>	<u>VDIPALQLIA</u>	<u>AVSTLTLLTL</u>	<u>AVIYRPLVLE</u>
151	<u>SIDPLFLKSV</u>	<u>GKGGLWHVL</u>	<u>FLVLVVMNLV</u>	<u>SGFQALGTLM</u>	<u>SVGLMMLPAI</u>
201	<u>TARLWAKHMG</u>	<u>ALILLSVLTA</u>	<u>LLCGSLGLLI</u>	<u>SYHIEIPSPG</u>	<u>AIILCCSVLY</u>
251	<u>FLSVLKGEG</u>	<u>GILTKWLKNH</u>	<u>RHHTT*</u>		

a281	99.2% identity in 204 aa overlap					
	10	20	30	40	50	60
m281.pep	MRYALASVFCLSLSAAPVGVLVMMRMSLIGDALSHAVLPGA	AVGYMFAGLSLPAMGLGG				
a281	MRYALASVFCLSLSAAPVGVLVMMRMSLIGDALSHAVLPGA	AVGYMFAGLSLPAMGLGG				
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVV	LVSKNGSSVDLLHLLFGSVLA				
a281	VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVV	LVSKNGSSVDLLHLLFGSVLA				
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIAAVSSLTLLTLAVIYRPLVLESIDPLFLK	SVGGKGLWHVFLVLVVMNLV				
a281	VDIPALQLIAAVSTLLTLAVIYRPLVLESIDPLFLK	SVGGKGLWHVFLVLVVMNLV				
	130	140	150	160	170	180

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	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

```

g282.seq
1  atgggattgg gtatggaat cggcaagctg attgtggctc ttttgggtgc
51  gatcaatccg tttagcgcgt tgctcgcttta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgata ggcggtgctg tattgaaggt
201 tttgggcata agcgtcgggt cgtttcaggt cggcggcggtg attttgggtgc
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa ggcgcgcccg cccgcaatgc
351 agggcgcatg gccgtcgtgc ccacgcctat accgatcacc atcggtcctg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatacgcg tgattatcgc ggccggtttg gtggtcagtg cgatttgta
501 tgccatttta atcgttgccg ggaaggtcag ccgcctgtg ggccgcagcg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggccggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattccgcg aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

```

g282.pep
1  MGLGMEIGKL IVALVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYT
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLG GATGLTILNR IMGMMLAAVS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

```

m282.seq
1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCGCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGTG GGCGCGACGG
551 GGCTGACGAT TTTAAACCGC ATTATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

```

m282.pep
1  MGLGMEIGKL IVAFLVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLG GATGLTILNR IMGMMLAAVS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng)

from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282.pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	:					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
m282.pep	70	80	90	100	110	120
	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	:					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
m282.pep	130	140	150	160	170	180
	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	:					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
m282.pep	190	200	210			
	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
g282	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282.seq

1	ATGGGATTGG	GCATGGAAAT	CGGCAAGCTG	ATTGTGGCTT	TTTTGGTGCT
51	GATTAATCCG	TTTAGCGCGT	TGTCGCTT	CCTTGACCTG	ACCAACGGGC
101	ACAGCACGAA	GGAGCGCAGG	AAGGTCGCGC	GGACGGCCGC	CGTTGCCGTG
151	TTTGCCGTGA	TTGCGGTATT	TGCGCTGATC	GGCGGTACGC	TGCTGAAGGT
201	TTTGGGCATC	AGCGTCGGTT	CGTTTCAGGT	CGGCGGCGGA	ATTTTGGTGT
251	TGCTGATTGC	CATTTCGATG	ATGAACGGCA	ACGACAATCC	CGCCAAGCAG
301	AATCTCGGCG	CGCAGCCGGA	AACGGGGCAG	GTGCGCCCCG	CCGCAATGC
351	CGGAGCGATT	GCCGTCGTGC	CCATCGCCAT	ACCGATCACC	ATCGGCCCGG
401	GCGGTATTTC	GACCGTGATT	ATTTACGCTT	CGGCGGCTAA	AACATACGGC
451	GACATCGCGT	TGATTATCGC	GGCCGGTTTG	GTGGTCAGTG	CGATTGTGTA
501	TGCCATTTTA	ATCGTTGCCG	GGAAGGTCAG	CCGCCTGCTG	GGTGCGACGG
551	GGCTGACGAT	TTTAAACCGT	ATCATGGGTA	TGATGCTGGC	GGCGGTATCG
601	GTGGAGATTA	TTGTGTCGGG	ACTGAAAATG	ATATTCCCGC	AACTGGCAGG
651	TTGA				

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282.pep

1	MGLGMEIGKL	IVAFVLINP	FSALSPLYLDL	TNGHSTKERR	KVARTAAVAV
51	FAVIAVFALI	GGTLLKVLGI	SVGSFQVGGG	ILVLLIAISM	MNGNDNPAKQ
101	NLGAQPETGQ	VRPARNAGAI	AVVPIAIPIT	IGPGGISTVI	IYASAAKTYG
151	DIALIIAAGL	VVSAICYAIL	IVAGKVSRL	GATGLTILNR	IMGMLAAVS
201	VEIIVSGLKM	IFPQLAG*			

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282.pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
a282	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m282 .pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQVRPARNAGAI					
	70	80	90	100	110	120
m282 .pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
m282 .pep	GATGLTILNRIMGMMLAAVSVETIIVSGLKTIFFPQLAGX					
a282	GATGLTILNRIMGMMLAAVSVETIIVSGLKMIFFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

```

g283 .seq
1  atgaactttg ctttatccgt catcacattt accctcgcct ctttcctgcc
51  cgtcccgccg gccggaaccg ccgtctttac ttggaagac ggcgccggca
101 acagctattc ggatgtgccg aaacagcttc atcccgacca gagccaaatc
151 ctcaacctgc ggacgctcca aaccaaacg gcggtcaagc ccaaacctgc
201 cgtcgatacg aatgcggaca gtgcgaagga aaacgaaaag gatatcgccg
251 agaaaaacg gcagcttgag gaagaaaaga aaaaattgc cgaaccgaa
301 cggcagaaca aagaagaaa ctgccggatt tcaaaaatga acctgaaggc
351 ggtgggaaac tcaaatgcga aaacaagga tgatttgatc cgtaataaca
401 ataacgccgt aaacaaatac tgccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

```

g283 .pep
1  MNFALSVITE TLASFLPVPP AGTAVFTWKD GGGNSYSVDP KQLHPDQSQI
51  LNLRLTQTKP AVKPKPAVDN NADSAKENEK DIAEKNGQLE EEKKKIAETE
101 RQNKEENCRI SKMNLKAVGN SNAKNKDDLI RKYNNAVNKY CR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

```

m283 .seq
1  ATGAACCTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGCGGGCA
101 ACAGCTATTG GGATGTACCG AACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACGGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAACTGC CGGATTTCAA AAATGAACCT
351 GAAGGCGGTG GGAAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

```

m283 .pep
1  MNFALSVIML TLASFLPVPP AGAAVFTWKD GGGNSYSVDP KQLHPDQSQI
51  LNLRLTQTKP AVKPAQADAG KRTDGAAQEN NPDTAENRQ LEEKKRIAE
101 TERQNKEENC RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283 .pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSVDPKQLHPDQSQILNLRLTQTKP					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSVDPKQLHPDQSQILNLRLTQTKP					
	10	20	30	40	50	60



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	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRIKMNLIKAV					
		:	:	: :	:	
g283	AVKPKPA-VDTNAD-SAKENEKDIAEKNGQLEEEKKRIAETERQNKEENCRIKMNLIKAV					
	70	80	90	100	110	
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNNAVNYCRYX					
g283	GNSNAKNKDDLIRKYNNNAVNYCRYX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1173>:

```

a283.seq
1  ATGAACTTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCACG
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAACTGCG CGGATTTCAG AAATGAACCT
351 GAAAGCGGTG GGAATTCAG ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1174; ORF 283.a>:

```

a283.pep
1  MNFALSVIML TLASFVPVPP AGAAVFTWKD GGGNSYSDDVP KQLHPDQSQI
51  LNLRTROTTP AVKPAQADAG KRTDGAQEN NPDTAEKNRQ LEEKKRIAE
101 TERQNKEENC RISKMNLIKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

m283/a283 100.0% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFVPVPPAGAAVFTWKDGGGNSYSDDVPKQLHPDQSQIILNLRTROTTP					
a283	MNFALSVIMLTLASFVPVPPAGAAVFTWKDGGGNSYSDDVPKQLHPDQSQIILNLRTROTTP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRIKMNLIKAV					
a283	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRIKMNLIKAV					
	70	80	90	100	110	120
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNNAVNYCRYX					
a283	GNSNAKNKDDLIRKYNNNAVNYCRYX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1175>:

```

g284.seq.
1  atgccgtctg aaactcgaaa tcggtttcag acggcattgg tttacgcggc
51  aggttggggc ttagcggtct ttgtaacggc attcgctttt gcctgcaaaa
101 gagtcgccgg ctttgcggtt gcctttgaag ccttcgccgg tttttttgaa
151 actgtcttct ttaaagcctt ctttcttgaa accttcgccg cgcgttttgc
201 cgccgaagcc ttctttgccc ggtttatgat cgccgcgcgc gccgcgggat
251 ttctatcgc ccagccgcc tttgccttgc ggcttgccgc ctgcggattt
301 gcgtttgcgc gccggctcca tgccttcgat ggtcagttcg gccagtttgc
351 ggtaaatgta tttttcgatt ttgtggactt tgacgtattc gttcacttcg
401 gcaaacgtaa tcgcaatacc cgtgcggcct gcgcggccgc tgcgcccgat
451 gcggtggacg tagtcttccg cctgtttcgc caggtcgtag tttatgacgt

```

645

```

501 gggtaatggt cggtagctca ataccgcgtg cggcaacgtc ggtggcaacc
551 aaaattttgc agcggccttt acgcaaattc gtcagcgtgc ggttgcgcca
601 gccctgcggc atatcgccgt gcaggcagtt ggcggcgaaa cctttttcgt
651 acaattcatc cgcgatgact tcggtcatcg ctttggtgga cgtgaaaatc
701 acacattggt cgatgttggc atcgcgcagg atgtggtcga gcaggcggtt
751 tttgtggcgc atatcgtcgc agtacaacaa ctgctcttcg attttgcctt
801 ggccgtccac gcgttcgact tcgataattt cagagtcttt ggtcagtttt
851 cgcgccagtt tgccgactgc gccgtcccaa gtggcggaga acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

```

g284.pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
51  TVFLKAFFLE TFAARFAAEA FFARFMIAP AAGFPIAPAA FAFRLAACGF
101 AFAGRLHAFD GQFGQFAVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFLFR QVVVDVNGG RYVNTACGNV GGNQNFAAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHFRFG RENHTLVDVG IAQDVVEQAV
251 FVAHIVAVQQ LFFDFALAVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

```

m284.seq..
1  ATGCCGTCTG AAACTCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51  AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTTCGAA
151 ACCGTCTCTC TTAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTGC
201 CGCCGAAGCC TTCTTGTCTC GGTTCATGAT CGCCGCGCCA ACCGCCGAT
251 TTACGATCGC CCCAGCCGCC TTTGCCTTTC GGCTTGCCGC CTGCGGATTT
301 GCGTTTTCGG GTCGGTTCCTA TGCCTTCGAT GGTCACTTCG GGCAGTTTTC
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCGGCCT GCGCGCCGGT TGCGCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACATC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT ACGCAAATCC ATCAGCGTGC GGTGCGCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT TCGCGCGAAA CCTTTTTCGT
651 ACAGTTCATC CGCAATGACT TCGGTCATGG CTTTGGTGGA CGTGAAATC
701 ACGCATTGAT CGATATTGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTTCTTCG ATTTTGCCTT
801 GATCGTCCAC GCGTTCGACT TCGATGATTT CAGGGTCTTT GGTCACTTTC
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCG CTCGGCGTTG CTTCCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAAATCAG CACTTCCAAA
1001 CGTTCAAAAT CAACTTTGCC GCTTTGCATC AGGTCCATCA GACGGCCCGG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGCT CAGGGCACGG GTTTGGTAGC
1101 CGAAAGACGC GCCGCCGACG ATGCTGACGG TGCGGAACCA ACGCATATTT
1151 TTGCATACG CCAGCGCGTT TTTCTCGACT TGAGCCGCCA GTTCGCGGGT
1201 CGGGGTCAAC ACCAAAGCAC GCGGCCCTTT GCCCGGTTTT TCGCTGCGTT
1251 TGGTCAGTTT TTGCAAAGTC GGTA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

```

m284.pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
51  TVSLKAFFLE TFAARFAAEA FFARFMIAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFHAFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFLFR QVVVDVNGG RYVDTACGNI GGNQNFAAAF TQIHQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFGR RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVQNG HFQTFKINFA ALHQVHQFAR
351 RGDNQIDRFA QGTGLVAERR AADDADGAEP THIFGIRQV FLDLSRQFAG
401 RGQHQSTRAF ARFFAAFGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

646

	10	20	30	40	50	60
m284 . pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284 . pep	TFAARFAAEAFFARFMIAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
g284	TFAARFAAEAFFARFMIAPPAAGFPIAPAAFAFRLAACGFAGRLHAFDGGQFGQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284 . pep	FFDFVDFDFVHFVHGKRNRTAACAAGAPDAVDVVFRLFRQVVVDNVGNRGYVDTACGNI					
g284	FFDFVDFDFVHFVHGKRNRTAACAAGAPDAVDVVFRLFRQVVVDNVGNRGYVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284 . pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNFAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHREFGGRENHTLVDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284 . pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLFFDFALAVHAFDFDNFRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284 . pep	LTVARRCFHDGFDVDKAHIQHTVGFVQNHQFQTKINFALHQVHQTARRGDNQIDREA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284 . seq
1  ATGCCGCTCTG AAACCTCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51  AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCCG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTCTTGAA
151 ACCGTCTCTC TTAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTTCG
201 CGCCGAAGCC TTCTTTGCTC GGTTTATGAT CGCCGCGCCA ACCGCCGGAT
251 TTACGATCGC CCCAGCCGCC TTTGCCCTTC GGCTGCGCGC CTGCGGATT
301 GCGTTTGCAG GTCCGTTCCA TGCCTTCGAT GGTCAGTTCG GGCAGTTTTC
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCGGCCT GCGCGGCCGG TGCGCCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACGTC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT GCGCAAATCC ATCAGCGTGC GGTTCGCCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT GCGCGCGAAA CCTTTTTCGT
651 ACAATTCATC CGCGATGACT TCGGTCATGG CTTTGGTGGA CGTGAAAATC
701 ACGCATTGAT CGATGTCGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTTCTTCG ATTTTGCCCT
801 GGTCGTCCAC GCGTTCGACT TCGATGATTT CAGGTCCTTT GGTCACTTTG
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCT TCCGGCGTGG CTTGACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAAATCAG CACTTCCAAG
1001 CGGGCGAAAT CGACTTTGCC GCTTTGCATC AAGTCCATCA GACGGCCCGG
1051 CGTGCGGACA ATCAGATCGA CCGGTTTGCT CAGGGCGCGG GTTTGGTAGC
1101 CGAACGATGC ACCACCGACG ATGCTGACGG TACGGAACCA ACGCATATTT
1151 TTGGCATACG CCAGCGCGTT TTTCTCGACT TGAGCCGCCA ATTCGCGGGT
1201 CGGCGTCAAC ACCAACGCGC GCGGGCCTTT GCCCGGTTTT TCGCTGCGTT
1251 TGCTCAGTCG CTGCAAAGTC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284 . pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE

```

647

```

51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFAHFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGFGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDFFDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNG HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDREA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRRARF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

	10	20	30	40	50	60
m284.pep	MPSETRNRFQ TALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
a284	MPSETRNRFQ TALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDQFGQFSVNV					
a284	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDQFGQFSVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVVFRLEFQVVVDNVGNGRYVDTACGNI					
a284	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVVFRLEFQVVVDNVGNGRYVDTACGNI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNFAAAF AQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDIG					
a284	GGNQNFAAAF AQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQ LFFDFALIVHAFDFFDFRVFGQFARQFADRAVPSGGEQQS					
a284	IAQDMIEQAVFVAHIVAVQQ LFFDFALVVHAFDFFDFRVFGQFARQFADRAVPSGGEQQS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m284.pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNGHFQTFKINFALHQVHQTARRGDNQIDRFA					
a284	LTVFRRGFDDGFDVVDKAHIQHTVGFVQNGHFQAGEIDFAALHQVHQTARRGDNQIDRFA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m284.pep	QGTGLVAERRAADDADGAEP THIFGIRQRVFLDLSRQFAGRGQHQS TRAFARFFAAGQF					
a284	QGAGLVAERCTTDDADGTEP THIFGIRQRVFLDLSRQFAGRRQHQRARAFARFFAAGQS					
	370	380	390	400	410	420
m284.pep	LQSRX					
a284	LQSRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

g285.seq
1 atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat tttggcagta

```

151 tgtttcctcg gctggatcgc cggtagcgaa gcaggtttgc gcttcgggct  
201 gtaccaaatac ccgtcctggt tcggcgtaaa catttcctcc caaaacctca  
251 aaggcacact gctcgacggc ttcgacggcg acaactggtc gatagaaacc  
301 gagggggcag accttaaaat cagccgcttc cgcttcgcgt ggaaccgctc  
351 cgaactgatg cgccgcagcc tgcacatcac cgacatctcc gccggcgaca  
401 tcgccatcgt aaccaaaccg actccgccta aagaagaacg cccgcctcaa  
451 ggcttgcccg acagcataga cctgcccgcc gctgtctatc tcgaccgctt  
501 cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaaccgtct  
551 atctcgaacg cctcaacgcg gcataccggt acgaccgtaa agggcaccgc  
601 ctcgacctga aggccgcgga cagcccggtg agcagttcgt cggggtcagc  
651 ctcggtcggc ttgaaaaaac cgtttgccct cgataccgcc atttacacca  
701 aaggcggatt cgaaggcgaa accatacaca gtacggcgcg gctgagcggc  
751 agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg  
801 cctctcgga aaatccgtca tccaccggtt tgccgaatca ttggataaaa  
851 cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc  
901 gtgccttccc tgcccgatgc cgggctgaat ttcgacctga ccgccatccc  
951 gtcgttttca gacggcatcg cgctggaagg ctcgctcgat ttggaaaaa  
1001 ccaaagcccg ctttgccgac cgcaacggca tccccgctcg tcagggtttg  
1051 ggccgctttg tcatccggca ggacggcacg gtgcatacgc gcaatacgtc  
1101 cgccgccctg ctcggacggg cgggcatcag gctgtcgggc aaaaatcgaca  
1151 ccgaaaaaga catccttgat ttaaatatag gcatcaactc cgtcggcgcg  
1201 gaagacgtgc tgcaaacgcg gttcaaaagg aggttgagac gcagcatcgg  
1251 catcggcgcc acgaccgcct cgcccaaaat ctcttggaac ctcggcaccg  
1301 gcacggcacg cagggacggc agcctcccca tcgcaagcga ccccgcaaac  
1351 gaacagcgga aactggtgtt cgacaccgtc aacatctccg ccggggaagg  
1401 cagcctgacc gcgcaaggct atctcgagct gtttaaagac cgcctgctca  
1451 agctgggacat ccgttccgcg gcattcgacc cttcgcgcgt cgatccgcaa  
1501 tttccggcag gcaatatcaa cgttccgatt catcttgccg gtgaactggc  
1551 aaaagagaaa tttacgggca aaatgcgtt tttgcccggt acgttcaacg  
1601 gcgtgcccgt tgccggcagc gccgacattg tttacgagtc ccgccacctt  
1651 ccgcgcgcgg ccgtcgattt gcggttgggg cggaacatcg tcaaaacaga  
1701 cggcggtctc ggcaaaaaag gcgaccggct taacctcaat atcaccgcac  
1751 ccgattttatc ccgttccggt ttcggactcg cggggtcttt aaatgtacgc  
1801 ggacaccttt ccggcgattt ggacggcggc atccgaacct ttgaaaccga  
1851 cctttccggc acggcgcgca acttacacat cggcaaaagc gcagacatcc  
1901 gttcgtctga ttttaccctc aaaggctcac ccggcacaag ccgcccgatg  
1951 cgcgccgata tcaaggcgcg ccgcctttcc ctgtcggcgg gcgcggcggt  
2001 tgtcgatacc gccggcctga cgctggaagg tacggggcgcg cagcacgcga  
2051 tccgcacaca cgccgccatg acgtggacg gcaaacggtt caaactcgat  
2101 ttggacgctt caggcgcat caacagggaa cttaccgat ggaaaggcag  
2151 catcgcatc ctcgacatcg gcggcgcat caacctcaag ctgcaaaacc  
2201 gtatgacgct cgaagccggt gcggaacacg tggcggaag tcgggcaaat  
2251 tggcaggcaa tggcgcgag cctcaacctg caacactttt cttgggacag  
2301 gaaaaccggc atatcgga aaggcgcgcg acggcgctg cacatcgccg  
2351 agttgcacaa tttcttcaaa ccgcccttcg aacacaatct ggttttaaac  
2401 ggcgactggg atgtgcgcta cgggcacaa gcgcggcggt acctcaatat  
2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttgggtt  
2501 tgaacgcatt ttccctgaaa acgcgcttcc aaaaacgacc catcggaatc  
2551 ctgcttgacg gcggcgcgcg tttcgacgg attaacgcg atttgggcat  
2601 cggcaacgcc ttcggcgga atatggcaaa tacaccgctc ggcggcagga  
2651 ttacagcctc ctttcccgac ttggcgcat tgaagccctt tctgcccgcc  
2701 gccgcgcaaa acattaccgg cagcctgaat gcctccgcgc aaatcgcgcg  
2751 acgggtaggc tctccgtccg tcaatgccgc cgtcaacggt agcagcaact  
2801 acgggaaaaat caacggcaat atcaccgtcg ggcaagccg ctccttcgat  
2851 accgcacctt tggcgcgag gctcaacctg accgttgccg atgccgaagc  
2901 attccgcaac ttcctaccgg tcggacaaac cgtcaaaagg agcctgaatg  
2951 ccgcgtaac cctcgcgggc agcatcgccg acccgcaact gggcggcagt  
3001 atcaacggcg acaagctcta ttaccgcaac caaacccaag gcatcatctt  
3051 ggacaacggc tcgtgcggtt cgcatattgc aggcaggaaa tgggtaatcg  
3101 acagcctgaa attccggcac gaaggacg cggaactctc cggcacggtc  
3151 agcatggaaa acagcgtgcc cgatgtcgat atcgcgcgcg tgttcgacaa  
3201 ataccgcatc ctgtcccgcc ccaaccggcg cctgacggtt tccggcaaca  
3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggtatgatt  
3301 aaaactgatc agggcggtgt cggttcgcaa aaatcctcga tgcgctccgt  
3351 cggcgacgat gtcgtcgat tggcggaagt caagaaagag gcggcgcat  
3401 cgctccccgt caatatgaac ctgactttag acctcaatga cggcatccgc

649

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3451 ttctccggct acggcgcgga cgttaccata ggcggaacac tgaccctgac
3501 cgcgcaaccg ggcggaatg tgcgtggggt gggcacggtc cgcgtcatca
3551 aagggcggtt caaagcatac gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgct caacgacccc aacctgaaca tccgcgcgga
3651 acgcccgcct tcccccgctg gtgcgggctg ggaaatattg ggacagccta
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggacgaggca gcagcggcga
3801 caatgccgcc ctgtccgcag ccgacggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctgggt gatgatttgg gctttaccag caagcgagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtcggct aaactgattt accggctgac ccgcgccata
4051 cagggcggtg cccgtatcgg cagccggttc tcgggcggcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

```

g285.pep
1  MTDTPTPTD PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51  CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RSLHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLFA AVYLDRFETG KISMGKTFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGFEGE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFs DGIALEGS LD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSGIGIG TTASPKISWQ LGTGARTDGD SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRS AFDPSRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTDGGF GKKGDRLLNL ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLGG TARNLHIGKA ADIRSLDFTL KGSFPGTSRPM
651 RADIKGGRLS LSGGAADVDT AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKGSIGI LDIGGAFNLK LQNRMTLEAG AEHVAASAA
751 WQAMGGSNLN QHFSWDRKTG ISAKGGARGL HIAELHNFFK PPFHNLVLN
801 GDWDVAYGHN ARGYNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNITGSLN ASAQIGGRVG SPSVNAAVNG SSNYKINGN ITVGQSRFSD
951 TAPLGGRLNL TVADAEAFRN FLVPGQTVKG SLNAAVTLGG SIADPHLGGs
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAEISGTV
1051 SMENSVPDGD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GGKLTTLTAQ PGNVRGVGTV RVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEFMSEKD
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRLFGSDKK DSAGNGKGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

```

m285.seq
1  ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGGC
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTGCGCG GCACTGCTGT CTGTCCTGAT TTTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CCGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTTCTCTC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGCGAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTTA AAGAAGAAGC CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAAGC GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CAGCCGCTGG AGCAGTTCTG CGGGGGCGGC
651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAATGGCG ATCGACGGCG GCAATATCCG

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801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA  
 851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCTTC  
 901 GTGCCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC  
 951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG TTCGCTCGAT TTGGA AAAACA  
 1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGTCCG TCAGGTTTTA  
 1051 GGCGGCTTTG TCATCCGGCA GGACGGCAGC GTGCATATCG GCAATACGTC  
 1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTGCGGC AAAATCGACA  
 1151 CCGAAAAAGA CATCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG  
 1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG  
 1251 CATCGTGGC ACGACCGCCT CGCCAAAAT CTCTTGCGAA CTCGGCATCG  
 1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC  
 1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCEG CCGGGCAAGG  
 1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA  
 1451 AGCTGGACAT CCGTCCCGC GCATTGACG CTTCGCGCAT CGATCCGCAA  
 1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC  
 1551 AAAAGAGAAA TTACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG  
 1601 GCGTACCGAT TGCCGGCAGT GCGACATTG TTTACGAGTC CCGCACCTT  
 1651 CCGCGTGCCG CCGTCGATT GCGGCTGGGG CGGAACATTA TTA AAACAGA  
 1701 CGGCGGCTTC GGCAAAAAG GCGACCGGCT TAACCTCAAT ATCACCGCAC  
 1751 CCGATTTATC CCGTTTCGGT TTCGGAATCG CCGGGTCTTT AAATGTACGC  
 1801 GGACACCTTT CCGGTGATT GCGGCGGCG ATCCGAACCT TTGAAACCGA  
 1851 CCTTTCCGGC GCGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC  
 1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCCGATA  
 1951 CGCGCCGACA TCAAAGGCAG CCGCCTTCG CTGTGCGGCG GAGCGGCGGT  
 2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCACA  
 2051 TCGGCACACA CGCCGCCATG ACGCTGGATG GCAAAACGTT CAAATTCGAT  
 2101 TTGGACGCTT CAGGCGGCAT CAACAGGGA CTTACCCGAT GGAAGGCAG  
 2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC  
 2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAT  
 2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA  
 2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG  
 2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC  
 2401 GCGGACTGGG ATGTGCGCTA CCGGCGCAAC GCGCGCGGCT ACCTCAATAT  
 2451 CAGCCGGCAA AGCGCGGATG CCGTATTGCC CCGCGGCGAG GCTTTGGGTT  
 2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC  
 2551 CTGCTTGACG GCGGCGCGCG TTTGCGGCGG ATTAACGCCG ATTTGGGCAT  
 2601 CGCCAACGCC TTCGGCGGCA ATATGGCAAA TGCACCGCTC GGCGGCAGGA  
 2651 TTACCGCCTC CTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC  
 2701 CCGCGCAAAA ACATTACCGG CAGCTGAAT GCGCGCGCGC AAATCGGCGG  
 2751 ACGGGTAGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT  
 2801 ACGGGAAAAA CAACGGCAAC ATCACCCTCG GGCAAGCCG CTCTTTCGAT  
 2851 ACCGCGCCTT TGGGCGGCAG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT  
 2901 ATTCGCAAC TTCTTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG  
 2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGCAGC  
 3001 ATCAACGGCG ACAAACTCTA TTACCGCAAC CAAACCCAGG GCATCATCTT  
 3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG  
 3101 AGACCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTCT CCGTACGGTC  
 3151 GGTATGGA AAACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTGACAA  
 3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CTGACGGTT TCCGGCAACA  
 3251 CCGCCTGCG CTATTGCGCG CAAAAGGCA TATCCGTTAC CGGGATGATT  
 3301 AAAACGATC AGGGGCTGTT CGGTTGCAA AAATCCTCGA TGCCGTCGCT  
 3351 CGGCGACGAT GTCGTGCTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC  
 3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCGC  
 3451 TTGCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCTGAC  
 3501 CGCCCAATCG GCGGAAGCG TACGGGCGT GGCACGGTC CGCGTCATCA  
 3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCAG  
 3601 GTCTCCTTTG TCGGCCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA  
 3651 ACGCCGCTT TCCCGGCTCG GTGCGGCGT GGAATATTTG GGCAGCCTCA  
 3701 ACAGCCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGA AAAAGAC  
 3751 AAGCTCTCTT GGCTCATCCT CAACCGCGCC GGCAGCGGCA GCAGCGGCA  
 3801 CAATGCCGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAATCA  
 3851 ACACCGCAT CCGGCTGGTG GATGATTGG GCTTTACCAG CAAGCGCAGC  
 3901 CGCAACGCGC AAACCGGCGA ACTCAACCCG GCCGAACAGG TGCTGACCGT  
 3951 CGGCAAAACA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT  
 4001 CAGCGCGGA ACAGTCCGTC AAATGATT ACCGCGTGAC CCGCGCCATA  
 4051 CAGGCGGTTG CCGTATCGG CAGCGTTTCG TCGGCGGCG AGCTGACATA

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG  
4151 GAAACGGCAA AGGAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep  
1 MTDAPTDT PTENGTRKMP SEHRPTPEAK KRRPLLKLSA ALLSVLILAV  
51 CFLGWLAGE AGLRFGLYQI PSWFGVNIS QNLKGTLLDG FDGDNWSIET  
101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPL  
151 SLPDSIDLPA AVYLDRFETG KISMGAFFDK QTVYLERLDA SYRYDRKGHR  
201 LDLKAADTFW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG  
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF  
301 VPSLPDAGLN FDLTAIPSF S DGIALEGLD LENTKAGFAD RINGIPVRQVL  
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA  
401 EDVLQTAFFK RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN  
451 GQRKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ  
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TENGVPPIAGS ADIVYESRHL  
551 PRAAVDLRLG RNIKTDDGGF GKKGDRNLN ITAPDLSRFG FGLAGSLNVR  
601 GHLSGDLDDG IRTFETDLSG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI  
651 RADIKGSRLS LSGGAHVVDL ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD  
701 LDASGGINRE LTRWKSIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN  
751 WQAMGGSLNL QHFWDKKTG ISAKGGAHGL HIAELHNFFK PPFENHLVLN  
801 GDWDVAYGRN ARGYNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI  
851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFLPA  
901 AAQNTGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSD  
951 TAPLGRLNL TVADAEVFRN FLVPVQTVKG SLNAAVTLGG SIADPHLGG  
1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV  
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI  
1101 KTDQGLEFSQ KSSMPSVGGD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR  
1151 FAGYGADVTI GKKLTLLTAQS GGSVRGVGT VIKGRYKAY QQDLDTKGT  
1201 VSFVGPLNDP NLNIRAERL SPVGAGVEIL GSLNSPRITL TANEPMSKED  
1251 KLSWLILNRA GSGSSGDNA LSAAAGALLA GQINDRIGLV DDLGFTSKRS  
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI  
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNGKKG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDAPTDTPTENGTRKMPSEHRPTPEAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	:                 :                 :					
g285	MTDTTPTDPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGTE					
	10	20	30	40	50	60
m285.pep	AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM					
	:                 :					
g285	AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM					
	70	80	90	100	110	120
m285.pep	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYLDRFETGKISMGAFFDK					
	:                 :                 :					
g285	RRSLHITDISAGDIAIVTKPTPPKEERPPLQGLPDSIDLPAAYLDRFETGKISMGTGFDK					
	130	140	150	160	170	180
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTFWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
	:                 :                 :					
g285	QTVYLERLNAAYRYDRKGHRDLKAADTFWSSSSGSASVGLKKPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
m285.pep	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					
	250	260	270	280	290	300





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a285.seq
1  ATGACCGGATA  CCGCACCAGC  AGATACCGAT  CCGACCGAAA  ACGGCACGCG
51  CAAAATGCGC  TCTGAACACC  GCCTACCCC  GCCGGCAAAA  AAACGCCGCC
101 CGTGCTGTA  GCTGTCGGCG  GCACTGCTGT  CTGTTCTGAT  TTTGGCAGTA
151 TGTTTCTCG  GCTGGCTCGC  CCGCACCGBA  GCGGGTTTGC  GCTTCGGGCT
201 GTACCAATC  CGCTCTTGGT  TCGGCGTAAA  CATTTCCTCC  CAAAACCTCA
251 AAGGCAAGCT  GCTCGACGGC  TTCGACGGCG  ACAACTGGTC  GATAGAAACC
301 GAGGGGGCAG  ACCTTAAAAA  CAGCCGCTTC  CGCTTCGCGT  GGAACACGCT
351 CGAATCGATG  CGCCCGCAGC  TGCACTATAC  CGAAATTTCC  GCGGCGGACA
401 TCGCCTCGT  TACCAACAAC  ACTCCGCTA  AAGAAGAACG  CCCGCCGCTC
451 AGCCTTCCCG  ACAGCATAGA  CCTGCCTGCC  GCCGTCTAT  TCGACCGGCT
501 CGAGACGGGC  AAAATCAGCA  TGGGCAAGC  CTTTGACAAA  CAAACCGTCT
551 ATCTCGAAGC  GCTGGATGCT  TCTACCGGT  ACGACGCGAA  AGAACACGCG
601 CTCGACCTGA  AGGCTGCCGA  CACGCCGTGG  AGCAGTTCGT  CGGGGTCAGC

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651 CTCGGTCGGC TTGAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA  
 701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC  
 751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGCGC GCAATATCCG  
 801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA  
 851 CATTGGAAGA AGTACTGGTC AAAGGTTCA ACATCAATCC GTCCGCCTTC  
 901 GTGCCTTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC  
 951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGAAAAACA  
 1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCG TCAGGTTTTA  
 1051 GGCAGCTTTG TCATCCGGCA GGACGGCACG GTGCATATCG GCAATACGTC  
 1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA  
 1151 CCGAAAAAGA CATCCTCGAT TTAATATAG GCATCAATC CGTCGGCGCG  
 1201 GAAGACGTAC TGCAAAACCG GTTCAAAGGC AGGTTGGACG GCAGCATCGG  
 1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGCCAA CTCGGCATCG  
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 1351 GCACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG  
 1401 CAGCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGTCTA  
 1451 AGCTGGACAT CCGTTCCCGC GCATTGACC CTTGCGCAT CGATCCGCAA  
 1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC  
 1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG  
 1601 GCGTACCGAT TGCCGGCAGT GCGGACATTG TTTACGAGTC CCGCCACCTT  
 1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTTAAACAGA  
 1701 CCGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCGCAC  
 1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CCGGGTCTTT AAATGTACGC  
 1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA  
 1851 CCTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC  
 1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCCGATA  
 1951 CCGCGCGACA TCAAAGGCG CCGCCTTCG CTGTGCGGCG GAGCGGAGGT  
 2001 TGTCGATACC GCGGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGCA  
 2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT  
 2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAGGCGAG  
 2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC  
 2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAT  
 2251 TGGCAGGCAA TGGGCGGCG CCTCAACCTG CAACACTTTT CTTGGGATAA  
 2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG  
 2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC  
 2401 GCGGACTGGG ATGTGCGCTA CCGGCGAAAC GCGCGGCGCT ACCTCAATAT  
 2451 CAGCCGCAA AGCGCGCATG CCGTATTGCC CCGCGGCGAG GCTTTGGGTT  
 2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC  
 2551 CTGCTTGACG GCGGCGCGCG TTTGCGGCGG ATTAACGCGG ATTTGGACAT  
 2601 CCGCAACGCC TTCGGCGGCA ATATGGCAAA TGCACCGCTC GCGGCGAGGA  
 2651 TTACCGCCTC CCTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC  
 2701 GCGCGGCAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG  
 2751 ACGGGTCGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT  
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 2851 ACCGCGCCTT TGGGCGGCG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT  
 2901 ATTCCGCAAC TTCCTACCGG TCGGACAAC CGTCAAGGC AGCCTGAATG  
 2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCATT GGGCGGCAGC  
 3001 ATCAACGCGC ACAAACCTCTA TTACCGCAAC CAAACCCAAG GCATCATCTT  
 3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG  
 3101 ACAGCCTGAA ATTCGGGCAC GAAGGGACGG CGGAACCTCT CCGTACGGTC  
 3151 GGTATGGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTGACAA  
 3201 ATACCGCATC CTGTCCCGCC CCAACCGCGC CCGTACGGTT TCCGGCAACA  
 3251 CCCGCTGCG CTATTGCGCG CAAAAGGCA TATCCGTTAC CCGGATGATT  
 3301 AAAACGGATC AGGGGCTGTT CGGTTGCGAA AAATCCTCGA TGCCGTCCGT  
 3351 CCGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC  
 3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CCGCATCCGC  
 3451 TTCGCCGGT ACGGCGCGGA CGTTACCATA GCGGCGAAAC TGACCCTGAC  
 3501 CGCCCAATCG GCGGGAAGCG TCGGGGCGT GGGCACGGTC CGCGTCATCA  
 3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGACATTAC CAAAGGCACG  
 3601 GTCTCCTTTG TCGGCCCGCT CAACGACCCC AACCTCAACA TCCGCGCGCA  
 3651 ACGCCGCCCT TCCCCGTCG GTGCGGCGT GGAATATTG GGCAGCTCA  
 3701 ACAGTCCGCG CATTACGCTG ACGGCAAACG AACCAGTGA TGA AAAAGAC  
 3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGCGCA  
 3801 CAATGCCGCC CTGTCCGCG CCGCGGCGC GCTGCTTGCC GGGCAATCA  
 3851 ACGACCGCAT CCGGCTGGTG GATGATTGG GCTTTACCAG CAAGCGCAGC  
 3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT

655

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3951 CGGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAAGTATT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTG CCCGTATCGG CAGCCGTTTC TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

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a285.pep
1  MDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51  CFLGWLAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPL
151 SLPDSIDLPA AVYLDRFETG KISMGAFAFK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSES DGIALEGLSD LENTKAGFAD RNGIPVRQVL
351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFAK RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIIKTGGGF GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRLS LSGGAEVVDI ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKSIGI LDIGGAFLNK LQNRMTLEAG AERVAASAAN
751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PFFEHLNLVLN
801 GDWDVAYGRN ARGYNISRQ SGDAVLPGGQ ALGLNAFLSK TRFQNDRIGI
851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFPLPA
901 AAQNTGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRFSD
951 TAPLGGRLNL TVADAEVFRN FLVPGQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGKLTLTQS GGSVRGVGTV RVIKGRYKAY QQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVAGVEIL GSLNSPRITL TANEPMSEKD
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTGVKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNSKKGK*

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m285/a285 99.4% identity in 1389 aa overlap

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          10      20      30      40      50      60
m285.pep  MDTAPTDTDPTENGTRKMPSEHRPTPPAKRRPLLKLSAALLSVLILAVCFLGWLAGTE
          |||
a285      MDTAPTDTDPTENGTRKMPSEHRPTPPAKRRPLLKLSAALLSVLILAVCFLGWLAGTE
          10      20      30      40      50      60

          70      80      90      100     110     120
m285.pep  AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM
          |||
a285      AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM
          70      80      90      100     110     120

          130     140     150     160     170     180
m285.pep  RRSLLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYLDRFETGKISMGAFAFK
          |||
a285      RRSLLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYLDRFETGKISMGAFAFK
          130     140     150     160     170     180

          190     200     210     220     230     240
m285.pep  QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK
          |||
a285      QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK
          190     200     210     220     230     240

          250     260     270     280     290     300
m285.pep  TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF
          |||

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656

a285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPPAESLDKTL EEVLVKGFNINPSAF
	250 260 270 280 290 300
	310 320 330 340 350 360
m285.pep	VPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTKAGFADRNGIPVRQVLGGFVIRQDGT
	:
a285	VPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTKAGFADRNGIPVRQVLGSFVIRQDGT
	310 320 330 340 350 360
	370 380 390 400 410 420
m285.pep	VHIGNTSAALLGRGGIRLSGKIDTEKDILDLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
	:
a285	VHIGNTSVALGRGGIRLSGKIDTEKDILDLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
	370 380 390 400 410 420
	430 440 450 460 470 480
m285.pep	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
	:
a285	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
	430 440 450 460 470 480
	490 500 510 520 530 540
m285.pep	RLKLDIRSFADPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
	:
a285	RLKLDIRSFADPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
	490 500 510 520 530 540
	550 560 570 580 590 600
m285.pep	ADIVYESRHLPRAAVDLRLGRNIIKTGGFGKKGDRLNLNITAPDLSRFGFGLAGSLNVR
	:
a285	ADIVYESRHLPRAAVDLRLGRNIIKTGGFGKKGDRLNLNITAPDLSRFGFGLAGSLNVR
	550 560 570 580 590 600
	610 620 630 640 650 660
m285.pep	GHLSGDLDDGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
	:
a285	GHLSGDLDDGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
	610 620 630 640 650 660
	670 680 690 700 710 720
m285.pep	LSGGAAVVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
	:
a285	LSGGAEVVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
	670 680 690 700 710 720
	730 740 750 760 770 780
m285.pep	LDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMGGSLNLQHFSWDKKTGISAKGGAHGL
	:
a285	LDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMGGSLNLQHFSWDKKTGISAKGGAHGL
	730 740 750 760 770 780
	790 800 810 820 830 840
m285.pep	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
	:
a285	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
	790 800 810 820 830 840
	850 860 870 880 890 900
m285.pep	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
	:
a285	TRFQNDRIGILLDGGARFGRINADLDIGNAFGGNMANAPLGGRITASLPDLGLTKPFLPA
	850 860 870 880 890 900
	910 920 930 940 950 960
m285.pep	AAQNITGSLNAAAQIGGRVGSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN
	:

657

a285	AAQNITGSLNAAAQIGGRVGS	PSVNAAVNGSSNYGKINGNITVGQSR	SFDTAPLGGRLNL			
	910	920	930	940	950	960
m285.pep	970	980	990	1000	1010	1020
	TVADAEVERNF	LPVGQTVKGS	LNAAVTLGG	SIADPHLGG	SINGDKLY	YRNQTQGI
a285	TVADAEVERNF	LPVGQTVKGS	LNAAVTLGG	SIADPHLGG	SINGDKLY	YRNQTQGI
	970	980	990	1000	1010	1020
m285.pep	1030	1040	1050	1060	1070	1080
	SLRSHIAGR	KWVIDSLK	ERHEGTAEL	SGTVGMEN	SGPDVDIG	AVFDKYRIL
a285	SLRSHIAGR	KWVIDSLK	ERHEGTAEL	SGTVGMEN	SGPDVDIG	AVFDKYRIL
	1030	1040	1050	1060	1070	1080
m285.pep	1090	1100	1110	1120	1130	1140
	SGNTRLRY	SPQKGISV	TGMIKTDQ	GLFGSQKS	SMPSVGDD	VVVLGEVK
a285	SGNTRLRY	SPQKGISV	TGMIKTDQ	GLFGSQKS	SMPSVGDD	VVVLGEVK
	1090	1100	1110	1120	1130	1140
m285.pep	1150	1160	1170	1180	1190	1200
	LTLDLNDG	IRFAGYG	ADVTIGG	KLTLTAQ	SGGSVRG	VGTVRVIK
a285	LTLDLNDG	IRFAGYG	ADVTIGG	KLTLTAQ	SGGSVRG	VGTVRVIK
	1150	1160	1170	1180	1190	1200
m285.pep	1210	1220	1230	1240	1250	1260
	VSVFGPLN	DPNPNL	NIRAERRL	SPVGAGVE	ILGSLNSP	RITLTANE
a285	VSVFGPLN	DPNPNL	NIRAERRL	SPVGAGVE	ILGSLNSP	RITLTANE
	1210	1220	1230	1240	1250	1260
m285.pep	1270	1280	1290	1300	1310	1320
	GSGSSGD	NAALSA	AAGALLA	GGQINDRI	GLVDDL	LGFTSKRS
a285	GSGSSGD	NAALSA	AAGALLA	GGQINDRI	GLVDDL	LGFTSKRS
	1270	1280	1290	1300	1310	1320
m285.pep	1330	1340	1350	1360	1370	1380
	LTGKLYI	GYEYIS	SAEQSVK	LIYRLTR	AIQAVAR	IGSRSSG
a285	LTGKLYI	GYEYIS	SAEQSVK	LIYRLTR	AIQAVAR	IGSRSSG
	1330	1340	1350	1360	1370	1380
m285.pep	1390					
	DSAGNGK	GKX				
	:					
a285	DSAGNSK	GKX				
	1390					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51 CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACATGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAC CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATCACCGACA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTAAGGCCT
351 GCCCGACAGC ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAACAACAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGCG ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG

```

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551 TCGGCTTGAA AAAACCGTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTCGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG GCGGCCGAAC TGACGATCGA GCGCGGCAAT ATCCGCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTGCGG AATCATTGGA TAAACATTG
751 GAAGAAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTGGA CCTGACCGCC ATCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAA
901 GCGGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTGGGCGG
951 CTTTGTCTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCCTGTCTCGG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTAA TATAGGCATC AACTCGGTCG GCGCGGAAGA
1101 CGTGCTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CACCGGCAGC
1201 GCACGCACGG ACGGCAGCCT cgcCATCGCA AGCGAcCCCG CAAACGAACA
1251 GCGGAAACTG GTGTTGACA CCGTCAACAT CTCGCCGGG GAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCGGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAATTTCC
1401 GGCAGGCGat atCAACGGTT CGATTCTCT. TGCCGGTGAA CTGGCAAAA
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTG CCGGTACGTT CAACGGCGTG
1501 CCGATTGCCG GCAGCGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 GCGCGCCGTC GATTGCGGT TGGGGCGGAA CATCGTCAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCAGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGG GATTGAGCG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCCGTTCT
1801 CTCGATTTTA CCCTCAAAGG CTCACCCGGC ACAAGCCGCC CGATGCGCGC
1851 CGATATCAAG GCGGCGCGCC TTTCCCTGTC GGGCGGCGCG GCGGTTGTCG
1901 ATACCGCCGG CCTGACGCTG GAAGGTACGG GCGCGCAGCA CCGCATCCGC
1951 ACACACGCCG CCATGACGCT GGACGGCAA CCGTTCAAAC TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAG GGCAGCATCG
2051 GCATCCTCGA CATCGCGGCG GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGCGG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTTCTTGG GACAGGAAA
2201 CCGGCATATC GGCAAAAGGC GCGCGACGCG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGCAACAC AATCTGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG GGGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGCATCG GAATCTGCT
2451 TGACGGCGGC GCGCGTTTCG GACGGATTAA CGCCGATTG GGCATCGGCA
2501 ACGCCTTCGG CCGCAATATG GCAATACAC CGCTCGCGCG CAGGATTACA
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCGCGCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCTC CGCGCAAAAT GCGGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGTAGCAG CAACTACGGG
2701 AAAATCAACG GCAATATCAC CGTGGGCAA AGCCGCTCTC TCGATACGGC
2751 ACCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTCC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATCGCGCC
2851 GTAACCTCG GCGGACGAT CGCCGACCCG CACTTGGGCG GCAGTATCAA
2901 CCGCGACAAG CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTCGCAT ATTGCAGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTC GGCACGAAGG GACGGCGGAA CTCTCCGGCA CGGTACGAT
3051 GGAACACAGC GTGCCGATG TCGATATCGG GCGGTTGTT GACAAATACC
3101 GCATCCTGTC CGGCCCAAC CGCCGCCTGA CCGTTTCCGG CAACACCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAARAC
3201 TGATCAGGGG CTGTTCCGTT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTGGGC GAAGTCAAGA AAGAGGCGGC GGCATCGCTC
3301 CCCGTCAATA TGAACCTGAC TTAGACCTC AATGACGGCA TCCGTTCTC
3351 CCGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGGCG
3401 AACCGGGCGG AATGTGCGT GGGGTGGGCA CCGTCCGCGT CATCAAAGG
3451 CGTTACAAAG CATAACGGCA GGATTAGAC ATTACCAAAG GCACAGTCTC
3501 CTTTGTGCGC CCGCTCAACG ACCCAACCT GAACATCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAT TATTGGGCG CCTCAACAGC
3601 CCGGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCTCAACC GTGCCGGCAG CGGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC CGCAGCGGCA GCGCGCTGCG TTGCCGGGCA AATCAACGAC
3751 CGCATCGGCG TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGGAACCTA ACCCGCGCGA ACAGGTGCTG ACCGTGCGCA
3851 AACCACTGAC CGGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTTACCGG CTGACCCGCG CCATACAGG
3951 GGTGCGCCGT ATCGGCAGCC GTTCGTCGGG GCGCGAGCTG ACATACACCA
4001 TACGTTTGA CCGCCTCTTC GGTTCGGACA AAAAAGACTC CGCAGGAAAC
4051 GGCAAGGGA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:  
g285-1 pep

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1  LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAVYLD RFETGKISMG KTFDKQTYYL
151 ERLNAAARYD RKGHRLDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GEGETIHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGTGT
401 ARTDGLAIA SDPANEORKL VFDTVNISAG EGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAG LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFLAG SLNVRGHLGS DLDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKSGSP TSRPMRADIK GGRSLSLGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDDASG GINRELTRWK GSGIGLDIGG AFNLKLQNRM
701 TLEAGAEHVA ASANWQAMG GSLNLQHFSW DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIGNAFGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNASAQI GGRVGSFSVN AAVNGSSNYG
901 KINGNITVQG SRSFDTAPLG GRNLNTVADA EAFRNFLPVG QTVKGSLNAA
951 VTLLGGSADP HLGGSSINGDK LYRNRQTQGI ILDNGLSRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSMP SVGGDDVVVLG EVKKEAASL
1101 PYNMNLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR GVGTVRVIKG
1151 RYKAYGQDL DITKGTVSFVG PLNDPNLNR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLF GSDKKDSAGN
1351 GK GK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATTT CCTCCAAAA CCTCAAAGGC
151 ACCTGCTCGC ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCGCTT CGCGTGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCCGG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCCGT CTATCTCGAC CGTCTCAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG GCGGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGAATCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAATAT CGTCATCCAC CCGTTTGGCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGGCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGAC TGAATTTTGA CCTGACCGCC ATCCCGTCGT
851 TTTGAGACGG CATCGCGCTG GAAGGTTTCG TCGATTGGA AAACACCAA
901 GCCGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTGAGG TTTTAGGCGG
951 CTTTGTGATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCTGTCTCGG ACGGGCGGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCCGCTTCA AAGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGACGGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACGCGCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATT CGACCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCCGTC GATTGCGGC TGGGGCGGAA CATTATTAAG ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCCGGT GATTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGCGGCAGC CATCCGTTCC
1801 CTCGATTTCA CGCTCAAAGG TTCGCCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTGCTGTGC GGGCGGAGCG GCGGTTGTCG
1901 ATACCGCCGA CCTGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCGG CCAATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGAACCTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGCGGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAA  
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 2251 CACAATTTCT TCAAAACCGCC CTTGGAACAC AATCTGGTTT TAAACGGCGA  
 2301 CTGGGATGTC GCCTACGGGC GCAACGCGCG CGGCTACCTC AATATCAGCC  
 2351 GGCAAAGCGG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC  
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 2451 TGACGGCGCG GCGCGTTTCG GGCAGATTAA CGCCGATTG GGCATCGCCA  
 2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCGG CAGGATTACC  
 2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTCTGCG CCGCCGCCGC  
 2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAATC GCGGACGGG  
 2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGACGAG CAACTACGGG  
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 2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCG  
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 2851 GTAACCTCTG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA  
 2901 CGGCGACAAA CTCTATTACC GCAACCAAA CCAAGGCATC ATCTTGACA  
 2951 ACGGCTCGCT CGCTTCGCAT ATCGCGGCGA GGAATGGGT AATCGACAGC  
 3001 CTGAAATTCC GGCACGAAGG GACGCGGAA CTCTCCGTA CGGTCGGTAT  
 3051 GGAACACAGC GGACCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC  
 3101 GCATCCTGTC CCGCCCCAAC CGCCGCTGA CGGTTTCCGG CAACACCCGC  
 3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAC  
 3201 GGATCAGGGG CTGTTCCGTT CGCAAAATC CTGATGCCG TCCGTCGGCG  
 3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC  
 3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC  
 3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAACTGACC CTGACCGCCC  
 3401 AATCGGGCGG AAGCGTACGG GCGTGGGCA CGGTCGCGT CATCAAAGG  
 3451 CGTTATAAGG CATACGGGCA GGATTGGAC ATTACCAAG GCACGGTCTC  
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 3701 CCGCCCTGTC TGCAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC  
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 3801 CGGCAAAACC GCGCAACTCA ACCCCGCCGA ACAGGTGCTG ACCGTGCGCA  
 3851 AACCACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC  
 3901 CGCGAAGAGT CCGTCAAACT GATTACCGG CTGACCCGCG CCATACAGGC  
 3951 GGTGCCCCGT ATCGGCGAGC GTTCGTCGGG CGGCGAGCTG ACATACACCA  
 4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAGACTC CGCCGAAAC  
 4051 GGCAAGGAA AATAA

This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pep

1 LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG  
 51 TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA  
 101 IVTKPTFPKE ERPFLSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL  
 151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG  
 201 GLEGKTIHST ARLSGSLKDV RAELAIDGNN IRLSGKSVIH PFAESLDKTL  
 251 EEVLVKGFNI NPAAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK  
 301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE  
 351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT  
 401 ARTDGLSLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLKL  
 451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV  
 501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD  
 551 LSRFGFGLAG SLNVRGHLG DLDGGIRTFE TDLGSAARNL HIGKAADIRS  
 601 LDFTLKGSPP TSRRPIRADIK GSRLSLSGGA AVVDATLML DGTGVQHRIR  
 651 THAAMTLGDK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRN  
 701 TLEAGAERVA ASANWQAMG GSLNLQHFSW DKKTGISAKG GAHGLHIAEL  
 751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPPGGQALGLN  
 801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRT  
 851 ASLPDLGALK PFLPAAQNI TGSLNAAAI GGRVGSFVN AAVNGSSNYG  
 901 KINGNITVGO SRSFDTAPLG GRLNLTADA EVFRNPLPVG QTVKGSNLAA  
 951 VTLGGSIAFP HLGGSSINGDK LYYRNQTQGI ILDNGLSRSH IAGRKVIDS  
 1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR  
 1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDVVVLG EVKKEAAAPL  
 1101 PYNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGSVR GVGTVRVIKG  
 1151 RYKAYQDLD ITKGTVSFVG PLNDPNLNR AERRLSFVGA GVEILGSLNS  
 1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND  
 1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS  
 1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRDFRS GSDKKDSAGN  
 1351 GKKG\*

g285-1/m285-1 96.5% identity in 1354 aa overlap

10 20 30 40 50 60

661

g285-1.pep	LKLSAALLSVLILAVCFLGWIAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDN
m285-1	LKLSAALLSVLILAVCFLGWLAGEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDN
	10 20 30 40 50 60
g285-1.pep	70 80 90 100 110 120
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDS
	70 80 90 100 110 120
g285-1.pep	130 140 150 160 170 180
m285-1	IDLPAAYLDRFETGKISMGTDFDKQTVYLERLNAAYRYDRKGHRLDLKAADTPWSSSSG
	130 140 150 160 170 180
g285-1.pep	190 200 210 220 230 240
m285-1	SASVGLKKPFALDTAIYTKGGFEGETIHSTARLSGSLKDVRALTDGGNIRLSGKSVIH
	190 200 210 220 230 240
g285-1.pep	250 260 270 280 290 300
m285-1	PFAESLDKLTLEEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK
	250 260 270 280 290 300
g285-1.pep	310 320 330 340 350 360
m285-1	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSALLGRGGIRLSGKIDTEKDILDLNIGI
	310 320 330 340 350 360
g285-1.pep	370 380 390 400 410 420
m285-1	NSVGAEDVLQTAFAKGRLDGSIGIGTTASPKISWQLGTGTARTDGLAIASDPANEQRKL
	370 380 390 400 410 420
g285-1.pep	430 440 450 460 470 480
m285-1	VFDTVNISAGEGSLTAQGYLEFKDRLLKLDIRSRAFDPSRIDPQFPAGDINGSIHLAGE
	430 440 450 460 470 480
g285-1.pep	490 500 510 520 530 540
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIVKTDGGFGKKGD
	490 500 510 520 530 540
g285-1.pep	550 560 570 580 590 600
m285-1	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTFTDLSGTARNLHIGKAADIRS
	550 560 570 580 590 600
g285-1.pep	610 620 630 640 650 660
m285-1	LDFTLKGSPTSRPMDIKGGRLSLSGGAADVDTAGLTLEGTGAQHRIRTHAAMTLDGK
	610 620 630 640 650 660
g285-1.pep	670 680 690 700 710 720
m285-1	PFKLDLDASGGINRELTRWKGSGIGLDIGGAFNLKLNRMTEAGAERVAASAANWQAMG
	670 680 690 700 710 720
g285-1.pep	730 740 750 760 770 780
m285-1	GSLNLQHFSWDRKTGISAKGGAGLHIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYL
	GSLNLQHFSWDRKTGISAKGGAGLHIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYL

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	730	740	750	760	770	780
g285-1.pep	790	800	810	820	830	840
m285-1	NISRQSGDAVLPGGQALGLNAFLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
	790	800	810	820	830	840
g285-1.pep	850	860	870	880	890	900
m285-1	ANTPLGGRITASLPDLGALKPFLPAAQONITGSLNAAQIGGRVGSPSVNAAVNGSSNYG					
	850	860	870	880	890	900
g285-1.pep	910	920	930	940	950	960
m285-1	KINGNITVGQSRSFDTAPLGGRLNLTVADAEAFRNFLPVGQTVKGSLSNAAVTLGGSIAADP					
	910	920	930	940	950	960
g285-1.pep	970	980	990	1000	1010	1020
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVMENS					
	970	980	990	1000	1010	1020
g285-1.pep	1030	1040	1050	1060	1070	1080
m285-1	VPDVGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
g285-1.pep	1090	1100	1110	1120	1130	1140
m285-1	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVITGGKLTTLTAQPGGNVR					
	1090	1100	1110	1120	1130	1140
g285-1.pep	1150	1160	1170	1180	1190	1200
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLIRAEERLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
g285-1.pep	1210	1220	1230	1240	1250	1260
m285-1	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
g285-1.pep	1270	1280	1290	1300	1310	1320
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
g285-1.pep	1330	1340	1350			
m285-1	IGSRSSGGELTYTIRFDRFSGDDKDSAGNGKGK					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

```

1 CTGAAGCTGT CGGCGGCACT GCTGCTGTCT CTGATTTTGG CAGTATGTTT
51 CCTCGGCTGG CTCGCCGGCA CGGAAGCGGG TTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTCCGCGCGG CGACATCGCC
301 ATCGTTACCA AACCAGACTCC GCCTAAAGAA GAACGCGCCG CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCGGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGAAGTGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAATAAT CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCGG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAAA
901 GCGCGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAAG TTTAGGCAG
951 CTTTGTCTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCT
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAG CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCAGC
1201 GCGCGCAGCG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCGATT CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGCTC GATTGCGGC TGGGGCGGAA CATTATTAAG ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCGGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGGC GATTGAGCG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCCGTTCC
1801 CTCGATTTCG CGCTCAAAGG TTGCGCCGAC ACAAGCCGCC CGATACGGCG
1851 CGACATCAAA GGCAGCCGCC TTTCGCTGTC GGGCGGAGCG GAGGTTGTCT
1901 ATACCGCCGA CCTGATGCTG GACGGCAGCG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGCGGCG GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGCGG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GGCAGCACAG GTCTGCATAT CGCCGAGTTG
2251 CACAAATTTT TCAAACCGCC CTTGGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAGACGCG CGATGCCGTA TTGCCCCGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGTATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GCGGATTAA CGCCGATTG GACATCGGCA
2501 ACGCCTTCGG CCGCAATATG GCAATGCAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTCTGCG CCGCCGCCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCCG CGCGCAAATC GCGGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCCGCTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG CGCGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT GCGTTCGAT ATCGCGGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCG GGCACGAAGG GACGGCGGAA CTCTCCGTA CCGTCGGTAT
3051 GGAACACAGC GGACCCGATG TCGATATCGG CCGGTTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCCTGA CCGTTTCCGG CAACCCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAC
3201 GGATCAGGGG CTGTTCCGTT CGCAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGCGGCG GGCACCGCTC
3301 CCGCTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGTTCCG
3351 CCGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGGCC
3401 AATCGGGCGG AAGCGTGCGG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTGAGC ATTACCAAAG GCACGGTCTC
3501 CTTTGTCCGG CCGCTCAACG ACCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAT TATTGGGCG CCTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCCTCAACC GCGCCGGCAG TGGCAGCAGC GCGGACAAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGCT TTGCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CCGGCAAAAC GCGGAACTCA ACCCCGCCGA ACAGGTGCTG ACCGTCGGCA
3851 ACAAACCTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAAC TATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCCGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCTG CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 AGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

## a285-1.pep

```

1  LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPPLSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLRGGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGLSLAI SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGAARNL HIGKAADIRS-
601 LDTLKGSPD TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWQAMG GSLNLQHFWS DKKTGISAKG GAHGLHIAEL
751 HNFEEKPFEP NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSCLKTRFQN DRIGILDGG ARFGRINADL DIGNAFGGNM ANAPLGGGRIT
851 ASLPDLGTLK PFLPAAQNI TGSLNAAAI GGRVGSPPSVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRNLTVADA EVFRNPLPVG QTVKGSNLAA
951 VTLLGGSADP HLGGSINGDK LYRNQTQGI ILDNGSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVE DKYRLSRPN RRLTVSGNTR
1051 LRYSPQGIS VTGMKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAPL
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYGQDLD ITRGTVSFVG PLNDPNLNR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGVEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRDFRS GSDKKDSAGN
1351 SKGK*

```

a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	10	20	30	40	50	60
a285-1.pep	70 WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDS	80	90	100	110	120
m285-1	70 WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDS	80	90	100	110	120
	70	80	90	100	110	120
a285-1.pep	130 IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG	140	150	160	170	180
m285-1	130 IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG	140	150	160	170	180
	130	140	150	160	170	180
a285-1.pep	190 SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH	200	210	220	230	240
m285-1	190 AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH	200	210	220	230	240
	190	200	210	220	230	240
a285-1.pep	250 PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK	260	270	280	290	300
m285-1	250 PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK	260	270	280	290	300
	250	260	270	280	290	300
a285-1.pep	310 AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLRGGGIRLSGKIDTEKDILDLNIGI	320	330	340	350	360
m285-1	310 AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLRGGGIRLSGKIDTEKDILDLNIGI	320	330	340	350	360
	310	320	330	340	350	360
a285-1.pep	370 NSVGAEDVLQTAFKGRLDGSGIGGTTASPKISWQLGIGTARTDGLSLAIASDPANGQRKL	380	390	400	410	420
m285-1	370 NSVGAEDVLQTAFKGRLDGSGIGGTTASPKISWQLGIGTARTDGLSLAIASDPANGQRKL	380	390	400	410	420
	370	380	390	400	410	420
	430	440	450	460	470	480

665

a285-1.pep	VLDTVNIAAGQGS	SLTAQGYLE	FKDRLLK	LDIRSR	AFDPSRID	PQLPAGNINGS	INLAGE
m285-1	VLDTVNIAAGQGS	SLTAQGYLE	FKDRLLK	LDIRSR	AFDPSRID	PQLPAGNINGS	INLAGE
	430	440	450	460	470	480	
a285-1.pep	LAKEKFTGKMR	FLPGTFNG	VPIAGSAD	IVYESRHL	PRAAVDL	RRLGRNI	IKTDGGFGKKGD
m285-1	LAKEKFTGKMR	FLPGTFNG	VPIAGSAD	IVYESRHL	PRAAVDL	RRLGRNI	IKTDGGFGKKGD
	490	500	510	520	530	540	
a285-1.pep	RLNLNITAPDL	SRFGFLAG	SLNVRGHL	SGDLGG	IRTFTDL	SGAARNL	HIGKAADIRS
m285-1	RLNLNITAPDL	SRFGFLAG	SLNVRGHL	SGDLGG	IRTFTDL	SGAARNL	HIGKAADIRS
	550	560	570	580	590	600	
a285-1.pep	LDFTLKGS	PDTSRPIR	ADIKGSRL	SLSGGAE	VVDATD	MLDGTG	VQHRIRTHAAMTLDGK
m285-1	LDFTLKGS	PDTSRPIR	ADIKGSRL	SLSGGAE	VVDATD	MLDGTG	VQHRIRTHAAMTLDGK
	610	620	630	640	650	660	
a285-1.pep	PFKFDLDAS	GGINREL	TRWKSIG	ILDIGGA	FNKLQNR	MILEAGA	ERVAASAANWQAMG
m285-1	PFKFDLDAS	GGINREL	TRWKSIG	ILDIGGA	FNKLQNR	MILEAGA	ERVAASAANWQAMG
	670	680	690	700	710	720	
a285-1.pep	GSLNLQHFS	WDKKTG	ISAKGGA	HGLHIAE	LHNFFK	PPFEHNL	VLNGDWDVAYGRNARGYL
m285-1	GSLNLQHFS	WDKKTG	ISAKGGA	HGLHIAE	LHNFFK	PPFEHNL	VLNGDWDVAYGRNARGYL
	730	740	750	760	770	780	
a285-1.pep	NISRQSGDA	VLPGGQAL	GLNAFSL	KTRFQND	RIGILLD	GGARFGR	INADLDIGNAFGGNM
m285-1	NISRQSGDA	VLPGGQAL	GLNAFSL	KTRFQND	RIGILLD	GGARFGR	INADLDIGNAFGGNM
	790	800	810	820	830	840	
a285-1.pep	ANAPLGGRI	TASLPDL	GLTKPFL	PAAQNI	TGSLNAA	QIGGRV	GSPSVNAAVNGSSNYG
m285-1	ANAPLGGRI	TASLPDL	GLTKPFL	PAAQNI	TGSLNAA	QIGGRV	GSPSVNAAVNGSSNYG
	850	860	870	880	890	900	
a285-1.pep	KINGNITV	GQSRSD	TAPLGG	RNLTVAD	AEVFRN	FLPVGQ	TVKGSLNAAVTLGGS
m285-1	KINGNITV	GQSRSD	TAPLGG	RNLTVAD	AEVFRN	FLPVGQ	TVKGSLNAAVTLGGS
	910	920	930	940	950	960	
a285-1.pep	HLGGSING	DKLYRN	QTQGI	ILDNGS	LRSHIAG	RKWVID	SLKFRHEGTAELSGTVGMENS
m285-1	HLGGSING	DKLYRN	QTQGI	ILDNGS	LRSHIAG	RKWVID	SLKFRHEGTAELSGTVGMENS
	970	980	990	1000	1010	1020	
a285-1.pep	GPDVDIG	AVFDKYR	ILSRPN	RRLTVS	GNTRLR	YSPQK	GISVTGMIKTDQGLFGS
m285-1	GPDVDIG	AVFDKYR	ILSRPN	RRLTVS	GNTRLR	YSPQK	GISVTGMIKTDQGLFGS
	1030	1040	1050	1060	1070	1080	
a285-1.pep	SVGDDVV	VLGEVK	KEAAAP	LPVNMN	LTLDL	NDGIRF	AGYADVITGGKLT
m285-1	SVGDDVV	VLGEVK	KEAAAP	LPVNMN	LTLDL	NDGIRF	AGYADVITGGKLT
	1090	1100	1110	1120	1130	1140	
a285-1.pep	GVGTVRV	IKGRYK	AYGQD	LDITK	GTVSF	VGPLND	PNLNIRAERRLS
m285-1	GVGTVRV	IKGRYK	AYGQD	LDITK	GTVSF	VGPLND	PNLNIRAERRLS
	1150	1160	1170	1180	1190	1200	

666

	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTANEPMSKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSSGGELTYTIRFDRFSGSDKDSAGNSKGKX					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKDSAGNSKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

g286.seq

```

1  atgcagaaca ccggtaccat gatgatcaaa ccgaccgccc tgctcctgcc
51  ggctttatatt ttctttccgc acgcatacgc gcctgcgccc gacctttccg
101 aaaacaaggc ggcggttttc gcattgttca aaagcaaaag ccccgacacc
151 gaatcagtc aattaaaacc caaattcccc gtcgcgcatcg acacgcagga
201 cagtgaatc aaagatatgg tcgaagaaca cctgcgctc atcacgcagc
251 agcaggaaga ggttttgat aaggaacaga cgggattcct tgccgaagaa
301 gcaccggaca acgttaaac aatgctccgc agcaaaaggct atttcagcag
351 caaggtcagc ctgacggaaa aagacggagc ttatacgggtg cacatcacac
401 cgggcccgcg caccaaaatc gccaacgtcg gcgtcgccat cctcggcgac
451 atcctttcag acggcaacct cgccgaatac taccgcaacg cgctggaaaa
501 ctggcagcag ccggtaggca gcgatttcga tcaggacagt tgggaaaaaca
551 gcaaaacttc cgtcctcggc gcggtaacgc gcaaaaggcta cccgcttgcc
601 aagctcggca acaccgggc gccgtcaac cccgataccg ccaccgcca
651 tttgaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701 aaatcaccgg cacacagcgt taccccaac aaaccgtctc cggcctggcg
751 cgcttccaac cgggcacgcc ctacgacctc gacctgctgc tcgacttcca
801 acaggcgctc gaacaaaacg ggcattatc cggcgcgctc gtacaagccg
851 acttcgaccg cctcccaagg ggaccgcgtc cccgtcaaa gtagcgtaac
901 cgaggtcaaa cgccacaaac tcgaaaccgg catccgcctc gattcggaat
951 acggtttggg cggcaaaatc gcctacgact attacaacct cttcaacaaa
1001 ggctatatcg gctcggctcg ctgggatatg gacaaatag aaaccacgct
1051 tgccgcccgc atcagccagc cgcgcaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaaccgt tcgaccaccc aaaacctcga aaaacgcgcc
1151 ttctccggcg gcatctggtg tgtgcgcgac cgcgcgggca tcgatgccag
1201 gctgggggcg gaatttctcg cagaaggccg gaaaaatccc ggctcggatg
1251 tcgatttggg caacagccac gccacgatgc tgaccgcctc ttggaacgc
1301 cagctgctca acaacgtgct gcaccccga aacggccatt acctcgacgg
1351 caaaatcggg acgactttgg gcacattcct gtcctccacc gcgctaattc
1401 gcacctctgc ccgcgcaggt tatttcttca cgcccga aaaactc
1451 ggcacgttca tcatacgcgg acaagcgggt tacaccgttg cgcgcgacaa
1501 tgccgatgtc ccctcggggc tgatgttccg cagcggcgcc gcgtcttccg
1551 tgcgcgggta cgaacttga

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This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

g286.pep

```

1  MONTGTMKIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKSKSPDT
51  ESVKLKPFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101  APDNVKTMLR SKGYFSSKVS LTEKDGYTV HITPGPRTKI ANVGVAIGLD
151  ILSDGNLAEY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201  KLGNTAAVN PDTATADLNV VDSGRPIAF GDFEITGTQR YPEQTVSGLA
251  RFQPGTPYDL DLLLDFQAL EQNGHYS GAS VQADFDRLPR GPRPRQSQRN
301  RGQTPQTRNR HPPRFGIRFG RQNRLLRLQ LQQRLYRLGR LGYGQIRNHA
351  CRRHQPAQAL SGQLLDKQRF LQPFDPKPR KTRLLRRHLV CARPRGHRCQ
401  AGGGISRRLR ENPRLGCRFG QPRHDADRL LETPAAQQA AFRKRPLPRR

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451 QNRDDFGHIP VLHRANPHLC PRRLFLHARK QKTRHVHHTR TSGLHRCTRQ  
501 CRCLPGADVQ QRRRVFRARL RT\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq  
1 ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC  
51 GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG  
101 AAAACAAGGC GCGGGTTTC GCATTGTTC AAAACAAAAG CCCCGACACC  
151 GAATCAGTCA AATTAACC CAAATCCCC GTCTCATCG ACACGCAGGA  
201 CAGTGAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCAGCAGC  
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCTC CGCCGAAGAA  
301 GCGCCGGACA ACGTTAAAC GATGCTCCGC AGCAAAGGCT ATTTCAGCAG  
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC  
401 CGGGCCCGCG CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC  
451 ATCCTTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA  
501 CTGGCAGCAG CCGGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAAACA  
551 GCAAAACTTC CGTCTCGGC GCGGTAAACG GCAAAGCCTA CCCGCTTGCC  
601 AAGCTCGGCA ATACGCAGGC GGCCGTCAAC CCCGATACCG CCACGCGCGA  
651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GGCGACTTTG  
701 AAATCACCAG CACACAGCGT TACCCGAAC AAATCGTCTC CGGCCTTGCG  
751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA  
801 ACAGGCGCTC GAACAAAACG GGCATTATTC CGGCGCTCC GTACAAGCCG  
851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC  
901 GAGGTCAAAC GCCACAACT CGAAACCGGC ATCCGCCTCG ATTCGGAATA  
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG  
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAATACGA AACCACGCTT  
1051 GCCGCCGGCA TCAGCCAGCC GCGCAACTAT CCGGGCAACT ACTGGACAAG  
1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCGCCT  
1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG  
1201 CTGGGGGCGG AATTCTCGC AGAAGGCCGG AAAATCCCCG GCTCGGCTGT  
1251 CGATTGGGCG AACAGCCAGC CCACGATGCT GACCGCTCT TGGAAACGCC  
1301 AGCTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CCTCGACGGC  
1351 AAAATCGGTA CGACTTTGGG CACATTCCTG TCCTCCACCG CGCTGATCCG  
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTAC GCCCGAAAAC AAAAACTCG  
1451 GCACGTTTCA CATACGCGGA CAAGCGGTT ACACCGTTGC CCGCGACAAT  
1501 GCCGACGTTT CTTAGGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT  
1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGGCCCG AACGGATCGG  
1601 TCCTGCCCGA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG  
1651 TTTACGCGCA CCCTTCCCG CGCGGTGTT CACGATATGG GCGATGCCGC  
1701 CGCCAATTTT AAACGTATGA AGCTGAAACA CGGTTCCGGA CTGGGCGTGC  
1751 GCTGGTTCAG CCCGCTTGGC CCGTTTCTCT TCGACATCGC CTACGGGCAC  
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep  
1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT  
51 ESVKLPKFP VLIDTQDSEI KDMVEHLPL ITQQQEEVLD KEQTGFLAEE  
101 APDNVKTMLR SKGYFSSKVS LTEKDGYTV HITPGPRTKI ANVGVAILED  
151 ILSDGNLAEY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA  
201 KLGNTQAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA  
251 RFQPGMPYDL DLLLDFQQAL EQNGHYS GAS VQADFDRLQG DRVPVKVSVT  
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKGYSVSV WMDKYETTL  
351 AAGISQPRNY RGNWTSNVS YNRSTQNL KRAFSGGVWY VRDRAGIDAR  
401 LGAEFLAEGR KIPGSAVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG  
451 KIGTTLGTFLL SSTALIRTS RAGYFFTPEN KKLGTFIIRG QAGYTVARDN  
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP  
551 FTRLTGSAVF HMDGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH  
601 SDKKIRWHIS LGTRF\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap



	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKN	KS	PD	TESV	KLKPKFP
g286	MQNTGTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKS	K	SP	DTESV	KLKPKFP
	10	20	30	40	50	60
m286.pep	VLIDTQDSEIKDMVEEHLPLIT	QQQEEVL	DKEQTGFLAEEAPDNVKTML	RSKGYFSSKVS		
g286	VRLDTQDSEIKDMVEEHLPLIT	QQQEEVL	DKEQTGFLAEEAPDNVKTML	RSKGYFSSKVS		
	70	80	90	100	110	120
m286.pep	LTEKDGAYTVHITPGPRTKIAN	VGVAILG	DILSDGNLAEYYRNALENWQ	QPVGSDF	QD	QDS
g286	LTEKDGAYTVHITPGPRTKIAN	VGVAILG	DILSDGNLAEYYRNALENWQ	QPVGSDF	QD	QDS
	130	140	150	160	170	180
m286.pep	WENSKTSVLGAVTRKAYPLAK	LGNTQA	AVNPD	TATADLNVVDSGRPIA	FGDFEITGTQR	
g286	WENSKTSVLGAVTRKGYPLAK	LGNTRA	AVNPD	TATADLNVVDSGRPIA	FGDFEITGTQR	
	190	200	210	220	230	240
m286.pep	YPEQIVSGLARFQPGMPYDL	LLLD	FQQA	LEQNGHYS	SGASVQAD	FDRL-QGDRVPVKVSV
g286	YPEQTVSGLARFQPGTFYDL	LLLD	FQQA	LEQNGHYS	SGASVQAD	FDRLPRGFRPRQSQRN
	250	260	270	280	290	299
m286.pep	TEV	KRHKLETGIRLDSEYGLG	GKIAYD	YNNLFN	KGYIGSVVWMDK	YETTLAAGISQPRN
g286	RGQTPQTRNRHPPRF	GIRFG	RQNRRL	LQLQ	RLYRLGRLGYQIRNHACRR	HQPAAQL
	310	320	330	340	350	360

a286.seq

seq	1	ATGCACGACA	CCCGTACCAT	GATGATTAAA	CCGACCGCCC	TGCTCCTGCC
51	GGCTTTATTT	TTCTTTCCGC	ACGCATACGC	GCCTGCCGCC	GACCTTCCG	
101	AAAACAAGGC	GGCGGGTTTC	GCATTGTTC	AAAAAAGAG	CCCCGACACC	
151	GAATCAGTTA	AATTAATAAC	CAAAATCCCC	GTCCGCATCG	ACACGCAGGA	
201	TAGTGAATC	AATGAATATG	TCGAAGAACA	CTCGCCGCTC	ATTACGCAG	
251	AGCAGGAAGA	AGTATTGGAC	AAGGAACAGA	CGGGCTTCCT	CGCCGAAGAA	
301	GCACCGGACA	ACGTTAAATC	AATGCTCCGC	AGCAAAGGCT	ATTTACGACG	
351	CAAGTCAGC	CTGACGGAAA	AAGACGGGAC	TTATACGGTA	CACATCACAC	
401	CGGGCCCGCG	CACCAAAATC	GCCAACGTGC	CGCTCGCCAT	CCTCGCGCAC	
451	ATCCTTTAG	CGCCAACTC	CGCCGAATAC	TACCGCAACG	CGCTGGAAAA	
501	CTGGCAGCAG	CCGGTAGGCA	GTGATTTCGA	TCAGGACAGT	TGGGAAAAACA	
551	GCAAAATCTC	CGTCTCCGG	CGCGTAAACG	GCAAAGCCTA	CCCGCTTGCC	
601	AAGTCGGCA	ACACCCGGGC	GGCGCTCAAC	CCCGATACCA	CCGACGCCGA	
651	TTTGAACGTC	TCGTGTGACA	CGGCGCCGCT	CATCGCCTTC	GGCGACTTTG	
701	AAATTACCGG	CACGCAGCGT	TACCCCGAAC	AAATCGTCTC	CGGCTTGGCG	
751	CGCTTCCAAC	CGGGCAGCCG	CTACGACCTC	GACCTGTGTC	TGCAGTTCCA	
801	ACAGGCGCTC	GAACAACAGC	GGCATTTATC	CGGCGCGTCC	GTACAAGCCG	
851	ACTTCGACCG	CTCCAAGGCG	GACGCGTCC	CCGTCAAAGT	CAGCGTAAAC	
901	GAGGTCAAAC	GCCACAAGCT	CGAAACCGGC	ATCCGCGCTCG	ATTTCGGAATA	
951	CGGTTTGGGC	GGCAAAATCG	CCTACGACTA	TTACAACCTC	TTCAACAAAG	
1001	GCTATATCCG	TTCGGTTCGTG	TGGGATATGG	ACAAATACGA	AACCAACGCTT	
1051	GCCGCCGGCA	TACGACGACC	GGCAACTATC	CGGGGCAACT	ATGTGACAAAG	
1101	CAACGTTTCC	TACAACCGTT	CGACCACCCA	AAACCTCGAA	AAACGCGCCT	
1151	TCTCCGGCGG	CATCTGGTAT	GTGCGCGACC	GCGGGGGCAT	CGATGCCAGG	
1201	CTGGGGGCGG	AGTTTCTCGC	AGAAGGCCCG	AAAATCCCCG	GCTCGGATAT	
1251	CGATTTTGGG	AACAGCCACG	CCACGATGCT	GACGCGCTCT	TGGAAACGCC	
1301	AGCTGCTCAA	CACGTCGTG	CATCCCGAAA	ACGGCCATTA	CTCGACGGG	

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1351 AAAATCGGTA CGACTTTGGG CGCATTCTCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTCAT CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCC AACGGATCGG
1601 TCCTGCCCCG ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTT CACGATATGG GCGACGCCGC
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTGCGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTCTCT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

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-- This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

```

a286.pep
1  MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51  ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGF LAEE
101 APDNVKTMLR SKGYFSSKVS LTEKD GAYTV HITPGPRTKI ANVGVA I LGD
151 ILS DGNLA EY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLG NTRAAVN PDTATADLNV VDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLLDFQQA LEQNGHYS GASVQADFRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKG YIGSVV WMDKYETTL
351 AAGISQPRNY RGNYWTSNVS YNRSTTQNL E KRAFSGGIWY VRDRAGIDAR
401 LGAEFLA EGR KIPGSDIDL G NSHATMLTAS WKRQLNNVL HPENGHYLDG
451 KIGTTLGAFL SSTALIRTS A RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRL SGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

m286/a286 98.7% identity in 615 aa overlap

10 20 30 40 50 60
m286.pep MHDTRTMMIKPTALLLPALFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP
|||||
a286 MHDTRTMMIKPTALLLPALFFPHAYAPAADLSENKAAGFALEFKNKSPDTESVKLPKFP
10 20 30 40 50 60

70 80 90 100 110 120
m286.pep VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGF LAEEAPDNVKTMLRSKGYFSSKVS
| |||||
a286 VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGF LAEEAPDNVKTMLRSKGYFSSKVS
70 80 90 100 110 120

130 140 150 160 170 180
m286.pep LTEKD GAYTVHITPGPRTKIANVGVAILGDILSDGNLA EY YRNALENWQQPVGSDFDQDS
|||||
a286 LTEKD GAYTVHITPGPRTKIANVGVAILGDILSDGNLA EY YRNALENWQQPVGSDFDQDS
130 140 150 160 170 180

190 200 210 220 230 240
m286.pep WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPD TATADLNVVDSGRPIAFGDFEITGTQR
|||||
a286 WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPD TATADLNVVDSGRPIAFGDFEITGTQR
190 200 210 220 230 240

250 260 270 280 290 300
m286.pep YPEQIVSGLARFQPGMPYDL DLLLDFQQA LEQNGHYS GASVQADFRLQGDRVPVKVSVT
|||||
a286 YPEQIVSGLARFQPGTPYDL DLLLDFQQA LEQNGHYS GASVQADFRLQGDRVPVKVSVT
250 260 270 280 290 300

310 320 330 340 350 360
m286.pep EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKG YIGSVVWMDKYETTLAAGISQPRNY
|||||
a286 EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKG YIGSVVWMDKYETTLAAGISQPRNY
310 320 330 340 350 360

370 380 390 400 410 420

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670

m286.pep	RGNYWTSNVSYNRSTQNLEKRAFGSGGVVYVRDRAGIDARLGAEFLAEGRKIPGSAVDLG
a286	RGNYWTSNVSYNRSTQNLEKRAFGSGGIWYVRDRAGIDARLGAEFLAEGRKIPGSDIDLG
	370 380 390 400 410 420
m286.pep	NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
a286	NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
	430 440 450 460 470 480
m286.pep	KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNPNSVLPERAL
a286	KKLGTFIIRGQAGYTVARDNANVPNSGLMFRSGGASSVRGYELDSIGLAGPNPNSVLPERAL
	490 500 510 520 530 540
m286.pep	LVGSLLEYQLPFTRTLGAVFHDMDGAAANFKRMKLGSGLVGRWFSPLAPFSFDIAYGH
a286	LVGSLLEYQLPFTRTLGAVFHDMDGAAANFKRMKLGSGLVGRWFSPLAPFSFDIAYGH
	550 560 570 580 590 600
m286.pep	SDKKIRWHISLGRFX
a286	SDKKIRWHISLGRFX
	610

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

g287.seq

```

1 atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51 ctgtgtggggc ggccgtggcg gatcgcccga tgtcaagtcg gcggacacgc
101 cgtcaaaacc ggccgcccc gttgttgctg aaaatgccgg ggaagggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgccgcaagc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 tttcggcaga aaatacaggc aatggcgggt cggaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaaa atgccgcga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 cccccgcgtc aaaccctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaatataac
501 gttgaccacc tgtaaaggcg attcttgtaa tggtgataat ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attagcgat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gcttccggcc
751 gagattccgc tgattcccgt caatcaggcc gatacgctga ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgcccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcggatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttgttgg
951 cacggccgtg tacaacggcg aagtgtgca tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggg aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatggaaa cggctttaag gggacttga
1151 cggaataatg cggcggggat gtttccgga ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattccgc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

g287.pep

```

1 MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV
51 LPKEKKDEEA AGGAPQADTQ DATAGEGSDQ MAAVSAENTG NGGAATTDNP
101 KNEDAGAQND MPQNAAESAN QTGNQFAGS SDSAPASNPA PANGGSDFR

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671

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151 TNVGNVSVID GPSQNLTLH CKGDSNNGDN LLDEEAPSKS EFEKLSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGNTKYI IFYTDKPPTR SARSRRSLPA
251 EIPLIPVNOA DTLIVDGEAV SLTGHSGNIF APEGNYRYLT YGAEKLPGGS
301 YALRVQGEPA KGEMLVGTAV YNGEVLHFHM ENGRPYPSGG RFAAKVDFGS
351 KSVGDIIDSG DLHMGTKQF KAAIDGNGFK GTWTENGGGD VSGRFYGPAG
401 EEVAGKYSYR PTDAEKGFGF VFAGKKDRD*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1 ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTGG CCCTTTCAGC
51 CTGCGGGGGC GGCGGTGGCG GATCGCCCGA TGTCAGTCCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTCTCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAATAACAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGGCA GCGGGGCAAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGGTT
551 CTTAGATCC CATCCCCGCG TCAAACCTTG CACCTGCGAA TGGCGGTAGC
601 AATTTTGGA GGGTTGATT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGA TGAGAAGTA CAGCTAAAAT CAGAATTGTA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTGCGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGAT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCGGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGCGCA
1101 ACCGCGAAAA GGCGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCAGG
1201 TTTGCCGCAA AAGTCGATT CGGCAGCAA TCTGTGGACG GCATTATCGA
1251 CAGCGCGCAT GATTTCATA TGGGTACGCA AAAATTCAAA GCCGCCATCG
1301 ATGGAAACGG CTTTAAGGGG ACTTGGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTTGCCGGCA
1451 AAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAK
51 EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMANAA
151 DGMQGDPSA GGQNAAGTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFRVVDLANG VLIDGPSQNI TLTHCKGDSG SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRS
301 ARSRRSLPAE MPLIPVNQAD TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTKQFK AADGNGFKG TWTENGSGDV
451 SGKIFYGPAGE EVAGKYSYRP TDAEKGFGV FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

          10      20      30      40      49
m287.pep MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETEAK
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287      MFKRSVIAMACIFLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKKDEEA
          10      20      30      40      50      60

```

	50	60	70	80	90	100	109
m287.pap	KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKEDEVAQNMPQNAAGT						
	:	::					
g287	AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQNDMPQNA--						
	70	80	90	100	110		
	110	120	130	140	150	160	169
m287.pap	DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMAAADGMQGGDPSAGGQNAAGTA						
g287	-----						
	170	180	190	200	210	220	229
m287.pap	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNTILTHCKGDS						
	::   :						
g287	-ESANQTGNNQAGSSDSAPASNPAPANGGSDFGRNVGNSSVIDGPSQNTILTHCKGDS						
	120	130	140	150	160	170	
	230	240	250	260	270	280	289
m287.pap	CSGNNFLDEEVQLKSEFEKLSDADKISNYKKDKGKNDKFVGLVADSVQMGKINQYIIFYKP						
	:: :    :		::		::		:
g287	CNGDNLLDEEAPSKSEFEKLSDDEEKIKRYKKDEQRENFGVLVADRVKKDGTNKYIIFYTD						
	180	190	200	210	220	230	
	290	300	310	320	330	340	349
m287.pap	KPTSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLT						
	:						
g287	KPPT-----RSARSRRSLPAEIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLT						
	240	250	260	270	280	290	
	350	360	370	380	390	400	409
m287.pap	YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGS						
g287	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFAAKVDFGS						
	300	310	320	330	340	350	
	410	420	430	440	450	460	469
m287.pap	KSVVDGIIDSGDDLHMGTKQFKAAIDGNGFGKGTWTENGSGDVSGKFYGPAGEEVAGKYSYF						
g287	KSVVDGIIDSGDDLHMGTKQFKAAIDGNGFGKGTWTENGSGDVSGRIFYGPAGEEVAGKYSYF						
	360	370	380	390	400	410	
	470	480	489				
m287.pap	PTDAEKGFGVFAGKKEQDX						
g287	PTDAEKGFGVFAGKKDRDX						
	420	430					

a287.seq

1	ATGTTTAAAC	GCAGTGTGAT	TGCAATGGCT	TGTATTGTTG	CCCTTTCAGC
51	CTGTGGGGGC	GGCGGTGGCG	GATCGCCCGA	TGTTAAGTCG	CGGGACACGC
101	TCTCAAAACC	TGCGGCCCTT	GTGTTTACTG	AAGATGTCGG	GGAAGAGGTG
151	CTGCCGAAAG	AAAAGAAAGA	TGAGGAGGCG	GTGAGTGGTG	CGCGCGAAGC
201	CGATACGCAG	GACGCAACCG	CCGGAAAAGG	CGGTCAAGAT	ATGGCGGCAG
251	TTTCGGCAGA	AAATACAGGC	AATGGCGGTG	CGGCAACAAC	GGATAATCCC
301	GAAATAAAG	ACGAGGGACC	GCAAAATGAT	ATGCGCGAAA	ATGCCGCCGA
351	TACAGATAGT	TCGACACCGA	ATCACACCCC	TGCACCGAAT	ATGCCAACCA
401	GAGATATGGG	AAACCAAGCA	CCGATGCGCG	GGGAATCGGC	ACAACCGCGA
451	AACCAACCGG	ATATGGCAAA	TGCGGCGGAC	GGAAATGCAGG	GGGACGATCC
501	GTCGGCAGGG	GAAATGCGCG	GCAATACGCG	AGATCAAGCT	GCAAAATCAAG
551	CTGAAAAACA	TCAAGTGGCT	GGCTCTCAAA	ATCCTGCCTC	TTCAACCAAT
601	CCTAACGCCA	CGAATGGCGG	CAGCGATTTT	GGAAGGATAA	ATGTAGCTAA
651	TGGCATCAAG	CTTGACAGCG	GTTTCGGAATA	TGTAACGTTG	ACACATTGTA
701	AAGACAAAGT	ATTCGATAGA	GATTTCTTAG	ATGAAGAAGC	ACCACCAAAA
751	TCAGAATTTG	AAAAATTAAG	TGATGAAGAA	AAAAATTAATA	AAATATAAAAA

a287.pep

1	MFKRSVIAMA	CIVALSACGG	GGGSGPDVKS	ADTLSPAAP	VVTEDVGEEV
51	LPKEKKDEEA	VSGAPOADTQ	DATAGKGGQD	MAAVSAENTG	NGGAATTDPN
101	ENKDEGPOND	MPQNAADTDS	STPNHTPAPN	MPTRDMGNQA	PDAGESAQPA
151	NQPMDMAAAD	GMQGDDPSAG	ENAGNTADQA	ANQAEENNQVG	GSQNPASSTN
201	PNATNGSSDF	KINXYANGIK	LDSGSENVTL	THCKDKVCOR	DFLDEEAPPK
251	SFEKLSDSEE	KINKYKKDEQ	RENFVGLVAD	RVEKNGTNKY	VIIYKDKSAS
301	SSSARFRRSA	RSRRSLPAEM	PLIPVNQADT	LIVDGEAVSL	TGHSNGTFAP
351	EGNYRYLTYG	AELKSGGSYA	LSVQGESPAK	EMLAGTAVYN	GEVLHFFHMN
401	GRPSPSGGRF	AAKVDFGSKS	VDGIIDSGDD	LHMGTKQKFA	VLDNGFGFKGT
451	WTENGSGDVS	GFRYFGPAGEE	VAGKYSYRPT	DAEKGGFGVF	AGKKEQD*

m287/a287 77.2% identity in 501 aa overlap

	10	20	30	40	49
m287.pep	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPV	VSSE-----	KETE		
a287	MFKRSVIAMACIVALSACGGGGGGSPDVKSADTLSPKPAAPV	VTEDVGEEVLPKEKKDEEA			
	10	20	30	40	50
	60	70	80	90	100
m287.pep	KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQN	DMPQNAAGT			
a287	VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATTDNFENKDEGP	QNDMPQNAADT			
	70	80	90	100	110
	120	130	140	150	160
m287.pep	DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDP	SAGGQNAAGNTA			
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGGDP	SAG--ENAGNTA			
	120	130	140	150	160
	170	180	190	200	210
m287.pep	AQGANQAGNNGAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQ	NITLTHCKGDS			
a287	DQAAQAEENNQVGGSQNPASSTNPATNGGSDFRINVANGIKLDSGSENV	LTHCKDKV			
	180	190	200	210	220
	230	240	250	260	270
m287.pep	CSGNNFLDEEVQLKSEFEKLSADKISNYKKDGNKDNKEVGLVADSVQMK	GINQYIIFYKP			
a287	CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNG	TNKYVIIYKD			
	240	250	260	270	280
	290	300	310	320	330
m287.pep	KP--TSFARFRRSARSRSLPAEMPLIPVNQADTLIVDGEAVSLTGHS	GNIFAPEGNYRY			
a287	KSASSSARFRRSARSRSLPAEMPLIPVNQADTLIVDGEAVSLTGHS	GNIFAPEGNYRY			
	300	310	320	330	340
	350				

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	350	360	370	380	390	400
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287.pep	GSKSVDGIIDSGDDLHMGTKQKFAAIDGNGFKGTWTENGSGDVSQKFGYPAGEEVAGKYS					
a287	GSKSVDGIIDSGDDLHMGTKQKFAVIDGNGFKGTWTENGSGDVSQKFGYPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287.pep	YRPTDAEKGFGVFAGKKEQDX					
a287	YRPTDAEKGFGVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1  atgcacaccg gacaggcggg aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgtcaag caacctacc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttgtct tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcgggt cgcccttacc gcaccttttc
201 acccttgctt gtgctgcaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccg cgcgcggcgg ttaaccggca ttctaccctg
301 cggagcccg actttcctcc ccgtatgcct tacgcgatac gcgcgactg
351 tctgcccgtc ccgtgtgcgg cgcggattat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacagggt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgtc caagtcgccc tccaatacgg
501 ctttgtggtt gccgacttcg tagcctgtac gcaagtcttt gatgctga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPFRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTGTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCggttttg CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCTCTC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPFRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
g288	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAVQYGFVADFVACTQVF					
	130	140	150	160	170	180

m288.pep	DTX
g288	DAX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

```

a288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTGCCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTGTTGCTT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTGCTT GTGCTGCCAA AGCAGCCATC GCGCGTTTTC CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC GCAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TAAAGCCGTC CAAGTCGCGG TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTGC GCAAGTCTTT AATGCGTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1210; ORF 288.a&gt;:

```

a288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHA
151 LFQAGFDKAV QVAVQYGFV ADFVACAQVF NA*

```

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					



```

a288      PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADFVACAQVF
           130      140      150      160      170      180

m288.pep   DTX
           ::
a288      NAX

```

-- The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

```

g290.seq
1  atggcaaaaa tgatgaaatg ggcggctgtt gcgcggtcg cgcgggcagc
51  ggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata
101 ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg
151 ggcgagattt cgccgtccaa cctggtatcg gtcggcgcgc aggcttcggg
201 gcagattaaa aagctttatg tcaaactcgg gcaacaggtc aaaaaggcg
251 atttgattgc ggaatcaat tcgaccacgc agaccaacac gatcgatatg
301 gaaaaatcca aattggaac gtatcaggcg aagctggtgt ccgcacagat
351 tgcatgtggc agcgcgga aaaaatataa gcgtcaggcg gcgttgtgga
401 aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggaatgcgctt
451 gccgcccgc aagccaatgt tgccgagttg aaggctttaa tcagacagag
501 caaaatttcc atcaataccg ccgagtcgga tttgggtac acgcgcatta
551 ccgcgacgat ggacggcacg gtggtggcga ttcccggtga agaggggcag
601 actgtgaacg cggcgagtc tacgccgacg attgtccaat tggcgaatct
651 ggatatgatg ttgaacaaaa tcgagattgc cgaggcgcat attaccaagg
701 tgaaggcggg gcaggatatt tcgtttacga tttgtccga accggatacg
751 ccgattaagg cgaagtcga cagcgtcgac cccgggtga ccacgatgtc
801 gtcggggcgc tacaacagca gtacggatac ggcttccaat gcggtctatt
851 atatgccc ttcgtttgtg ccgaatccgg acggcaaaact cgccacgggg
901 atgacgacgc agaatacggg tgaatcgac ggtgtgaaaa atgtgttgc
951 tattccgtcg ctgaccgtga aaaatcgcg cggaaggcg ttcgtacgcg
1001 tgttgggtgc ggacggcaag gcagtgaac gcgaaatccg gaccggtatg
1051 aaagacagta tgaataccga agtgaaaagc ggggtgaaag agggggacaa
1101 agtgggtcat tccgaaataa ccgccgccga gcagcaggaa agcgggcaac
1151 gcgccctagg cggcccgcgc gccgataa

```

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

```

g290.pep
1  MAKMMKWAAY AAVAAAAVWG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQVQ KKGDLIAEIN STTQNTIDM
101 ESKSLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATSK EDLESAQDAL
151 AAAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEGQ
201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYYARFV PNPDKLATG
301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM
351 KDSMNTVEKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

```

m290.seq (partial)
1  ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
51  ACTCGGGCAA CAGGTTAAAA AGGGCGATT TATTGCGGAA ATCAATTCTGA
101 CCTCGCAGAC CAATACGCTC AATACGGAAA AATCCAAGTT GGAAACGTAT
151 CAGGCGAAGC TGGTGTCGGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
201 ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG
251 ATTTGGAAAG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC
301 GAGCTGAAGG CTTTAATCAG ACAGAGCAAA ATTTCATCA ATACCGCCGA
351 GTCGGAATTG GGCTACACGC GCATTACCGC AACGATGGAC GGCACGGTGG
401 TGGCGATTCT CGTGAAGAG GGGCAGACTG TGAACCGGC GCAGTCTACG
451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAAATGCA
501 GATTGCCGAG GCGGATATTA CCAAGGTGAA GCGGGGCAG GATATTTCTG
551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC
601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GCGGTTTACA ACAGCAGTAC
651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCGTTTC TTTGTGCCGA

```

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```

701 ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGA AAAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TCGCGGTGTT GGGTGGCGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
1 ..VSVGAAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
51 QAKLVSAQIA LGSAEKKYKR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTMSG GYNSSTDSTA SNAVYYARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLII PSLTVKNRGG KAFVRVLGAD GKAEREIRT GMRDSMNTVE
301 KSGLKEGDKV VISEITAAEQ QESGERALGG PRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

m290.pep				10	20	30
				VSVGAAQASGQ	IKILYVKLGQ	QVKKGDLIAE
g290	PQAA	YITE	AVRR	GDIS	RTVS	ATGEIS
	30	40	50	60	70	80
m290.pep		40	50	60	70	80
		INSTSQNTNL	NTEKSKLETY	QAKLVSAQIA	LGSAEKKYKR	QAALWKENAT
g290		INSTTQNTNL	IDMEKSKLETY	QAKLVSAQIA	LGSAEKKYKR	QAALWKDDAT
	90	100	110	120	130	140
m290.pep		100	110	120	130	140
		AFAAAKANVA	ELKALIRQSK	ISINTAESEL	GYTRITATMD	GTVVAILVEE
g290		ALAAAKANVA	ELKALIRQSK	ISINTAESDL	GYTRITATMD	GTVVAIPVEE
	150	160	170	180	190	200
m290.pep		160	170	180	190	200
		PTIVQLANLD	MMLNKMQIAE	GDITKVKAGQ	DISFTILSEP	DTPIKAKLDS
g290		PTIVQLANLD	MMLNKMQIAE	GDITKVKAGQ	DISFTILSEP	DTPIKAKLDS
	210	220	230	240	250	260
m290.pep		220	230	240	250	260
		GGYNSSTDSTA	SNAVYYARS	FVPNPDGKLA	TGMTTQNTVE	IDGVKNVLII
g290		GGYNSSTDSTA	SNAVYYARS	FVPNPDGKLA	TGMTTQNTVE	IDGVKNVLLI
	270	280	290	300	310	320
m290.pep		280	290	300	310	320
		KAFVRVLGAD	GKAEREIRT	GMRDSMNTVE	KVSEITAAEQ	QESGERALGG
g290		KAFVRVLGAD	GKAEREIRT	GMRDSMNTVE	KVSEITAAEQ	QESGERALGG
	330	340	350	360	370	380
m290.pep						
		PPRRX				
g290		PPRRX				
		390				

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1  ATGGCAAAAA TGATGAAATG GGCGGCTGTT GCGGCGGTCG CCGCGGCAGC
51  GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAAC GGTACAGGCG GGCGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AAACCTTATG TCAAACTCGG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTGGA AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAAATTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATT
551 CCGCAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGA AGAGGGGCAG
601 ACTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGCGGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTTGTCCGA ACCGGATACG
751 CCGATTAAAG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGGCGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TTCGTTTGTG CCGAATCCGG ACGGCAAACT CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAATCGAC GGTGTGAAAA ATGTGCTGAT
951 TATTCGCTCG CTGACCGTGA AAAATCGCGG CCGCAGGGCG TTTGTGCGCG
1001 TGTTGGGTGC AGACGGCAAG GCGCGGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1  MAKMMKWAIV AAVAAAAVWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQQV KKGDLIAEIN STSQTNTLNT
101 ESKSKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAAKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNMKQIAEGD ITKVKGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYYARFV PNPDKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTGM
351 RDSMNTVEKS GLKEGDKVVI SEITAEQQE SGERALGGPP RR*
```

m290/a290 98.2% identity in 334 aa overlap

```

                                     10      20      30
m290.pep                               VSVGAQASGQIKLYVKLGQQVKKGDLIAE
a290      PQAAAYITETVRRGDISRTVSATGEISPSNLVSVGAQASGQIKLYVKLGQQVKKGDLIAE
          30      40      50      60      70      80

          40      50      60      70      80      90
m290.pep  INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
a290      INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATAKEDLESAQD
          90     100     110     120     130     140

          100     110     120     130     140     150
m290.pep  AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
a290      ALAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
          150     160     170     180     190     200

          160     170     180     190     200     210
m290.pep  PTIVQLANLDMMLNKMQIAEGDITKVKGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
a290      PTIVQLANLDMMLNKMQIAEGDITKVKGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
          210     220     230     240     250     260

          220     230     240     250     260     270
```

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```

m290.pep      GGYNSSTD TASNAVYYYARSFV PNP D GK LATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               |||||||
a290          GGYNSSTD TASNAVYYYARSFV PNP D GK LATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               270      280      290      300      310      320

               280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTVEVKSGLKEGDKV VISEITAAEQQESGERALGG
               :|||||
a290          KAFVRVLGADGKAAEREIRTGMRDSMNTVEVKSGLKEGDKV VISEITAAEQQESGERALGG
               330      340      350      360      370      380

m290.pep      PPRRX
               ||||
a290          PPRRX
               390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcttgccgct
51  gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttgaaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccgggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttgacaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaatctt atggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atgcgtaaag gcaaatcccg ggtcggcggc agcatctgcg acaatcccgt
651 cgcggaacc acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tcccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaacc cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSVAAALSKAR
51  LEKTYSAQDL KVLVSVETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLT EE RAADLNKIDF ASLPLDKAIK EVRNGNKLKV AVFSDPDPCF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPD
251 PTGGNHPOKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGA AAAAA CCTATTCCGC CCAAGATTG AAAGTGTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCgtcggcga ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGACAA AGCCATCAA GAAGTGC GCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATG CCGGCCTGCA CCCGATGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTGAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATCGGTAAAG GCAAAATCCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCC

```

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751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

This corresponds to the amino acid sequence &lt;SEQ ID 1220; ORF 292&gt;:

```

m292.pep
1  MKTKLIKILT PFTVLP LLAC GQTPVSNANA EPAVKAESAG KSVAA SLKAR
51  LEKTYSAQDL KVL SVSETPV KGIYEVV VSG RQIIYTD AEG GYMFV GELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQGFEN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILT PFTVLP LLAC GQTPVSNANA EPAVKAESAG KSVAA SLKAR LEKTYSAQDL					
g292	MKTKLIKILT PFTVLP LLAC GQTPVSNANA E SAVKAESAG KSVAA SLKAR LEKTYSAQDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVL SVSETPV KGIYEVV VSG RQIIYTD AEGGYMFV GELIN IDTRKNL TEERAADLNKIDF					
g292	KVL SVSETPV KGIYEVV VSG RQIIYTD AEGGYMFV GELIN IDTRKNL TEERAADLNKIDF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA					
g292	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQPDRAKAWTDWMRKGKFPVGG SICDNPVAET TSLGEQGFENG TPTLVFPNG					
g292	ARKAQILWCQPDRAKAWTDWMRKGKFPVGG SICDNPVAET TSLGEQGFENG TPTLRLPQR					
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSPMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHPQKPAVNPQX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
1  ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCCGCT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGACAA AGCCATCAA GAAGTGCGCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAACGCT TGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCAT TG CCGGCCTGCA CCCCGATGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTCAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATTCCT GGTGCGCGGC AGCATCTGCG ACAATCCGCT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCAACGGG GCGAGCCAAA GCGGCTACAG CCCGATGCCC
751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLAKAR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151  CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251  QLEEIIRKNQ *

m292/a292    100.0% identity in 260 aa overlap

              10      20      30      40      50      60
m292.pep      MKTKLIKILTPFTVLPLLACGQTPVSNANAEPAVKAESAGKSVASLAKARLEKTYSAQDL
a292           MKTKLIKILTPFTVLPLLACGQTPVSNANAEPAVKAESAGKSVASLAKARLEKTYSAQDL
              10      20      30      40      50      60

              70      80      90     100     110     120
m292.pep      KVLVSSETPVKGIYEVVVSQSGRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
a292           KVLVSSETPVKGIYEVVVSQSGRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
              70      80      90     100     110     120

              130     140     150     160     170     180
m292.pep      ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
a292           ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
              130     140     150     160     170     180

              190     200     210     220     230     240
m292.pep      ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLSGEQFGFNGTPTLVFPNG
a292           ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLSGEQFGFNGTPTLVFPNG
              190     200     210     220     230     240

              250     260
m292.pep      RSQSGYSPMPQLEEIIRKNQX
a292           RSQSGYSPMPQLEEIIRKNQX
              250     260
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
  1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtctggtc
 51  gggttcgggt gtcagaacat catcgaaacc ctttcctgcg gcgttacgac
101  gatattcgcc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151  tggcatcgcc tgcggcggtt caagtcgaat cggcggacgc gtggcgtgaa
201  gccgttgaaa aaaccttata tggcgagggg ggcggaatgc agatgcaggc
251  gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301  ccgagggcgt gcgggaagcg gtatgcggac atcggggggc atagtgtatc
351  aatccgtatc cgagttttcc ggttgagca tcgtatgagt atttatgcgc
401  tcgcgcacat catccacctg tattcgcca ccgcctttgt cggcggcgtg
451  ttttttgaa gctgtggttt gtccgtcctg catacgggac ggggtgtcgc
501  cgaggcgccg cgcgaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
551  tgatgccgtt tgcggtcgga ctgctgttcg ccagggaac tctagagtcg
601  actgcagcag catgccctc...
  
```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
  1  MRITCAPMSL LSAVWSVRA VRTSSNRFP ALRRYSAFRP TIFPKPAGTP
 51  WRRVRRFKSN RTRGVKPLK KPYLARGAEC RCRRWTALS HNIAERARES
101  PRRCGRYAD IGGSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151  FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFPAVG LLFARGTLES
201  TAAACP...
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

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m294.seq  
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC  
 51 GATTCGGGTT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC  
 101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT  
 151 TGGCATCGGG TCGCGCGGTT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA  
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC  
 251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG  
 301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGCGG ATAGTGATAC  
 351 AATCCGTATC CGAGTTTTCG GTTTGGAGCA TCGTATGAGT ATTTATGCCG  
 401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG  
 451 TTTTGTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTGCGG  
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTACAGG  
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG  
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG  
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT  
 701 TCGCCATCGC CGTCGTCAA AATGGCGGTT CCACACTGAC GGTCCGTTGG  
 751 TCGAAATACA TACACGCCGT CGTCTTTACC CATATGCTGC TGATTGTCTT  
 801 TTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep  
 1 MRITCAPMSL LSAAVWSIRV VRTSSNRFFA AFRYSAFQP TIFPKPADTP  
 51 WHRVRRFKSN RMRGGKPLK KPYRPRGGC RCRRWTALS HNIAERARES  
 101 PRCGKRYAD IGGSDTIRI RVFRLEHRMS IYAVAHIVHL YCAIAFVGGV  
 151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPEFVG LFFASGIVMA  
 201 ANRYSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTGVG  
 251 SKYIHAVVET HMLLIVFLAK AMFYISW\*

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSA	AVWSVRAVRTSS	NRFFAALRRYS	AFRPTIFPKPAG	TPWHRVRRFKSN	
m294	MRITCAPMSLLSA	AVWSIRVVRTSS	NRFFAALRRYS	AFRPTIFPKPAG	TPWHRVRRFKSN	
	10	20	30	40	50	60
g294.pep	RRTRGVKPLKKPY	LARGAECRCRR	WTALSHNIAER	ARESPRRCGKRY	ADIGGSDTIRI	
m294	RRMRGGKPLKKPY	RPRGGCRRRAW	TALSHNIAER	ARESPRRCGKRY	ADIGGSDTIRI	
	70	80	90	100	110	120
g294.pep	RVFRLEHRMSIY	AVAHIIHLYCAT	AFVGGVFFEV	LVLSVLHTGR	VSREARREVEK	AMSYR
m294	RVFRLEHRMSIY	AVAHIVHLYCA	IAFVGGVFFEV	LVLSVLHTGR	VSREARREVEK	AMSYR
	130	140	150	160	170	180
g294.pep	AVRVMPEFVGLL	FARGTLESTAA	ACP			
m294	AVRVMPEFVGLL	FASGIVMAANR	YLSILGEPFAT	SFGTMLTLKIL	LAFSVLAHFAI	AVVK
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq  
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC  
 51 GATTCGGGCT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC  
 101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT  
 151 TGGCATCGGG TCGCGCGGTT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA  
 201 GCCGTTGAAA AAAACTTATC GTCCGAGGAG GCGGGAATGC AGATGCAGGC  
 251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG  
 301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC  
 351 AATCCGTATC CGAGTTTTCG GTTTGGAGTA CCGTATGAGT ATTTATGCCG  
 401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTTGT CGGCGGCGTG  
 451 TTTTGTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTGCTG  
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTACAGG  
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG  
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG  
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

683

701 TCGCCATCGC CGTCGTCAA ATGGCGCGT CCACACTGAC CGTCGGCTGG  
 751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT  
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294.pep  
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAPRP TIFPKPAGTP  
 51 WHRVRRFKSN RRTGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES  
 101 PRYGGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV  
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMFVVG LLEFASGIVMA  
 201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW  
 251 SKYIHTVVFET HMLLIVFLAK AMFYISW\*

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294.pep	MRITCAPMSLLSAAVWSIRV	VRTSSNRFPAAFRYSAPR	PTIFPKPADTPWHRVRRFKSN			
a294	MRITCAPMSLLSAAVWSIRV	VRTSSNRFPAAFRYSAPR	PTIFPKPAGTPWHRVRRFKSN			
	10	20	30	40	50	60
	70	80	90	100	110	120
m294.pep	RRMRGGKPLKKPYRPRGGG	CRCRRAWTALSHNIAERARE	SPRRCKRYADIGGDS	DTIRI		
a294	RRTGGKPLKKTYRPRRAEC	RCRRARTALSHNIAERARE	SPRRYGGKRYADIGGDS	DTIRI		
	70	80	90	100	110	120
	130	140	150	160	170	180
m294.pep	RVFRLEHRMSIYAVAHIVH	LYCAIAFVGGVFEVLVLSV	LHTGRVSREARREVEKA	MSYR		
a294	RVFRLEYRMSIYAVAHIVH	LYCAIAFVGGVFEVLVLSV	LHTGRVSCEARREVEKA	MSYR		
	130	140	150	160	170	180
	190	200	210	220	230	240
m294.pep	AVRVMFVVGGLLFASGIVMA	ANRYLSILGEPFATSFGTML	TLKILLAFSVLAHFAIAVVK			
a294	AVRVMFVVGGLLFASGIVMA	ANRYLSILGEPFATSFGTML	TLKILLAFSVLAHFAIAVVK			
	190	200	210	220	230	240
	250	260	270			
m294.pep	MARSTLTVGWSKYIHAVVF	THMLLIVFLAKAMFYISW	X			
a294	MARSTLTVGWSKYIHTVVF	THMLLIVFLAKAMFYISW	X			
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295.seq  
 1 atgctcggga tggcgcggca cgacggccag cagggcatcg ccgcgatatt  
 51 gttgccacgc cgccagcagt tttccgcct cgtcttcgcc ccgataaacg  
 101 cgcgtgctgc cgacacggc aaccggccgg cctccgatgc gttttcaaa  
 151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg  
 201 tattgccgca cacctgcacg gatgccgcgc ccaatttcgc caaccgcgcc  
 251 gcattccgct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg  
 301 acggatcagg cggcggactt tcagataacc gttcagcgat tttccgaca  
 351 gccgcgcatt cgccaaaaac agcggcacac ccgctcgccg gcattccttc  
 401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcgggcg  
 451 gtgttcgcgc aaaaactgcc gtacccacgt tttttgtca tacggaagat  
 501 agcggcattg cgcatcgga aacagaactt gcgcggttc ccgtcccgtc  
 551 ggggtcatct gcgtcatcag cagcggcgca tcgggaaaac gccgcgcaa  
 601 ctgcggtatc aagggtggg cggcacgcgt ttctccgacc gaaacggcgt  
 651 gtatccaaac cgcccggtta acgggattcg gatgcggctt gccgaaacgc  
 701 tcgtccctat gcgcccggta tgccggggca cttccggagc gtttgtcaa  
 751 ataacgccgt atccatatcg gcgcaagcag ccacaataca tcataaagcc  
 801 attggaacat cttctattt cctgcaaaac aaatgccgtc cgaacgggtc  
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:



g295.pap  
 1 MLGMRHDDGQ QGIAAILLPR RQOFFRLVFA PINARAAAHG NRPASDAFFK  
 51 LPRQRFHVFR RHQVVFGLAA HLHGCRAQFR QPRRIRLRLR QTARQSRGCG  
 101 TDQAADFQIT VQRFFRQPRI RQKQRHTRSP AFLHQIGPDF GFHQNAEHRA  
 151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ  
 201 LAYQGLGGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ  
 251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVQTAFRQR NQIS\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq  
 1 ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCATATT  
 51 GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAAGC  
 101 CGCGTGTGTC CGCACACGGC AACCGGCCCG CCTCCGATGC GTTTTCAAA  
 151 CTGCCCCGCC AGCGTTTCA TCTGTTCCGA CGGTATGATG TCGTATTGG  
 201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC  
 251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTCAGCGAAG CGGCGGCAGG  
 301 ACGGATCAGG CGGCGGACTT TCAGATAACC GTTCAACGAT TTTTCCGACA  
 351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGCGCGCCG GCATTCCCTC  
 401 ATCAGGTTGG GCCAGATTTT GGTTCATC AAAATGCCGA ACATCGGGCG  
 451 GTGTTCCGCG AAAAAGTCC GTACCCACGT TTTTGTGCA TACGGAAGAT  
 501 AGCGGCATTG CGCATCGGGA AACAGAACTT GCGCGGTTT CCGCCCCGTC  
 551 GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAC GCCGCCGCA  
 601 CTCGCGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGCGT  
 651 GTATCCAAAC CGCGCCGTA ACGGGATTCT GATACGGCTT GCCGAAACGC  
 701 TCGTCCCGAT GCGCCCGATA TGCCGGGCA CTTCGGAGC GTTTGTCCAA  
 751 ATAACGCGGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC  
 801 ATTGAACAT CTTTCTATT CTGCAAAAC AAATGCCGTC TGAACGGTTC  
 851 AGACGGCATT TCGGCAACGG AATCAAATAT CGTAG

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pap  
 1 MLGMRHDDQ QRIAAAILLPR RQOFFRLVFT PINARAAAHG NRPASDAFFK  
 51 LPRQRFHLFR RYDVVFGLAA HLHGCRAQFR QPRRIRLCLR QTARQSRGGR  
 101 TDQAADFQIT VQRFFRQPRI RQKQRHTRAP AFPHQVGPDP GFHQNAEHRA  
 151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PPRRGLRHQ QRRIGKTPPQ  
 201 LAYQGLGGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ  
 251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV XTVQTAFRQR NQIS\*

m295/g295 93.9% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pap	MLGMRHDDQRIAAAILLPRRQOFFRLVFTPINARAAAHGNRPASDAFFKLPRQRFHLFR					
g295	MLGMRHDDGQGIQIAAILLPRRQOFFRLVFAPIANARAAAHGNRPASDAFFKLPRQRFHVFR					
	10	20	30	40	50	60
m295.pap	RYDVVFGLAAHLHGCRAQFRQPRRIRLCLRQTARQSRGGRTDQAADFQITVQRFFRQPRI					
g295	RHQVVFGLAAHLHGCRAQFRQPRRIRLRLRQTARQSRGGRTDQAADFQITVQRFFRQPRI					
	70	80	90	100	110	120
m295.pap	RQKQRHTRAPAFPHQVGPDPGFHQNAEHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
g295	RQKQRHTRSPAFPHQVGPDPGFHQNAEHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
	130	140	150	160	170	180
m295.pap	PPRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDRNGVYPNRAGNGIRIRLAETLVPMRPI					
g295	PSRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDRNGVYPNRAGNGIRMRLAETLVPMRPV					
	190	200	210	220	230	240
m295.pap	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTVQTAFRQRNQISX					
g295	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVRTVQTAFRQRNQIS					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGTGCG CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCGGA CGGCATCAGG TCGTATTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTGAGCGAAG CGGCGGCGAG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGTGCGCCG GCATTCTTTC
401 ATCAGATTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTTCGCG AAAAAGTACC GTACCCACGT TTTTGTGTC TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCGTC
551 GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAC GCTGCCGCAA
601 CTCGCGTATC AAAGTTGGG CGGCACGCGT TTCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGTA .ACGGGATTCG GATACGGCTT GCCGAAACGC
701 TCGCCCGGAT GCGCCCGATA TGCAGGGGCA CTTCCGGAGC GTTGTGCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1  MLGMARHDDQ QGIAAILLPR RQQFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRFHLFR RHQVVFGLAA HLHGCRAQFR QPRRIRLRLC QTARQSGGR
101 TDQAADFQIT V*RRFRQPRI RQQRHTRAP AFLHQIGPDF GFHQAETHRA
151 VFAQKLPYPR FVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLQP
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQ	QRIAAILLPR	RQQFFRLVFT	PINARAAAHG	NLRPASDAFFK	LPRQRFHLFR
a295	MLGMARHDDQ	QRIAAILLPR	RQQFFRLVFT	PINARAAAHG	NLPVSDAFFK	LPRQRFHLFR
	10	20	30	40	50	60
	70	80	90	100	110	120
m295.pep	RYDVVFGLAA	HLHGCRAQFR	QPRRIRLRLC	QTARQSGGR	TDQAADFQIT	VQRRFRQPRI
a295	RHQVVFGLAA	HLHGCRAQFR	QPRRIRLRLC	QTARQSGGR	TDQAADFQIT	VXRRFRQPRI
	70	80	90	100	110	120
	130	140	150	160	170	180
m295.pep	RQQRHTRAP	AFPHQVDFG	GFHQAETHRA	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
a295	RQQRHTRAP	AFHLQIGPD	GFHQAETHRA	VFAQKLPYPR	FFVIRKIAAL	CIRKQNLRGF
	130	140	150	160	170	180
	190	200	210	220	230	240
m295.pep	PSRRGHLRHQ	QRRIGKTP	QLAYQGLG	TRFSDNRGV	PNRAGNGIRI	LAETLVPMRPI
a295	PSRRGHLRHQ	QRRIGKTL	QLAYQRLG	TRFPDRNGV	PNRAGNGIRI	LAETLAPMRPI
	190	200	210	220	230	240
	250	260	270	280	290	
m295.pep	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	XTVQTAFRQR	NQISX
a295	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	RTVRTAFRQR	NQISX
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAATACG CGTGCGCGC
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51  GCTTGCCGTT TCGATTATTC TGGTgtcgGC GGCATACATT GCTtcgacag
101 aggggaccga ggcggtcaga ccgcAGCGCG TggaacaaAA ACTGCCGCCG
151 CTGTCTTGGg gcggaacagg CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGgacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGgcatt tGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCCA
351 CGGCAGTGCG CGCGAAGTGC AGTTTTttaC CGACGAAGAC GGCAGCGCA
401 aTctGGTCGC TTTGAAAAA AAAGCGGCA TATGGCGCGC GTCGGCTTCT
451 GATGCCGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGGCGGCA
701 CAACCCATCA GCGTTCCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGCG
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCgag CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCCG AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCA
1051 CAAGGCAATG TGC CGCGCGCG CGAGGTCATC GGTTTTGTG GTTCGACAGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGC GCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

```

g297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PQRVEQKLPP
51  LSWGGNGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGHAD
101 LRHLRADQSV HVLVGGDGSa REVQFTDED GERNLVALEK KGGIWRSSAS
151 DADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLLYD SLYFHGQOVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNYDEDEGRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGTpVRA SADGVITFKG RKGgyNAVM IRHANGVETL YAHLSAFSQA
351 QGNVRGGEVI GFVSGTGRST GPHLHYEARi NGQPVNPFVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

```

m297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
51  GCTTGCCGTT TCGATTATTT TGGTGTCCGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA CGCGTCAGA CCGCAGCGCG TGGAAACAAA TCTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGCACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCACGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TGC GTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCCA
351 CGCGCGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCAGCGCA
401 ATCTGGTCGC TTTGAAAAG AAAGCGGCA TATGGCGCGC GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGTTCCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGCG
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 CCCGCACCCG AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCG
1051 GAAGGCAATG TGC CGCGCGCG CGAGGTCATC GGTTTTGTG GTTCGACCGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGC GCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

```

m297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERVr PQRVEQNLPp
51  LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGHAD
101 LRHLRADQSV HVLVGGDGSa REVQFTDED GERNLVALEK KGGIWRSSAS
151 EADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK

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201 EGDVRLMYD SLYFHGQOVA AGDILAAEVV KGGTRHQAIFY YRSDKEGGGG  
 251 GNYDEDEGKV LQEKGGFNIE PLVYTRISSP FGVRMHPILH TWRLHTGIDY  
 301 AAPQGTTPVRA SADGVITFKG RKGGYGNVAM IRHANGVETL YAHLSAFSQA  
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPFVSV ALPTPELTQA  
 401 DKAAFAAQKQ KADALLARLR GIPVTVSQSD \*

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERVRPQVEQNLPPLSWGSGVQT					
g297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTEGTERVRPQVEQKLPLSWGNGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGGA					
g297	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTDDEGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEVPV					
g297	REVQFFTDDEGERNLVALEKKGGIWRRSASDADMKVLPTLRSVVVKTSARGSLARAEVPV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIFAGRFLDGLKEGDAVRLMYDSLYFHGQOVAAGDILAAEVVKGGTRHQAIFY					
g297	EIRESLSGIFAGRFLDGLKEGDAVRLLYDSLYFHGQOVAAGDILAAEVVKGGTTHQAIFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGGNYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGGNYDEDEGRVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTTPVRASADGVITFKGRKGGYGNVAMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTTPVRASADGVITFKGRKGGYGNVAMIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVGSTGRSTGPHLHYEARINGQPVNPFVSVALPTPELTQADKAAFAAQKQKADALLARLR					
g297	GFVGSTGRSTGPHLHYEARINGQPVNPFVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1	ATGGCTGTCT	TCCCACTTTC	GGCAAAACAT	CGGAAATACG	CGCTGCGCGC
51	GCTTGCCGTT	TCGATTATTT	TGGTGTCCGC	GGCATAACAT	GCTTCGACAG
101	AGAGGACGGA	GCGCGTCAGA	CCGCAGCGCG	TGGAACAAAA	ACTGCCGCCG
151	CTGTCTTGGG	GCGGCAGCGG	TGTTTCAGACG	GATATTGGG	TGCAGGAGGC
201	GGTGCAGCCA	GGCGACTCGC	TGGCGGACGT	GCTGGCGCGT	TCGGGTATGG
251	CGCGGGACGA	AATTGCCCGA	ATAACGGAAA	AATATGGCGG	CGAAGCCGAT
301	TTGCGGCATT	TGCGTGCCGA	CCAGTCGGTT	CATGTTTTGG	TCGGCGGCGA
351	CGCGCGGCGG	CGCGAAGTGC	AGTTTTTTAC	CGACGAAGAC	GGCGAGCGCA
401	ATCTGGTCCG	TTTGAAAAAA	AAAGCGGCA	TATGGCGGCG	GTCGGCTTCT
451	GAGGCGGATA	TGAAGGTTTT	GCCGACGCTG	CGTTCGGTCG	TGGTCAAAAC
501	GTCGGCGCGC	GGTTCGCTGG	CGCGGCGGGA	AGTGCCCGTC	GAAATTCGCG

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551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGCGGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCGG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACTTGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TGC GCGGCGG CGAGGTCATC GGT TTTGTCG GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GCGCGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCCGAATT GACGAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

```

a297.pep
1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV PQRVEQKLPP
51 LSWGGSGVQT AYWQEAQVQ GDSDLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGGG REVQFFTTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPFL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQQA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
251 GNYDDEGRV LQEKGGFNIE PLVYTRISSP FG YRMHPILH TWRLHTGIDY
301 AAPQGTTPVRA SADGVITFKG RKG YGNVAVM IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPVNPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/a297 99.3% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKH RKYALRALAVSIILVSAAYI ASTERTERV PQRVEQKLPP LSWGGSGVQT					
a297	MAVFPLSAKH RKYALRALAVSIILVSAAYI ASTERTERV PQRVEQKLPP LSWGGSGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWQEAQVQ GDSDLADVLAR SGMARDEIAR ITEKYGGEAD LRHLRADQSV HVLVGGDGGG					
a297	AYWQEAQVQ GDSDLADVLAR SGMARDEIAR ITEKYGGEAD LRHLRADQSV HVLVGGDGGG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTTDED GERNLVALEK KGGIWRRSASE ADMKVLPFL RSVVVKTSAR GSLARAEVPV					
a297	REVQFFTTDED GERNLVALEK KGGIWRRSASE ADMKVLPFL RSVVVKTSAR GSLARAEVPV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIF AGRFSLDGLKEG DAVRLMYDSLYFHGQQA AGDILAAEVV KGGTRHQAFY					
a297	EIRESLSGIF AGRFSLDGLKEG DAVRLIYDSLYFHGQQA AGDILAAEVV KGGTRHQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGG GNYDDEG KVLQEKGGFNIE PLVYTRISSP FG YRMHPILH TWRLHTGIDY					
a297	YRSDKEGGGG GNYDDEG RVLQEKGGFNIE PLVYTRISSP FG YRMHPILH TWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTTPVRA SADGVITFKG RKG YGNVAVMIRHANGVETLYAHLSAFSQA EGNVRGGEVI					
a297	AAPQGTTPVRA SADGVITFKG RKG YGNVAVMIRHANGVETLYAHLSAFSQA EGNVRGGEVI					
	310	320	330	340	350	360

689

	370	380	390	400	410	420
m297.pep	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTGCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTCAG ACGGCATCAA
201 AACCTTCCTG TCCGGCGAAA cgcgcgcac ggCTCAAGAC GCGGTTTCGG
251 CAGATATGCC GCCTGAAGCC GCCGCATCCG AAGCCGCCCC GCCGGCCGGC
301 GGAACAGAAT GGAACAAGG CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTGCGCGGAG ATTCGCTGAT GCAGGCGGTT GCGCCTTCG
401 TGCAAAAAAG CCTGAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCTTGAAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCC GAACGACCCG TGGGATTTC CCGTCGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACC CGT CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAATGCTTT CGGAACACT GAAAGGCAAA ATCATCCTGA TTCCACCGC
801 GCAAACTAGT AGCGGCGGGA AAGGccGCTA CACCGATTCC GTCACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAATAATA ATGGAATAA TCGTTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298.pep

```

1  MKNFLSLFAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKTFL SGETPPTAQD GGSADMPEEA AASEAAPPAG
101 GTEWKQGTGA AAVRSGDKVF FAGDSLMQGV APFVQKSLKQ QYGIESANLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNBP WDFPVGKRYL
201 KFASDEWAQE YLKRVDRILE AAHTRVQVW WLGIPLYMKKV KLDGQMRYLD
251 KLLSEHLKSK IILIPTAQLT SGGKGRYTDV VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTCTCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCGGAC GGCTCAAGAC GCGGTTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCCGTCCC TCAAACCGGT
301 GAAACAGAAT GGAACAAGA CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTTGTCGGCG ACTCGCTGAT GCAGGCGGTT GCCCCTTCG
401 TGCAAAAAAG CCTGAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGCAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACC CGT CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAATGCTTT CGGAACATTT GAAAGGCAAA ATCATCCTGA TTCCACCAC
801 GCACACCTGT AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAATAATA ATGGAATAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

```
m298.pep
1  MKNFLSLFSS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKAPL SGETPPTAQD GGSADMPSEA AASEAVPQTG
101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL
201 KFASDEWAQE YLKRVDRIE AAHTRVQVW WLGIPIYMKKA KLDGQMRYLD
251 KLLSEHLKGI IILIPTHTL SGGKDRYTDV VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*
```

m298/g298 94.8% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
g298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAPLSGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
g298	ALSDGIKAPLSGETPPTAQDGGSDMPSEAAASEAAPPAGGTEWKQDTEAAAVRSGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	FAGDSLMOGVAPFVQKSLKQQYGIESANLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWDFPVGKLYLKFASDEWAQEYLKRVDRIEAAHTRVQVWVWLGIPYMKKA					
g298	LAVFLGPNDPWDFPVGKRYLKFASDEWAQEYLKRVDRIEAAHTRVQVWVWLGIPYMKKV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLDKLLSEHLKGI IILIPTHTL SGGKDRYTDV VNVNGKPVRY RSKDGIHFTA					
g298	KLDGQMRYLDKLLSEHLKGI IILIPTAQL SGGKGRYTDV VNVNGKPVRY RSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	EGQKLLAEKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

```
a298.seq
1  ATGAAAACT TTCCTTCCCT TTTCGCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCTTG TCCGCGGAAA CGCCGCCGAC GGCTCAAGAC GCGGTTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACGCCCC TCAAACTGGC
301 GAAACAGAAT GGAAACAAAA CACCGAAGCC GCCGCCGTCC GAACAGGGGA
351 CAAAGTCTTT TTCGCCGGCG ACTCGCTGAT GCAGGGCGTT GCACCCTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGAAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT
551 TCCTCGGTCC GAACGACCCG TGGGATTTC CCGTTGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
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751  AAACTGCTTT CGGAATATTT GAAAGGCAAA ATCATCCTGA TTCCCACCGC
801  GCACACCCTG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851  ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901  GAAGGACAAA AACTGCTGGC GGCAAAAATA ATGGAAAAAA TCGTTTTTGA
951  ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
1   MKNFLSLFAS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AAPETAPQTG
101 ETEWKQNTA AAVRTGDKVF FAGDSLQGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDR WDFPVGKRYL
201 KFASDEWAE YLKRVDRIE AAHTHYVQVW WLGI PYMKKA KLDGQMRYL
251 KLLSEYLGK IILIPHTAL SGKDRYTDV VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRS	GAALQENAY				
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRS	GAALQENAY				
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAFISGETPPTAQDGGSDMPSEAAAPETAPQTGETEWKQNTA AAVRTGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLQGVAPFVQKSLKQYQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDSLQGVAPFVQKSLKQYQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDEWDFPVGKLYLKFADEWAEYLYKRVDRILEAAHTRVQVWVWLGIPYMKKA					
a298	LAVFLGPNDEWDFPVGKRYLKFADEWAEYLYKRVDRILEAAHTHYVQVWVWLGIPYMKKA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLKLLSEHLKGIILIPHTALSGGKDRYTDVNVNGKPVRYRSKDGIFHTA					
a298	KLDGQMRYLKLLSEYLGKIIILIPHTALSGGKDRYTDVNVNGKPVRYRSKDGIFHTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
a298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
1   ATGAACCCCA AACACTTCAT CGCATTTTCC GCCCTGTTCC CCGCCACGCA
51  GGCAGAAGCC CTGCCGCTCG CCTCCGTCAG CCCCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCGCGC CCTCGCCTTG GATGAAAAAA CTCCGATCCG TCGCACAAGG
201 CAGCGGCGAG GCCTTCCGCA TCCTGCAAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACGCC CTGCGCAAAC GCCTGCAAAA AACATGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCGGCGGTC CGTCACAGCG GCAACTGGCA AAGCTTCACC AGCAGGAACA
401 ATACCGGAGA TTTCCCGCTC GGCGGCATCC TCGCCCAAC CCGCAGCGGC
451 GGCGGCATGA CCCTGACCGC GTCTGACGGC AAAACCGGCA AACAGCGCGT

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501 TTCCCTGTTT GCCAAACCGC TGCTCGCCGA ACAAACCTTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGGCCAT ACAGACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTGACC CAGTGGTGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCC TTCAACAACA ACATCGACAT TGCCGATACC GAACAAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCCGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACGCGCCCC GTCCCTCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCC
1001 CCCGTCAGGG GCAGACGATG TTTTGGTCTT GGCAAAACGC AATGGGCGGC
1051 ATATGCAGCA TGAAAAACTG GCTCAACCAA GGATGGGCGC CCAAAGACGG
1101 CGTACACTTC TCCGCCAAG GCTACCGCGC CGCGGCGGAA ATGCTTGCCG
1151 ACAGCCTCGA AGAACTCGTC CGCGCGCGC CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1248; ORF 299.ng>:

```

g299.pep
1  MNPKHFIASF ALFAATQAEA LPVASVSPDT VTVSPSAPYT DTNGLLTDYG
51  NAAASPWMKK LRSVAQSGE AFRILQIGDS HTAGDFFTDA LRKRLQKTWG
101 DGGIGWVYPA NVKGQRMAAV RHSGNWQSF SRNNTGDFPL GGILAQTGSG
151 GGMTLTASDG KTGKQVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201 AALPLAIQTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGRTP VLLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKNLNLQ GWAADKGVHF SAQGYRRAE MLADSLEELV RAAAIRQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1249>:

```

m299.seq
1  ATGAACCCCA AACACCTCAT CGCATTITCC GCCCTATTCG CCGCCACGCA
51  GGCAGAAGCC CTACCTGTGC CCTCCGTGAG CCTCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAAA CTCCAATCCG TCGCACAAGG
201 CAGCGCGCAG ACCTTCCGTA TCCTGCAAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTGCAAAA AACTTGGGGC
301 GACGCGCGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GCGCGCGCTC CGGCACAACG GTAACCTGGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCTCGTC GCGCGCATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCTTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTGA AATGGCGTGC CGACCGTATG
751 AACGACCTCG CCCAAACCGG CGCCGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCT TTCAACAACA ACATCGACAT TGCCGACACC GAACAAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCTGC CGCCGGCATC
901 CTCATCATCG GCGCACCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCC
1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC CATGGGCGGC
1051 ATATGCAGCA TGAAAAACTG GCTCAACCAA GGATGGGCGC CCAAAGACGG
1101 CGTACACTTC TCCGCCAAG GCTACCGCGC CGCGGCGGAA ATGCTCGCCG
1151 ACAGCCTCGA AGAACTCGTC CGCTCCGCTG CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1250; ORF 299>:

```

m299.pep
1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
51  NASASPWMKK LQSVQSGE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101 DGGIGWVYPA NVKGQRMAAV RHNGNWQSLT SRNNTGDFPL GGILAHGTSG
151 GSMTLTASDG IASKQVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201 AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGRTP VRLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKNLNLQ GWAADKGVHF SAKGYRRAE MLADSLEELV RSAAIRQ*

```

m299/g299 95.5% identity in 397 aa overlap

```

10      20      30      40      50      60
m299.pep  MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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g299	MNPKHFIASFALFAATQAEALPVASVSPDTVTVSPSAPYTTDNGLLTDYGNAAASPWMKK
	10 20 30 40 50 60
m299. pep	LQSV AQSGSETFRILQIGDSHTAGDFFTD SLRKLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
g299	LRSAVQSGSEAFRILQIGDSHTAGDFFTDALRKLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
m299. pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
g299	RHSGNWQSFSTRNNTGDFPLGGILAHTGSGGSMTLTASDGTGKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299. pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
g299	TVNGNTVSANGGGWQVLDTGAAALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299. pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299. pep	LIIGAPESLKNTLGVCGRPVRLTEVQQMQRVARQGQTMFWSWQAMGGICSMKNWLNQ
	310 320 330 340 350 360
g299	LIIGAPESLKNTLGVCGRPVLLTEVQQMQRVARQGQTMFWSWQAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299. pep	GWAAKDGVHFSAGYRRAEMLADSLLEELVRSAAIRQX
	370 380 390
g299	GWAAKDGVHFSAGYRRAEMLADSLLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

a299. seq

1	ATGAACCCCA	AACACCTCAT	CGCATTTTCC	GCCCTATTCC	CGCCACGCA
51	GGCAGAAGCC	CTACCTGTCG	CCTCAGTCAG	CCTCGACACC	GTTACCGTTT
101	CCCCGTCCGC	CCCCTACACC	GATACAAACG	GGCTGCTGAC	CGACTACGGC
151	AACGCCTCCG	CCTCGCCTTG	GATGAAAAAA	CTCCAATCCG	TCGCACAAGG
201	CAGCGGCGAG	ACCTTCCGTA	TCCTGCAAAT	CGGCGACTCG	CATACCGCCG
251	GCGACTTCTT	TACCGACAGC	CTGCGCAAAC	GCCTACAAAA	AACTTGGGGC
301	GACGGCGGCA	TAGGCTGGGT	TTACCCCGCC	AACGTCAAAG	GGCAGCGCAT
351	GGCGGCCGTC	CGGCACAACG	GTAACCTGGCA	AAGCCTCACC	AGCAGGAACA
401	ACACCGGAGA	CTTCCCCTGC	GGCGGCATCC	TCGCCACAC	CGGCAGCGGC
451	GGCAGCATGA	CCCTGACCGC	ATCGGACGGC	ATAGCAAGCA	AGCAGCGCGT
501	TTCCCTGTTT	GCCAAACCCC	TGCTTGCCGA	ACAAACCCTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	GCGGCACTGC	CCCTGACCAT	ACACACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATC	GAAATCCCG	CCGGCGGCAT	TACCGTTTCC	GCGATGGGCA
701	TCAACGGCGC	ACAATTAACC	CAGTGGTCGA	AATGGCGTGC	CGACCGTATG
751	AACGACCTTG	CCCAAACCGG	CGCCGATCTA	GTCATCCTTG	CCTACGGTAC
801	CAACGAAGCC	TTCCGGCGACA	ACATCGACAT	TGCCGATACC	GAACAGAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCGCGACA	GCCTACCTGC	CGCCGGCATC
901	CTCATCATCG	GCGCGCCCGA	ATCCCTGAAA	AACACGCTCG	GCGTATGCGG
951	CACACGCCCC	GTCCGCCTGA	CCGAAGTCCA	ACAGATGCAG	CGGCGCATCG
1001	CCCGTCAGGG	GCAGACGATG	TTCTGGTCTT	GGCAAACGC	GATGGGCGGC
1051	GTTTGCGACA	TGAAAACTG	GCTCAACCAC	GGATGGGCGG	CCAAAGACGG
1101	CGTACACTTT	TCCGCCAAAG	GCTACCAACG	GTCGGCGGAA	ATGCTCGCCG
1151	ACAGCCTCGA	AGAACTCGTC	CGCTCCGCTG	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
  1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
 51  NASASPWMKK LQSV AQSGE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101  DGGIGWVYPA NVKGQMAAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151  GSMTLTASDG IASKQVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201  AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251  NDLAQTGADL VILAYGTNEA FGDNIADIAT EQKWLDTVRQ IRDSLPAAGI
301  LIIGAPESLK NTLGVCGRP VRLTEVQQMQ RRIARQQQM FWSWQNAMGG
351  VCSMKNWLNH GWAADGVHF SAKGYQSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

	10	20	30	40	50	60
m299.pep	MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
a299	MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
	10	20	30	40	50	60
m299.pep	LQSV AQSGETFRILQIGDSHTAGDFFTDSLRLKRLQKTWGDGGIGWVYPANVKQORMAAV					
a299	LQSV AQSGETFRILQIGDSHTAGDFFTDSLRLKRLQKTWGDGGIGWVYPANVKQORMAAV					
	70	80	90	100	110	120
m299.pep	LQSV AQSGETFRILQIGDSHTAGDFFTDSLRLKRLQKTWGDGGIGWVYPANVKQORMAAV					
a299	LQSV AQSGETFRILQIGDSHTAGDFFTDSLRLKRLQKTWGDGGIGWVYPANVKQORMAAV					
	70	80	90	100	110	120
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMILTASDGIASKQVSLFAKPLLAETL					
a299	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMILTASDGIASKQVSLFAKPLLAETL					
	130	140	150	160	170	180
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMILTASDGIASKQVSLFAKPLLAETL					
a299	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMILTASDGIASKQVSLFAKPLLAETL					
	130	140	150	160	170	180
m299.pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
a299	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
	190	200	210	220	230	240
m299.pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
a299	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
	190	200	210	220	230	240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI					
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIADIADTEQKWLDTVRQIRDSLPAAGI					
	250	260	270	280	290	300
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI					
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIADIADTEQKWLDTVRQIRDSLPAAGI					
	250	260	270	280	290	300
m299.pep	LIIGAPESLKNTLGVCGRPVRRLTEVQQMQRRVARQQQTMFWSWQNAMGGICSMKNWLNQ					
a299	LIIGAPESLKNTLGVCGRPVRRLTEVQQMQRRRIARQQQTMFWSWQNAMGGVCSMKNWLNH					
	310	320	330	340	350	360
m299.pep	LIIGAPESLKNTLGVCGRPVRRLTEVQQMQRRVARQQQTMFWSWQNAMGGICSMKNWLNQ					
a299	LIIGAPESLKNTLGVCGRPVRRLTEVQQMQRRRIARQQQTMFWSWQNAMGGVCSMKNWLNH					
	310	320	330	340	350	360
m299.pep	GWAADGVHFSAGYRRAEMLADSLEELVRSAAIRQX					
a299	GWAADGVHFSAGYQSAEMLADSLEELVRSAAIRQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
  1  ATGCACTCAA TATATTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
 51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101  TGCCGCACCC GGTTACGCTT TTTATATTT TCATTGTGTT ATGCTGATT
151  GCCTCTGCCG TCGGTGCGTA TTTCGACTA TCCGTCCCGC ATCCGCGTCC
201  TGTGTTGGGCG AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTCAGCC
251  TGCTCGATGC CGACGGTTTG ATCAAATCC TGACGCATAC CGTTAAAAAT
301  TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGGCGT
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351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCGTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACGCG TTTTATATGG
701 CAGCCAGTAC GTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCTTATCAA TCAGATTGT CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGGCT CATCTGAAA CAGGATTGGT
951 TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTATT TTCTGTTGT
1001 TTGCGCTGCC GGGCATTGTT TATGGCCGGA TAACCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TGCCCGCACA GTTTGTGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGTTTAA TTTTAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCTGCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTCG GGCTGATTAT GGCAGCGGTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTCTTCTT TAATTGCATG GATCGCCTTA TTCTGCATTT GGGTATTTGT
1551 TTTGGGTCGT CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1 MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTKSPRK LTTFMVVF TG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQI IHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIYPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYLIV IIFFAAQFVA FFWNTNIGQY IAVKGAVFLK
401 EVGLGGSVLF IGFIILICAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPQ
451 VIQAAYRIGD SVTNIITPMN SYFGLIMATV IKYKGDAGVG TLISMMLPYS
501 AFFLIWIAL FCIWVFLGL PVGPGTPTFY PVP*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1 ATGCACTCAA TATATTTT TT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51 GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTACGCTT TTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCG ATCCGCGCCC
201 TGTGTTGTCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACCGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCTG
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGATTGG TTATTTTGT ACTGAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GGCATTCCAA
801 TGAATACAGC CCTTTGGAAT ATAAAGGATT AATTTGGGCT GGCGTGGTGT
851 TTGTTGCCCT ATCCGCCCTA TTGGCTTGA GCATCGTCCC TGCCGACGGT
901 ATTTTGGCTC ATCCTGAAAC AGGATTGGTT TCCGGTTCGC CGTTTAAAT
951 ATCGATTGTT GTTTTATTT TCTGTTGTT TGCAGTGCY GGCmTGTGTT
1001 ATGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

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1051 ATGGCCGAAT CGATGAGTAC TCTGGsGCTT TmTTGswCA kcATCTTTTT
1101 TGCCGCACAG TTTGTGCGAT TTTTAAATTG GACGAATATT GGGCAATATA
1151 TTGCCGTTAA AGGGGCGACG TTCTTAAAAG AAGTCGGCTT GGGCGGCAGC
1201 GTGTTGTTTA TCGGTTTTAT TTTAATTTGT GCTTTTATCA ATCTGATGAT
1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAAC TGGCCCGATT TTCGTCCCTA
1301 TGCTGATGTT GGCCGGCTAC GCGCCCGAAG TCATTCAAGC CGCTTACCGC
1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTTCCG
1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GCGGTGGGTA
1451 CGCTGATTTC TATGATGTTG CCGTATCCG CTTTCTTCTT GATTCGCTGG
1501 ATTGCCTTAT TCTGCATTTG GGTATTTGTT TTGGGCCTGC CCGTCGGTCC
1551 CGGCGCGCCC ACATTCTATC CCGCACCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

```

m302.pep
1  MHSIYFFKEK QMSQTDQRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDPRPVGA KGRADDGLIY IVSLLNADGF IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTSPRK LTTFMVVFTG
151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 STIDPLLACI THQAAVVGPE ANWFFMVAST FVIALIGYFV TEKIVEPQLG
251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVFVLSAL LAWSIVPADG
301 ILRHPETGLV SGSPFLKSIV VFIFLLFALK GXVYGRVTRS LRGEQEVVNA
351 MAESMSTLXL XLXXIFFAAQ FVAFFNWTNI GQYIAVKGAT FLKEVGLGGS
401 VLFIFILIC AFINLMIGSA SAQWAVTAPI FVPMMLLAGY APEVIQAYR
451 IGDSVTNIIT PMMSYFGLIM ATVIKYKDA GVGTLSMML PYSAFFLIAW
501 IALFCIWVVF LGLPVGPGAP TFYPAP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng)

from *N. gonorrhoeae*:

m302/g302

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          10      20      30      40      50      60
m302.pep  MHSIYFFKEKQMSQTDQRDGRFLRTVEWLGNMPLPHPVTLFIIFIVLLLIASAVGAYFGL
          |||||:::|||||
g302      MHSIYFFKEKQMSQTDARRSGRFLRTVEWLGNMPLPHPVTLFIIFIVLLLIASAVGAYFGL
          10      20      30      40      50      60

          70      80      90      100     110     120
m302.pep  SVPDPRPVGA KGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLLGVGIA
          |||||:::|||||
g302      SVPDPRPVGA KGRADDGLIHVVSLLDADGLIKILTHTVKNFTGFAPLGTVLVSLLGVGIA
          70      80      90      100     110     120

          130     140     150     160     170     180
m302.pep  EKSGLISALMRLLLTKSPRKLTTFMVVFTGILSNTASELG YVVLIPLSAII FHSLGRHPL
          |||||:::|||||
g302      EKSGLISALMRLLLTKSPRKLTTFMVVFTGILSNTASELG YVVLIPLSAII FHSLGRHPL
          130     140     150     160     170     180

          190     200     210     220     230
m302.pep  AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI
          |||||:::|||||
g302      AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQAAQIIHPDYVVGPEANWFFMAASTFVI
          190     200     210     220     230     240

          240     250     260     270     280     290
m302.pep  ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVLSALLAW
          |||||:::|||||
g302      ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVLSALLAW
          250     260     270     280     290     300

          300     310     320     330     340     350

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m302.pep  SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      SIVPADGILRHPETGLVAGSPFLKSIVVFIFLLFALPGIVYGRITRSLRGEREVVNAMAE
          310      320      330      340      350      360

          360      370      380      390      400      410
m302.pep  SMSTLXLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFILICAFI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGAVFLKEVGLGGSVLFIGFILICAFI
          370      380      390      400      410      420

          420      430      440      450      460      470
m302.pep  NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      NLMIGSASAQWAVTAPIFVPMMLLAGYAPQVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          430      440      450      460      470      480

          480      490      500      510      520
m302.pep  IKYKKGAGVGTGLISMMLPYSAFFLIAWIALFCIWWFVLGLPVGPGAPTFFYPAPX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      IKYKKGAGVGTGLISMMLPYSAFFLIAWIALFCIWWFVLGLPVGPGPTPTFFYPVPX
          490      500      510      520      530

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATGTGTGT ATGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCGGAATA TCCGTCCCGC ATCCGCGCCC
201 TGTGGTGGCG AAAGGACGTG CCGATGACGG TTTGATTCAC GTTGTACAGC
251 TGCTCGATGC TGACGGTTTG ATCAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCGGTT GGAACGGGTG TTGTTTCTT TATGGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAATG CGCTTATTGC
401 TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTCGGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAAGTGG TTTTATATGG
701 TAGCCAGTAC GTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTTGT CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC TGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCTGAAA CAGGATTGGT
951 TTCCGGTTTC CCGTTTTTAA AATCAATTGT TGTTTTTATT TTCTTGTGT
1001 TTGCACTGCC GGGCATTGTT TATGGCCGGG TAACCGAAG TTTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTATAATT
1151 TGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTGTTT ATCGGTTTTA TTTAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCTGTCCT ATGCTGATGT TGGCCGGCTA CGCGCCCGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATTT GGGTATTGTT
1551 TTTGGGCTG CCCGTCGGTC CCGGCGCGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1  MHSIYFFKEK QMSQTDQTD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDRPVGVA KGRADDGLIH VVSLLDADGL IKIILHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLISALM RLLLTSPRK LTTFMVVFTG

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151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHNSEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIIVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMAE SMSTLGLYLV IFFAAQFVA FFNWTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIIITPM SYFGLIMATV IKYKDGAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

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## m302/a302 96.1% identity in 533 aa overlap

```

-- 100%
m302.pep      10      20      30      40      50      60
MHSIYFFKEKQMSQTDTRDGRFLRTVEWLGNMPLPHPVTLFIIFIVLLLIASAVGAYFGL
|||||
a302          10      20      30      40      50      60
MHSIYFFKEKQMSQTDTRDGRFLRTVEWLGNMPLPHPVTLFIIFIVLLLIASAAGAYFGL

m302.pep      70      80      90     100     110     120
SVPDPRPVGAKGRADDGLIYIVSLLNADGFIKILHTVKNFTGFAPLGTVLVSLGVGIA
|||||
a302          70      80      90     100     110     120
SVPDPRPVGAKGRADDGLIHVVSLLDADGLIKILHTVKNFTGFAPLGTVLVSLGVGIA

m302.pep     130     140     150     160     170     180
EKSGLISALMRLLLTKSPRKLTFMVVFTGILSNTASELG YVVLIPLSAI IFHSLGRHPL
|||||
a302         130     140     150     160     170     180
EKSGLISALMRLLLTKSPRKLTFMVVFTGILSNTASELG YVVLIPLSAI IFHSLGRHPL

m302.pep     190     200     210           220     230
AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI
|||||
a302         190     200     210     220     230     240
AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQQAQIIHPDYVVGPEANWFFMVASTFVI

m302.pep     240     250     260     270     280     290
ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVV FVALSALLAW
|||||
a302         240     250     260     270     280     290     300
ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVV FVALSALLAW

m302.pep     300     310     320     330     340     350
SIVPADGILRHPETGLVSGSPFLKSIIVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
|||||
a302         300     310     320     330     340     350     360
SIVPADGILRHPETGLVSGSPFLKSIIVFIFLLFALPGIVYGRVTRSLRGEQEVVNAMAE

m302.pep     360     370     380     390     400     410
SMSTLXLXLXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLF IGFILICAFI
|||||
a302         360     370     380     390     400     410     420
SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLF IGFILICAFI

m302.pep     420     430     440     450     460     470
NLMIGSASAQWAVTAPIFVPMMLAGYAPEVIQAAYRIGDSVTNIIITPMMSYFGLIMATV
|||||
a302         420     430     440     450     460     470     480
NLMIGSASAQWAVTAPIFVPMMLAGYAPEVIQAAYRIGDSVTNIIITPMMSYFGLIMATV

m302.pep     480     490     500     510     520
IKYKDGAGVGTLSMMLPYS AFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX
|||||
a302         480     490     500     510     520     530
IKYKDGAGVGTLSMMLPYS AFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

g305.seq  
 1 ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG  
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCCG  
 101 GCAATCTGAT TGGTTTTTAC AGCAATCACA AGGTTTTTGA AATTGCCATC  
 151 CAGCTCGGTG CCGTTTTTGGC GGTAGTGTTT GAATACCGGC AGCGTTTCAG  
 201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC  
 251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTGTTC  
 301 GACAAACAAA TCAAAGAGTA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT  
 351 GCTGGTTTTG GCGGTTTTT TATTTTTGTG GGTGGAGAAA CGCCAAAGCC  
 401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC  
 451 TTGATGATCG GTGTTGCCCA AGTGTGTTGCA CTGGTTCCGG GTACGTCCCG  
 501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA  
 551 CGGCAACGGA GTTTTCATTT TTCTTGCCCG TTCCGATGAT GGTTCGAGCA  
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT  
 651 CGGTTTGATT TTGATAGGCT TTATTGCCGC TTTTGTTCCT GGTTCGGTAG  
 701 CGGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCCGTTT  
 751 GCCTATTACC GCATTGTTT CCGCATTGTC ATCATAATAT TGTGTTGTC  
 801 GGGCTGGATA AGTTGGGAAT GA

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep  
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLI GFH SNHKVFEIAI  
 51 QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLAI AF IPAAVMGLLF  
 101 DKQIKEYL FN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA  
 151 LMIGVAQVFA LVPGTSRSGS TVMGMLWGI ERKTATEFSF FLAVPMVAA  
 201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF  
 251 AYYRIVFGIV IILWLSGWI SWE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)  
 1 ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG  
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCCG  
 101 GCAATCTGAT TGGTTTTTAC AGCAATCACA AGGTTTTTGA AATTGCCATC  
 151 CAGCTCGGTG CAGTTTTTGGC GGTAGTGTTT GAATACCGGC AACGTTTCAG  
 201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC  
 251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTGTTC  
 301 GGCWACAAA TCAAAGAGyA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT  
 351 GCTGGTtYTG GrcGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC  
 401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC  
 451 TTGATGATCG GCGTTGCCCA AGTGTGTTGCA CTGGTTCCGG GTACGTCCCG  
 501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA  
 551 CTGCGACAGA ATTCTCGTTT TTCTTGCTG TGCCGATGAT GGTGCGCGCA  
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT  
 651 CGGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTTC CA GGCTTGGTAG  
 701 CGGTAAAGC GTTGCTGAGG TTTGTTTCGG GTAC...

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)  
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLI GFH SNHKVFEIAI  
 51 QLGAVLAVVF EYRQRFSNVL HGLGKDRKAN RFVLNLAI AF IPAAVMGLLF  
 101 GXQIKEXL FN PLSVAVMLVL XGFXILWVEK RQSRAPKIA DVDALRPIDA  
 151 LMIGVAQVFA LVPGTSRSGS TIMGMLWGI ERKTATEFSF FLAVPMVAA  
 201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLI GFH SNHKVFEIAIQLGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLI GFH SNHKVFEIAIQLGAVLAVVF					
	10	20	30	40	50	60



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	70	80	90	100	110	120
g305.pep	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL					
	:					
m305	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTVMGMLWGI					
	:					
m305	XGFXILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLK					
	:					
m305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKNYIPFAYYRIVFGIVIIILWLSGWISWEX					
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1  ATGGATTTC  TGATTGTCCT  GAAAGCCCTG  ATGATGGGCT  TGGTAGAAGG
51  TTTTACCGAA  TTTTACCGA  TTCCAGCAC  CGGACATTG  ATTGTGTCG
101 GCAATCTGAT  TGATTTTAC  AGCAATCACA  AGGTTTTGA  AATTACCATC
151 CAGCTCGGTG  CGGTTTGGC  GGTAAGTGT  GAATACCGGC  AGCGTTTCAG
201 CAATGTGTTG  CATGGCGTGG  GAAAAGACCG  GAAAGCCAAC  CGTTTCGTCC
251 TTAATCTTGC  CATGCTTTT  ATACCTGCCG  CCGTGATGGG  GCTGTGTTC
301 GGCAACAAA  TCAAAGAGTA  TCTGTTAAC  CCCTTGAGTG  TTGCAGTCAT
351 GCTGTTTTG  GCGGTTTTT  TTATTTGTG  GGTGGAGAAA  CGCCAAAGCC
401 GAGCAGAGCC  TAAATGTGC  GATGTTGATG  CATTGCGTCC  GATTGATGCG
451 TTGATGATCG  GCGTTGCCA  AGTGTTCGA  CTGGTCCAG  GTACGTCCCG
501 TTCGGCAGT  ACGATTATGG  GCGGGATGCT  TTGGGGAATC  GAGCGGAAAA
551 CGGCAACGGA  GTTTTCATT  TTCTTGCCG  TTCCGATGAT  GGTTCAGCA
601 ACGGCTTATG  ATGTCCTGAA  GCATTACCG  TTTTTCACCC  TGCATGATGT
651 CGGTTTGATT  TTGATTGGCT  TTGTGCTGC  CTTTGTTC  GGCTTGCTGG
701 CCGTCAAAGC  GTTGCTGAGG  TTGTTTCCA  AGAAAAATTA  TATTCCTTTT
751 GCCTATTACC  GCATTGTTT  TGGTATTGCC  ATCATTATAT  TGTGGCTGTC
801 AGGCTGGATA  AGTTGGGAAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1  MDFLIVLKAL  MMGLVEGFTE  FLPISSSTGHL  IVFGNLIDFH  SNHKVFEITI
51  QLGAVLAVVF  EYRQRFNSVL  HGVGKDRKAN  REVLNLAI  IPAAVMGLLF
101 GKQIKEYLFN  PLSVAVMLVL  GGFFILWVEK  RQSRAPKIV  DVDALRPIDA
151 LMIGVAQVFA  LVPGTSRSGS  TIMGMLWGI  ERKTATEFSF  FLAVPMMVAA
201 TAYDVLKHYR  FFFLHDVGLI  LIGFVAAFVS  GLVAVKALLR  FVSKKNYIPF
251 AYYRIVFGIA  IILWLSGWI  SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
	:					
a305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSNHKVFEITIQLGAVLAVVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	:					
a305	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFGKQIKEYLFNPLSVAVMLVL					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m305.pep	XGFXILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
a305	GGFFILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAFVSGLVAVKALLR					
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

```

g306.seq
1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCGGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAAGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGGCGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TGCAGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAAGA
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGAGA  AAATGAAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651 CTGCAATGG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTCCGA  AGTGGTCGGC  TATCAGGCGG
751 GACATAAAAC  GCTTTACCGC  GTGCAAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```

g306.pep
1  MFMNKFSQSG  KGLSGFFFGL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREEDP  GQAVRKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEEKK  AAKEKVAPKP  TPEQILNSRS  IEXARSAAAK
201 EVQKMNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```

m306.seq (partial)
1  ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGAGC  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCGmAwAA  CCAGCyTAAG
151 GAAGACATCC  AACCTGAwCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201 TGCTGCGACA  GAGGCGAGAG  AGTCGGATGC  GGAAAawGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCCGACGG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAAw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAGCT
451 TCAAAAGAAG  AGAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTGCCG
551 CCGCCAAAGA  AGTGACAGAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```

702

601 ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG  
 651 CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA  
 701 GGCGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG  
 751 ATGCGGTGA

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

m306.pep (partial)

1 ..GLFFGLILAT VIIAGILFYLNQSGQNAFKI PASSKQPAET EILKPNQXX  
 51 EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP  
 101 EREEPDQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA  
 151 SKEEKKAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR  
 201 IICKWARMPT VRARKGSPVN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP  
 251 MR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

m306/g306

	10	20	30	40
m306.pep	GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKXP			
	:     :     :     :			
g306	MFMNKFSQSGKLSGFFGLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAETEILKLP			
	10	20	30	40
	50	60	70	80
m306.pep	NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
	:     :     :     :			
g306	NQPKEDIQPEPADQNALSEPDAEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
	70	80	90	100
	110	120	130	140
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAKEKVAPKP			
	:     :     :     :			
g306	GQAVRKKALTEEREQTVREKAQKKDAETVKKAVKPSKETEKKASKEEKKAKEKVAPKP			
	130	140	150	160
	170	180	190	200
m306.pep	TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSPVNWQSWA			
	:     :     :     :			
g306	TPEQILNSRSIEKARSAAAKEVQKMNFGQGSQRIICKWARMPTNPGARKGSPVNWQSWA			
	190	200	210	220
	230	240	250	
m306.pep	YLPRWSVIRRDIKRFTGCKAAICLPMRX			
	:     :			
g306	YLPKWSAIRRDIKRFTACKAAICPPMRX			
	250	260		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

a306.seq

1 ATGTTTATGA ACAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTT  
 51 CTTCGGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTATC  
 101 TGAACCAAGAG CGGTCAAAT GCGTTCAAA TCCCGGTTCC GTCGAAGCAG  
 151 CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCCTA AGGAAGACAT  
 201 CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA  
 251 AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT  
 301 GCCGACAAAG CCGACGAGGT TGAGGAAAAG GCGGACGAGC CGGAGCGGGA  
 351 AAAGTCGGAC GGACAGGCAG TCGCAAGAA AGCACTGACG GAAGAGCGTG  
 401 AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA  
 451 AAACAAGCGG TAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAGA  
 501 AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCGGAAC  
 551 AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGTGCCAAA

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```

601 GAAGTGCAGA AAATGAAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
701 ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTGCGTTAT CAGGCGGGAC
751 ATAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
801 A

```

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```

a306.pep
  1 MFMNKFSQSG KGLSGFFFL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
 51 PAETEILPKP NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD GQAVRKALT EEREQTVGEK AQKKDAETVK
151 KQAVKPSKET EKKASKEKK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

m306/a306 93.7% identity in 252 aa overlap

```

                                10      20      30      40
m306.pep                      GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX
                                |:|||||:|||||:|||||:|||||:|||||:|||||:
a306                          MFMNKFSQSGKLSGFFFLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPX
                                10      20      30      40      50      60

                                50      60      70      80      90      100
m306.pep                      NQKKEDIQXPADQNALSEPDAAEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP
                                |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a306                          NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD
                                70      80      90      100     110     120

                                110     120     130     140     150     160
m306.pep                      GQAVRKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
                                |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a306                          GQAVRKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETEKKASKEEKKAEKEKVAPKP
                                130     140     150     160     170     180

                                170     180     190     200     210     220
m306.pep                      TPEQILNSGSIEKARSAAAEVQKMKTPTRRKQRIICKWARMPTVRARKGSVFNWQSWAY
                                |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a306                          TPEQILNSGSIEKARSAAAEVQKMKTPTRRKQRIICKWARMPTAGARKGSVFNWQSWAY
                                190     200     210     220     230     240

                                230     240     250
m306.pep                      LPRWSVIRRDIKRFTGCKAAICLPMRX
                                |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a306                          LPRWSVIRRDIKRFTGCKAAICLPMRX
                                250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

```

g307.seq
  1  atgaaaacct tcttcaaac ctttcgacc gcgtcactcg cgctcatcct
 51  cgcagcctgc ggcggtcaaa aagacagcgc gcccgagcc tctgcgcgcg
101  ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
151  accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201  ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtgc
251  gcccgaatct ggcattggcg gagggcgagt tggacatcaa cgtcttccaa
301  cacaaaccct atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351  cgaagccttc caagtgcgca ccgcgccttt gggactgtat ccgggcaaac
401  tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgccaac
451  gacccgtcca acttcgcacg cgccttggtg atgctgaacg aactgggttg
501  gatcaaaact aaagacggca tcaatccgct gaccgcatcc aaagccgaca
551  tcgcggaaaa cctgaaaaac atcaaaatcg tcgagcttga agccgcacaa
601  ctgccgcgca gccgcgcgca cgtggatttt gccgtcgtca acggcaacta
651  cgccataagc agcggcatga agctgaccga agccctgttc caagagccga

```

704

```

701 gctttgccta tgtcaactgg tctgccgtca aaaccgccga caaagacagc
751 caatggccta aagacgtaac cgaggcctat aactccgacg cggttcaaagc
801 ctacgcgcac aaacgcttcg agggctacaa ataccctgcc gcatggaatg
851 aaggcgacgc caaataa

```

This corresponds to the amino acid sequence <SEQ ID 1272; ORF 307.ng>:

```

g307.pep
  1 MKTFFKTLST ASLALILAAC GGQKDSAPAA SAAAPSDNG AAKKEIVFGT
 51 TVGDFGDMVK EQIQAELEKK GYTVKLVEFT DYVRPNLALA EGELDINVFO
101 HKPYLDDFFK EHNLDITEAF QVPTAPLGLY PGKLSLEEV KDGSTVSAPN
151 DPSNFARALV MLNELGWIKL KGINPLTAS KADIAENLKN IKIVELEAAQ
201 LPRSRADVDF AVVNGNYAIS SGMKLTEALF QEPSFAYVNW SAVKTADKDS
251 QWLKDVTEAY NSDAFKAYAH KRFEGYKYP A WNEGAAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1273>:

```

m307.seq (partial)
  1 ..CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC
 51 CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCTGCC GCATGGAATG
101 AAGCGCAGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1274; ORF 307>:

```

m307.pep (partial)
  1 ..QWLKDVTEAY NSDAFKAYAH KRFEGYKSPA A WNEGAAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 307 shows 97.4% identity over a 38 aa overlap with a predicted ORF (ORF 307.ng)

from *N. gonorrhoeae*:

```

m307/g307

                                10      20      30
m307.pep                                QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
g307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKYP
              230      240      250      260      270      280

                                39
m307.pep      A WNEGAAKX
              |||||
g307      A WNEGAAKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1275>:

```

a307.seq
  1 ATGAAAACCT TCTTCAAAC CCTTCCGCC GCCGCACTCG CGCTCATCCT
 51 CGCCGCTGCG GCGGTCAAA AAGATAGCGC GCCCGCCGCA TCCGCTTCTG
101 CCGCCGCCGA CAACGGCGCG GCGAAAAAAG NAATCGTCTT CGGCACGACC
151 GTCGGCGACT TCGGCGATAT GGTCAAAGAA CAAATCCAAC CCGAGCTGGA
201 GAAAAAAGGC TACACCGTCA AACTGGTCGA GTTACCGAC TATGTGCGCC
251 CGAATCTGGC ATTGGCTGAG GCGAGTNGG ACATCAACGT CTTCCAACAC
301 AAACCCATATC TTGACGACTT CAAAAAGAA CACAATCTGG ACATCACCGA
351 AGTCTTCCAA GTGCCGACCG CGCCTTTGGG ACTGTACCGG GGCAAGCTGA
401 AATCGCTGGA AGAAGTCAA GACGGCAGCA CCGTATCCGC GCCCAACGAC
451 CCGTCCAAC TCGCCGCGGT CTTGGTGATG CTCGACGAAC TGGGTTGGAT
501 CAAACTCAA GANGGCATCA ATCCGCTGAC CGCATCCAAA GCGGACATTG
551 CCGAAAACCT GAAAAACATC AAAATCGTCG AGCTTGAAGC CGCGCAACTG
601 CCGCGTAGCC GCGCCGACGT GGATTTTGNC GTCGTCAACG GCAANTACGC
651 CATAAGCAGC GGCATGAAGC TGACCGAAGC CCTGTTCCAA GAACCGAGCT
701 TTGCCTATGT CAACTGGTCT GCCGTCAAAA CCGCCGACAA AGACAGCCAA
751 TGGCTTAAAG ACGTAACCGA GGCCTATAAC TCCGACGCGT TCAAAGCCTA
801 CGGCACAAA CGCTTCGAGG GCTACAAATC CCCTGCCGCA TGAATGAAG
851 GCGCAGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1276; ORF 307.a>:

```

a307.pep
  1 MKTFFKTLA AALALILAAC GGQKDSAPAA SASAAADNGA AKKXIVFGTT

```

705

```

51  VGDFGDMVKE QIQPELEKKG YTVKLVEFTD YVRPNLALAE GEXDINVFOH
101 KPYLDDFKKE HNLDITEVFQ VPTAPLGLYP GKLKSLEEVK DGSTVSAPND
151 PSNFARVLVM LDELGWIKLK XGINPLTASK ADIAENLKNI KIVELEAAQL
201 PRSRADVDFX VVNGXYAISS GMKLTEALFQ EPSFAYVNWS AVKTADKDSQ
251 WLKDVTEAYN SDAFKAYAHK RFEGYKSPAA WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                      QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
          220      230      240      250      260      270

                                39
m307.pep      AWNEGAAKX
              |||||
a307          AWNEGAAKX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTGTGA
51  TCCGTGTTTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGAAGT
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCGGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGC CGGA
501 AACGCGCGTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAGCGCGAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1278; ORF 308.ng&gt;:

```

g308.pep
1  MLNRVIFYRIL GVADNLYPCL SDFCFFTIIA GLPLQAVLWE RRMVRRLLII
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFQDNLNLT
151 ADVVLKERRR LVLMVRETPL NLAHLNLMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTGTGA
51  TCCGCGTTTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGAAGT
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGcT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGC CGGA
501 AACGCGCGTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GwAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGcTt TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCArgGAATG gcG...

```

This corresponds to the amino acid sequence &lt;SEQ ID 1280; ORF 308&gt;:

m308.pep (partial)

706

```

1  MLNRFVYRIL  GVADNLYPRL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNMR  XTEMGGVFP  PVPAMYRKPQ
201 TADDIVAHSV  AHALSFLGID  TPDSAQWGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRFVYRILGVADNLYPRLSDFCFFTI	IAAGLPLQAVLWERRMMVRRLLII	GISGASGFQY			
g308	MLNRFVYRILGVADNLYPRLSDFCFFTI	IAAGLPLQAVLWERRMMVRRLLII	GISGASGFQY			
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADFVHPIGNIGACIASGTF				
g308	GVKALELLRAQDVETHLVVSKGAEMARASE	TDYTKDEVYALADFVHPIGNIGACIASGTF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRA	ADVVLKERRRLVLMVRETPLNLAHLNMR				
g308	KTDGMLVAPCSMRTLASVAHGFGDNLTRA	ADVVLKERRRLVLMVRETPLNLAHLNMR				
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVFPVPVPAMYRKPQTADDIVAH	SVAHALSFLGIDTPDSAQWGM				
g308	VTEMGGVFPVPVPAMYRKPQTADDIVAH	SIHTLSFLGIDTPDLAQWGMADX				
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTCT  GTTTTTCAC  TATAATAGCC  GGTGTTGCCG
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCCCT  GGTCGTGCAC  GGCTTCGGCG  ACAACCTCTT  TACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTCTCTG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNMR  VTEMGGVFP  PVPAMYRKPQ
201 TADDIVAHSV  AHALSFLGID  TPDSAQWGM  AD*

```

m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRFYRILGVADNLYPRLSDFCFFTTI	AGLPLQAVLWERRMMVRRLL	IGISGASGFQY			
a308	MLNRIFYRILGVADNLYPRLSDFCFFTTI	AGLPLQAVLWERRMMVRRLL	IGISGASGFQY			
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADFVHPIGNIGACIASGTF				
a308	GVKALXLLRAQDIETHLVVSKGAEMARASE	TXYARDXVYALADKVHPIGNIGACIASGTF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGF	GDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNLMKR				
a308	KTDGMLVAPCSMRTLASVHGF	GDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNLMKR				
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPAMYRK	PQTADDIVAHSLVHALSLFGIDTPD	SAEWQGM			
a308	VTEMGGVVFPVPAMYRK	PQTADDIVAHSLVHALSLFGIDTPD	SAEWQGMAD			
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGTGTTTA TCGGATTCTT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGAAC
201 TTTGCCGCGC CAAGATGTCT AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCGGA
401 CGCTTGCCCT TGTGCGGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTGAAGGA AAGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCT CGATGTACCG CAAGCCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTGCTGTT
651 CCGAATCGAT ACGCCGGAAT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRFYRIL GVADNLYPCL SDFCFFTTIA GLPLQAVLWE RRMVRRLLI
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
151 ADVVLKERRR LVLVRETPL NLAHLNLMKR VTEMGGVVFP PVPAMYRKPK
201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTCTT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGAAC
201 TTTGCCGCGC CAAGATGTCT AAACGCACCT TGTGGTATCG AAAGGTCGCG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCTGT TCGATGCGGA
401 CGCTTGCCCT TGTGCGGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTGAAGGA AAGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCT CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTGCTGTT
651 CCGAATCGAT ACGCCGGAAT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRFYRIL GVADNLYPRL SDFCFFTTIA GLPLQAVLWE RRMVRRLLI

```



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51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA  
 101 LADVFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA  
 151 ADVVLKERRR LVLMVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKQ  
 201 TADDIVAHSV AHALSFLGID TPDSAEWQGM AD\*

m308-1/g308-1 97.0% identity in 232 aa overlap

	10	20	30	40	50	60
m308-1.pep	MLNRFYRILGVADNLYPRLSDFCFF	IIAGLPLQAVLWERRMMVRR	LIIGISGASGFQY			
g308-1	MLNRFYRILGVADNLYPRLSDFCFF	IIAGLPLQAVLWERRMMVRR	LIIGISGASGFQY			
	10	20	30	40	50	60
m308-1.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADVFVHPIGNIGACIASGTF				
g308-1	GVKALELLRAQDVETHLVVSKGAEMARASE	TDYTKDEVYALADVFVHPIGNIGACIASGTF				
	70	80	90	100	110	120
m308-1.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADVFVHPIGNIGACIASGTF				
g308-1	GVKALELLRAQDVETHLVVSKGAEMARASE	TDYTKDEVYALADVFVHPIGNIGACIASGTF				
	70	80	90	100	110	120
m308-1.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAAD	VVLKERRRLVLMVRETPLNLAHLDNMKR				
g308-1	KTDGMLVAPCSMRTLASVAHGFGDNLTRAAD	VVLKERRRLVLMVRETPLNLAHLDNMKR				
	130	140	150	160	170	180
m308-1.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAAD	VVLKERRRLVLMVRETPLNLAHLDNMKR				
g308-1	KTDGMLVAPCSMRTLASVAHGFGDNLTRAAD	VVLKERRRLVLMVRETPLNLAHLDNMKR				
	130	140	150	160	170	180
m308-1.pep	VTEMGGVVFPVPAMYRKQPTADDIVAHSAH	ALSFLGIDTPDSAEWQGMADX				
g308-1	VTEMGGVVFPVPAMYRKQPTADDIVAHSAH	LSLFGIDTPDLAEWQGMADX				
	190	200	210	220	230	
m308-1.pep	VTEMGGVVFPVPAMYRKQPTADDIVAHSAH	ALSFLGIDTPDSAEWQGMADX				
g308-1	VTEMGGVVFPVPAMYRKQPTADDIVAHSAH	LSLFGIDTPDLAEWQGMADX				
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA  
 51 TCCGTATTTA TCGGATTCTT GTTTTTTCAC TATAATAGCC GGTTTGCCGT  
 101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC  
 151 GGCATCAGTG GGGCGAGCGG TTTCCAATAC GCGTGAAGG CTTTGGANCT  
 201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG  
 251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC  
 301 TTGGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG  
 351 CCGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCGGA  
 401 CGCTTGCCCT GGTGCTGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG  
 451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCAGCA  
 501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA  
 551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCCTG CGATGTACCG CAAACCGCAG  
 601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTCGCTGTT  
 651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGAATG GCGGATTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1288; ORF 308-1.a&gt;:

a308-1.pep

1 MLNRFYRIL GVADNLYPYL SDFCFFIIIA GLPLQAVLWE RRMVRRLLI  
 51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA  
 101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVH GFGDNLTRA  
 151 ADVVLKERRR LVLMVRETPL NLAHLDNMXR VTEMGGVVFP PVPAMYRKQ  
 201 TADDIVAHSV AHALSFLGID TPDSAEWQGM AD\*

a308-1/m308-1 96.1% identity in 232 aa overlap

	10	20	30	40	50	60
a308-1	MLNRFYRILGVADNLYPYLSDFCFF	IIAGLPLQAVLWERRMMVRR	LIIGISGASGFQY			
m308-1	MLNRFYRILGVADNLYPRLSDFCFF	IIAGLPLQAVLWERRMMVRR	LIIGISGASGFQY			
	10	20	30	40	50	60
a308-1	GVKALXLLRAQDIETHLVVSKGAEMARASE	TXYARDXVYALADXVHPIGNIGACIASGTF				
m308-1	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADVFVHPIGNIGACIASGTF				
	70	80	90	100	110	120
a308-1	GVKALXLLRAQDIETHLVVSKGAEMARASE	TXYARDXVYALADXVHPIGNIGACIASGTF				
m308-1	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADVFVHPIGNIGACIASGTF				
	70	80	90	100	110	120
a308-1	KTDGMLVAPCSMRTLASVHGF	GDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR				
m308-1	KTDGMLVAPCSMRTLASVHGF	GDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR				
	130	140	150	160	170	180
a308-1	KTDGMLVAPCSMRTLASVHGF	GDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR				
m308-1	KTDGMLVAPCSMRTLASVHGF	GDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR				
	130	140	150	160	170	180

```

m308-1      KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVKERRRLVLMVRETPNLNLAHLNDNMKR
              130      140      150      160      170      180
a308-1      VTEMGGVFPVPVPMYRKPTADDIVAHSAHALSLFGIDTPDSAEWQGMADX
              190      200      210      220      230
m308-1      VTEMGGVFPVPVPMYRKPTADDIVAHSAHALSLFGIDTPDSAEWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

g311.seq

```

1  atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgcgtgccg gcgcgctttg ggggtgttgg
101 gtttggaaac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggcg gcattctgat tgaacagtc agggcgggcg gtaaaacggt
201 tgccgtggtc ggatcggca tcaatttcgt gctgcccag gaagtggaaa
251 acgccgcttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta atgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgctggt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgttct
501 gcacttgga acggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
601 gaacgttttt tgctgttga aggcgggaac agccggctca agtggcggtg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgccg taccgcgatt
701 tgtcgccttt gggcgcgga tggcgggaaa aggcggatgg aaatgtccgc
751 atcgctcggt gcgcgctgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttccgca caggctttgg
851 gcatacgcaa ccactaccgc caccgccgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgctcg
951 cagttgcggc acggcggtta cggttgacgc gctcaccgat gacggacatt
1001 atctcgcgcg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
1151 gcggctcgat aatgatgatg cacggccgtt tgaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggcgcgcgcg cgaaagtcgc
1251 cgaagccctg ccgcctgcat ttttgccgga aaataccgtg gcgctggcgg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

g311.pep

```

1  MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGILITV RAGGKTAVV GIGINFVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLET LLAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGT VKG VDGRGVLHLE TAEGETVVS GEISLRPDNR SVSVPKRPDS
201 ERFLLEGGN SRLKWAVEN GTFATVGSAP YRDLSP LGAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNLGSRFRFS RNACVVVSCG TAVTVDALTD DGHYLG GTIM PGFHLMKESL
351 AVRTANLNRP AGKRYPFPTT TGNVASGMM DAVCGS IMM HGRLEKNGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

m311.seq (partial)

```

1  ATGTTCAAGT TTGCTGGGT GTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTCGCTT GTTGC GG CAG TGGCGTGTGC GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCAATTAAAG TGGCCCAATG ATTTGGTTGT CGGACGCGAC
151 AAATGGGCGC GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CTGCCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG CGGGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAAT
351 CAGCCTGCGG TCCGACnACA GGCCGGTTTC CGTGnCGAAG CGGCGGGATT

```

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```

401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAA ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTGCGCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TCGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCGGACC
701 GCTGGTTCAA CGCCTTGGGC AGCCGCGGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCAAGT GCGGCACGGC GGTAAACGTT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrGGAACCA TCATGCCCGG TTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTTTCGGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAAACCG
1001 GGGCGGGCAA GCCTGTCGAT GTCATCATT CCGGCGCGGG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGG GCGGAAAATA CCGTGCCTGT
1101 GCGGACAAC CTCGTCATTT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGAATA TGAACAT....

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
51 KLGGILIETV RTGGKTAVAV GIGINFVLPX EVENAASVQS LFQTASRRGN
101 ADAAVLLXXX XXXXEISLR SDXRPVSXK RRDSEFLLL DGGNSRLKWA
151 WVNGTFATV GSAPYRDLSP LGAWEAKAD GNVRIVCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPPTTGNV ASGMDAVCG SVMMHGRLK EKTGAGKPDV VIITGGGAAK
351 VAEALPPAFL AENTVRVADN LVIYGLLNMI AEGREYEH....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311

m311.pep      10      20      30      40      50      60
MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311          10      20      30      40      50      60
MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPNDLVVGRDKLGGILIETV

m311.pep      70      80      90      100     110
RTGGKTAVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADAVALLLXXX-----
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311          70      80      90      100     110     120
RAGGKTAVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADAVALLETLLAELGAVLEQ

m311.pep      -----XXXXXXXXX
g311          130     140     150     160     170     180
YAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDRGVHLHLETAEGEQTVVS

m311.pep      120     130     140     150     160     170
XEISLRSDXRPVSXKRRDSEFLLL DGGNSRLKWAWVNGTFATVGSAPYRDLSP LGAE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311          190     200     210     220     230     240
GEISLRPDNRSVSPKRPDSERFLLLEGGNSRLKWAWVNGTFATVGSAPYRDLSP LGAE

m311.pep      180     190     200     210     220     230
WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311          250     260     270     280     290
WAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR

```

711

	240	250	260	270	280	290
m311.pep	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR					
g311	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
m311.pep	HAGKRYFPFTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPDVVIITGGGAAKVAEA					
g311	PAGKRYFPFTTTGNAVASGMMDAVCGSIMMHGRLEKKTGAGKPDVVIITGGGAAKVAEA					
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLNIAAEGREYEH					
g311	LPPAFLAENTVRVADNLVIHGLLNIAAEGGESEHAX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1  ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTT
51  GCTGTGCGCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGAAAAC GCAATCAAG TGGCCAAACG ATTTGGTCGT CGGACGCGAC
151 AAATTGGGCG GCATCTGAT TGAACCGT CAGGACGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTCTG GCTGCCCAAG GAAGTGGAAA
251 ACGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGAAAT
301 CCGCATGCGG CCGTGTGCT GGAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTGCAA TATGCGCGGG ACGGATTTCG GCCTTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC GTGGACGGAC AAGGCGTTCT
501 GCACTTGGAA ACGGCAGAGG GCAAACAGAC GGTCTGCAGC GGCGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTTCCG TGCCGAGCG GCGGGATTCT
601 GAACGTTTTC TGCTGTTGGA CGGCGGCAAC AGCCGGCTCA AGTGGGCGTG
651 GGTGGAAGAA GGCACGTTTC CAACCGTCGG TAGCGCGCCG TACCGGATT
701 TGTCGCTTTC GGGCGCGGAG TGGGCGGAAA AGGTGGATGG AAATGTCCGC
751 ATCGTCGGTT GCGCCGTGTG CGGAGAATTC AAAAAGGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAATCG AGTGGCTGCC GTCTTCCGCA CAGGCTTTGG
851 GCATACGCAA CCACTACCGC CACCCGAAG AACACGGTTC CGACCGCTGG
901 TTCAACGCCT TGGGCAGCCG CCGCTTCAGC CGCAACGCCT GCGTCGCTCG
951 CAGTTGCGGC ACGGCGGTAA CCGTTGACGC GCTCACCGAT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCCGAA CCGCAACCT CAACCGGCAC GCCGTAAGC GTTATCCTTT
1101 CCGGACCACA ACGGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 GCGGCTCGGT TATGATGATG CACGGCGGTT TGAAAGAAAA AACCAGGGCG
1201 GGCAAGCCTG TCGATGTCAT CATTACCGGC GCGGCGCGCG CAAAAGTTGC
1251 CGAAGCCCTG CCGCTGTCAT TTTTGGCGGA AAATACCGTG CGCGTGGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTGCCGC CGAAGGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1  MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGGILIETV RTGGKTVAVV GIGINEVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLETL LAELDAVLLQ YARDGFAPFV AEYQANRDH GKAVLLLRDG
151 ETVFEGTVKG VDGQGVHLHE TAEGKQTVVS GEISLRSDDR PVSVPKRDRS
201 ERFLLLDGGN SRLKWAVVEN GTFATVGSAP YRDLSPGLAE WAEKVDGNVR
251 IVGCAVCGEF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRH AGKRYFPFTT TGNASGMM DAVCGSVMMH HGRLEKKTGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

	10	20	30	40	50	60
m311.pep	MFSFGWVFD RPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV					
a311	MFSFGWVFD RPQYELGSLSPVAAVACRRALSRLGLKTQIKWPNDLVVGRDKLGGILIETV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADA AVLXXXXXXXX-----					
a311	RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADA AVLLETLAELDAVLLQ					
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGV DGQGV LHLETAEGKQTVVS					
	130	140	150	160	170	180
	120	130	140	150	160	170
m311.pep	-EISLRSDXRPVSVXKRRDSERFLLLDGGSRLKAWVENGTFATVGSAPYRDLSP LGAE					
a311	GEISLRSDDRPVSVPKRRDSERFLLLDGGSRLKAWVENGTFATVGSAPYRDLSP LGAE					
	190	200	210	220	230	240
	180	190	200	210	220	230
m311.pep	WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYRHPEEHGSDR					
a311	WAEKVDGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR					
	250	260	270	280	290	
	240	250	260	270	280	290
m311.pep	WFNALGSRFRSRNACVVVSCGTAVTVDALTDG HYLGGTIMGFHLMKESLAVRTANLNR					
a311	WFNALGSRFRSRNACVVVSCGTAVTVDALTDG HYLGGTIMGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYFPFPTTGNASGMMDAVCGSVMMMHGRLKEKTGAGKPV DVIITGGGAAKVAEA					
a311	HAGKRYFPFPTTGNASGMMDAVCGSVMMMHGRLKEKTGAGKPV DVIITGGGAAKVAEA					
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPPAFLAENTVRVADNLVIYGLLN MIAAEGREYEH					
a311	LPPAFLAENTVRVADNLVIHGLLN LIAAEGGESEHTX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1   ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGCGG GACATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GGAAGGTCG GGTTCAGCAG
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCCT GATGTTTCAGT TTCGGCTGGG CGTTTGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA CTTGCGTGCC GCGCGGCTTT
501 GGGGTGTTTG GGTTTGGAAG CGCAAATCAA GTGGCCAAAC GATTGTCGTC
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAAACGGT TTGCGGTGGT CGGTATCGGC ATCAATTTCTG TGCTGCCCAA
651 GGAAGTGGAA AACGCGCTT CCGTGCAGTC GCTGTTTCAG ACGGCATCGC
701 GCGGGGCGAA TGCCGATGCC GCCGTATTGC TGGAAACATT GCTTGCAGAA
751 CTGGGCGCGG TGTTGGAACA ATATGCGGAA GAAGGGTTCTG CGCCATTTTT

```

```

801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGCAGCG CGAAACCGTG TCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGCACCTGGA AACGGCAGaa ggCGAACAGA cggtcGtcag
951 cggcGaaATC AGcCTGCGGc CCGacaacag gtcggtttcc GTgccgaagc
1001 gGccggaTTC Ggaacgtttt tTGCTgttgg aaggcgggaa cagccggctc
1051 aAGTGGcggt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGCgCC
1101 gtaCCGCGAT TTGTGCGCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TCGCGCGTGT GCGGAGAATC CAAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TCGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCCCT TCCCGACCAC AACGGGCAAC GCCGTGCGAA CGCGCATGAT
1551 GGACGCGGTT TCGGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1  MTVLKPSHWR VLAELADGLP OHVSQLAREA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTLKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLEMS FGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIETVRAG
201 GKTVAUVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVDDG
301 RGVHLLETAE GEQTVVSGEI SLRPDNRVS VPKRPDSERF LLEGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIWG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAL GIRNHYRHE EHGSDRWFFNA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDG YLGGTIMGF HLMKESLAVR TANLNRPAKG
501 RYPPFTTTGN AVASGMMDAV CGSIMMMHGR LKEKNGAGKP VDVITGGGA
551 AKVAELPFA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1  ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATAACGGGG
151 CTGTTGCCGC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGCG TGACCCACCT
351 GCAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTGTTGACC GCCCGAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA GTGGCGTGTC GGCGCGCCTT
501 GTCGCGTTTA GGTTTGATG TGCAGATTAA GTGGCCCAAT GATTTGGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCGTGGT CGGTATCGGC ATCAATTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGCGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGCAGCG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCACCTGGA AACGGCAGAG GGCAACAGA CGGTCGTCAG
951 CGCGGAAATC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCCGAAGC
1001 GGCGGGATTG GGAACGTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAATA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TCGCTGTGT CCGGAGAATT CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TCGCTGCTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTGCGCA CGCGCATGAT
1551 GGATGCGGTT TCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGCG GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTTACGG GTTGTGAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1298; ORF 311-1&gt;:

m311-1.pep

```

1  MTVLKLSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVFDAPQY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILIETVRTG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGV
301 QGVHLHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSSAQAL GIRNHYRHFE EHGS DRWFNA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGHL YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTGN AVASGMMDAV CGSVMMHGR LKERTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*

```

m311-1/g311-1 93.9% identity in 591 aa overlap

m311-1.pep	10	20	30	40	50	60
g311-1	10	20	30	40	50	60
m311-1.pep	70	80	90	100	110	120
g311-1	70	80	90	100	110	120
m311-1.pep	130	140	150	160	170	180
g311-1	130	140	150	160	170	180
m311-1.pep	190	200	210	220	230	240
g311-1	190	200	210	220	230	240
m311-1.pep	250	260	270	280	290	300
g311-1	250	260	270	280	290	300
m311-1.pep	310	320	330	340	350	360
g311-1	310	320	330	340	350	360
m311-1.pep	370	380	390	400	410	420
g311-1	370	380	390	400	410	420
m311-1.pep	430	440	450	460	470	480
g311-1	430	440	450	460	470	480
m311-1.pep	490	500	510	520	530	540
g311-1	490	500	510	520	530	540
	550	560	570	580	590	

```

m311-1.pep  VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNMI AEGREYEHIX
              |||||
g311-1      VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLI AEGGESEHAX
              550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1  ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCCGC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTC
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGTG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTTCA GTTGGCTGGG TGTGTTGACC GCCCGAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA GTGGCGTGCC GCGCGCCTT
501 GTCGCGTTTG GGTGTTGAAA CGCAATCAA GTGGCCAAAC GATTGTTGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTTC TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGAAT TGCCGATGCC GCCGTGTTGC TGGAAACGGT GTTGGCGGAA
751 CTTGATGCGG TGTGTTGCA ATATGCGCGG GACGGATTTC CGCCTTTTGT
801 GCGCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCCGACGCG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGACGGA
901 CAAGGCGTTC TGCACTTGA AACGGCAGAG GGCAAACAGA CGGTCGTAG
951 GCGCGGAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GCGCGGATTC GGAACGTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGTGGAATA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGTGGATG
1151 GAAATGTCCG CATCGTCGGT TCGCGCGTGT GCGGAGAATT CAAAAGGCA
1201 CAAATGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGGA GAAACAGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCAG
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTT CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCGACACAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGTATCGGTT TCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGCGGCGG
1651 GCAAAGATTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGGCTGGCG GACAACCTCG TCATTACCG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1  MTVLKPSHWR VLAELADGLP QHVSQALMA DMKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGER SFGQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKS HRLGECLMF FGVVDRPQY
151 ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGRDKLG GILIVRTG
201 GKTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QANRDHGKA VLLLRDGETV FEETVKGVDG
301 QGVHLHETAE GKQTVVSGEI SLRSDRPVS VPKRRDSERF LLDGGSRL
351 KWAVVENGTF ATVGSAFYRD LSPLGAWEAE KVDGNVRIVG CAVCGEFKKA
401 QVQELARKI EWLPSSAQAL GIRNHYRHE EHGSDRWFA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGHI YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

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a311-1/m311-1 98.5% identity in 591 aa overlap

```

              10      20      30      40      50      60
a311-1.pep  MTVLKPSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
              |||||
m311-1      MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
              10      20      30      40      50      60

              70      80      90      100     110     120
a311-1.pep  LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              |||||
m311-1      LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              70      80      90      100     110     120

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716

	130	140	150	160	170	180
a311-1.pep	GRGRQGRKWSHRLGEC	LMFSFGWVDRPQYELG	SLSPVAACRRALSRL	GLKTQIKWPN		
m311-1	GRGRQGRKWSHRLGEC	LMFSFGWVDRPQYELG	SLSPVAACRRALSRL	GLDQIKWPN		
	130	140	150	160	170	180
a311-1.pep	DLVVGRDKLGGIL	ETVRTGGKTVAVVG	IGINFLPK	EVENAASVQSL	FQTASRRGNADA	
m311-1	DLVVGRDKLGGIL	ETVRTGGKTVAVVG	IGINFLPK	EVENAASVQSL	FQTASRRGNADA	
	190	200	210	220	230	240
a311-1.pep	AVLLETLLAELDA	VLLQYARDGFAPF	VAEYQAANRDH	GKAVLLLRDGE	TVFEGTVKGVDG	
m311-1	AVLLETLLAELDA	VLLQYARDGFAPF	VAEYQAANRDH	GKAVLLLRDGE	TVFEGTVKGVDG	
	250	260	270	280	290	300
a311-1.pep	QGVHLHLETAEG	KQTVVSGEISLR	SDRPVSVPKRR	DSEFLLLDG	GN SRLKWAV	ENGTF
m311-1	QGVHLHLETAEG	KQTVVSGEISLR	SDRPVSVPKRR	DSEFLLLDG	GN SRLKWAV	ENGTF
	310	320	330	340	350	360
a311-1.pep	ATVGSAPYRDL	SPLGAEWA	EKV DGNVR	IVGCAVCGE	FKKAQVQE	LARKIEWLP
m311-1	ATVGSAPYRDL	SPLGAEWA	EKV DGNVR	IVGCAVCGE	FKKAQVQE	LARKIEWLP
	370	380	390	400	410	420
a311-1.pep	GIRNHYRHPEE	HGSDRWFNAL	GSRRFSRNAC	VVVSCGTAV	TDALTD	DDGHYLG
m311-1	GIRNHYRHPEE	HGSDRWFNAL	GSRRFSRNAC	VVVSCGTAV	TDALTD	DDGHYLG
	430	440	450	460	470	480
a311-1.pep	HLMKESLAVRT	ANLNRHAGK	RYFPFTTGN	AVASGMMDA	VC	SVMMHGR
m311-1	HLMKESLAVRT	ANLNRHAGK	RYFPFTTGN	AVASGMMDA	VC	SVMMHGR
	490	500	510	520	530	540
a311-1.pep	VDVIITGGGA	AKVAEALPPA	FLAENTVR	VADNLVI	HGLNLIAE	GGSEHTX
m311-1	VDVIITGGGA	AKVAEALPPA	FLAENTVR	VADNLVI	HGLNLIAE	GREYEHX
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTaccat cggcaTTgaT ttgcacgact
101 gcacgagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggtcg gcaaagactT GGTGGCAacg Gcgaaacacc tTccgcCAA
201 ATACGCGGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAGGTA TGTGCGCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGCGAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTCTGTC AACCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTGCGCGT
651 ATCCGGTCCA GGCGTGGTCA AAGCCGCGCT GGAAAATTCG GACGCGGTCA
701 GCCTGACCGA GGTGCGCCGA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGCGG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTGTG CGCTGGCACC GACCCCGGCC GTCGGCGACT
851 CCGTGGCGCG CATTCCTGAA GAAATGGGCT TGAGCGTCTG CCGTACGCAC

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901 GGCACAAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGC CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCGGTC TGCTCCGTTG GTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGCG AAAAGAAGGT TCGTGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

... This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1 MSIQSGEILE TVKMVADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51 TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FCGAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCETH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGQLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1 ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51 CCAGAAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GCGCGAAACT
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAGGGA TGTGCGcTTC GGATGAGGTG TTAATCCGCT
401 CCATTCGCCA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACcGTc AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAATAATTGT CGTGTCTGTC AACCGGTGG AAGACAACCC GTTTwTGGCG
601 GCGCGGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTCG GCGTATCCGG
651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAACTG CTTTCAAAT TACCCGCGTG
751 GCGGAACTCA TCGGCCGCGA AGCcTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTGCGCGA CCCC GCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAACTC
1051 GAAGCCATGA CCGCCGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAt GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CAcGGTCGAG TTCGGCGGCT TGTGGGCTA
1251 CGCGCCTGTG ATGCCGGTCA AAGAAGGTTG GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
51 TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCX SIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FCGAKIVVFC NAVEDNPFXA
201 GAFHGSGLAV INVGVSGPGV VKAALENS DA TLTTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCETHGTTA
301 ALALLNDAVK KGGMMASAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIIVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLGYAPV MPVKEGSCEV FVNRGGRI PA PVQSMKN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

m312.pep	10	20	30	40	50	60
	MSIQSGEILETVKQVADQNFVDRITITIGIDLHDCISSDINVLNQNIYNKITTGVKDLVTT					
g312	MSIQSGEILETVKQVADQNFVDRITITIGIDLHDCISTDIDVLNQNIYNKITTGVKDLVAT					
	10	20	30	40	50	60
m312.pep	70	80	90	100	110	120
	AKYLSAKYGVPIVNRISVTPIAQIAAATHADSYVSVQAQTLDKAAKAIGVSFIGGFSALV					
g312	AKHLSAKYGVPIVNRISVTPIAQIAAATKADSYVSVQAQTLDKAAKAIGVSFIGGFSALV					
	70	80	90	100	110	120
m312.pep	130	140	150	160	170	180
	QKGMSPSDEVLIRSIPEAMKTTDIVCXSNIGSTRAGINMDAVKLAGETVKRTAEITPEG					
g312	QKGMSPSDEVLIRSVPEAMKTTDIVCSSNIGSTRAGINMDAVKLAGETIKRTAEITPEG					
	130	140	150	160	170	180
m312.pep	190	200	210	220	230	
	FGCAKIVVFCNAVEDNPFKXAGAFHSGS--DAVINVGVSQPGVVKAALENS DATTLTEVAE					
g312	FGCAKIVVFCNAVEDNPFMAGAFHSGSEADAVINVGVSQPGVVKAALENS DAVSLTEVAE					
	190	200	210	220	230	240
m312.pep	240	250	260	270	280	290
	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
g312	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTAVGDSVARILEEMGLSVCGTH					
	250	260	270	280	290	300
m312.pep	300	310	320	330	340	350
	GTTAALALLNDVAVKKGGMMASAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
g312	GTTAALALLNDVAVKKGGMMASAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
m312.pep	360	370	380	390	400	410
	CSVGLDMIIVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTIVGDTVEFGGLLG					
g312	CSVGLDMIIVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTIVGDSVEFGGLLG					
	370	380	390	400	410	420
m312.pep	420	430	440			
	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
g312	YAPVMPAKEGSCEVFVNRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

1	ATGAGTATCC	AATCCGGCGA	AATTTTAGAA	ACCGTCAAAA	TGGTTGCCGA
51	CCAGAATTTC	GATGTCCGCA	CCATTACCAT	CGGCATTGAT	TTGCACGACT
101	GCATCAGCAC	CGACATCGAC	GTGTTGAACC	AAAATATTTA	CAACAAAATT
151	ACCACGGTCG	GCAAAGACTT	GGTGGCGACA	GCAAAATATC	TGTCTGCCAA
201	ATACGGCGTG	CCGATTGTGA	ATCAGCGCAT	TTCTGTCACG	CCGATTGCCC
251	AAATCGCGGC	GGCCACCCAT	GCTGATTCTT	ACGTCAGCGT	GGCGCAAATC

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```

301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATTG GCGGCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGCGCGCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTCTGCG AACGCGGTGG AAGACAACCC GTTTATGGCG
601 GCGCGCTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGCCCC GGTGTCGTAA AAGCCGCGTT GGAAAATTCG GATGCAACGA
701 CATTGACCGA AGTTGCCGAA GTTGTGAAGA AAACCGCCTT CAAAATTACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGGCGACT
851 CGGTGGCGCG CATCTTTGAA GAAATGGGTT TGAGCGTCTG CCGTACGCAC
901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAAGCAGG CGTGCTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTCGGTCG GCTTGGATAT
1101 GATTGCCGTT CCCGGCGACA CACCCGCGCA CACCATTTCC GGCATCATTG
1151 CCGACGAAGC CGCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATTCGGG TAACCGGTAA AACCCTCGGC GACAGCGTCG AGTTCGGCGG
1251 CCTGTTGGGC TACGCGCCTG TAATGCCGGT AAAAGAAGGC TCATGCGAAG
1301 TGTTCTGCAA CCGGGCGCGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

```

a312.pep
  1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISTDID VLNQNIYNKI
 51 TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FCGAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GP VVKAALENS DATTLEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSVVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

m312/a312 96.7% identity in 451 aa overlap

m312.pep	10	20	30	40	50	60
a312	10	20	30	40	50	60
m312.pep	70	80	90	100	110	120
a312	70	80	90	100	110	120
m312.pep	130	140	150	160	170	180
a312	130	140	150	160	170	180
m312.pep	190	200	210	220	230	
a312	190	200	210	220	230	240
m312.pep	240	250	260	270	280	290
a312	240	250	260	270	280	290

720

	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDVAVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDVAVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAPVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAPVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

g313.seq

```

1  atggacgacc cgcgcaccta cggatcgggc aatcccggcg cgaccaatgt
51  tttaacgcagc ggcaaaaaaa aggcggccgc gctgacgctc ttgggcgatg
101 cgcgcaaaagg tttggttgcc gttttgcttg cagcgctgct tcaagaaccg
151 ctcggtttat cgcacagcgc aatcgccgcc gtcgcactcg ccgcgctggt
201 cgggcatatg tggccggtgt ttttcggatt taaggcgccg aaaggcggtg
251 caacggcatt gggcgctgct ctggcactct ctctgcaac tgccttggtc
301 tgcgcgttga tttggcttgt gatggcattc ggcttcaaag tatcctccct
351 tgcgcgctg gtcgccacaa ccgcgcggcc ccttgccgca ctgtttttaa
401 tgcgcacata ttcttggtat ttcgcaaccc tcgcaatcgc catattggtg
451 ttgctccgcc ataagagcaa catcctcaac ctgattaaag gcaaagaaag
501 caaatcggc gaaaaacgct ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

g313.pep

```

1  MDDPRTYGS NPGATNVLRS GKKAALTL LGDAAGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATAGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL VATTAAPLAA LFFMPHTSWI FATLAIALLV
151 LLRHKSNILN LIKGESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

m313.seq

```

1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTAGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGCT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCGCAAC TGCCTTGCTC
301 TGCGCGTTGA TTTGGCTTGT TATGGCATTG GGCTTCAAGG TGCTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTGCGCGCA TCCTTCTTTA
401 TGCCGCACGT CTCGTGGGTT TGGCGACCG TCGCCATTGC TTTGCTGGTG
451 TTGTTCCGCC ACAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
501 CAAATCGGC GGCAGCCGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

m313.pep

```

1  MDDPRTYGS NPGATNVLRS GKKAALTL LGDAAGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATAGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL TATIAAPVAA SFFMPHVSWS WATVAIALLV
151 LFRHKSNIKV LEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

from *N. gonorrhoeae*:

	10	20	30	40	50	60
m313.pep	MDDPRTYGS	GNPGATNVL	RS	GKKKAAAL	TLLGDAAKGL	VAVLLARVLQ
g313	MDDPRTYGS	GNPGATNVL	RS	GKKKAAAL	TLLGDAAKGL	VAVLLARVLQ
	10	20	30	40	50	60
m313.pep	VALAALVGH	MWPVFFG	FKGKG	GVATALG	VLLALSP	ATALVCALI
g313	VALAALVGH	MWPVFFG	FKGKG	GVATALG	VLLALSP	ATALVCALI
	70	80	90	100	110	120
m313.pep	WMAFGFKV	SSLAAL				
g313	WMAFGFKV	SSLAAL				
	70	80	90	100	110	120
m313.pep	TATIAAPV	AASFFMPH	VS	WVWATVA	IA	ALLVLF
g313	TATIAAPV	AASFFMPH	VS	WVWATVA	IA	ALLVLF
	130	140	150	160	170	
m313.pep	FRHKSNIV	KL	LEGRESK	IGGSRX		
g313	VATTAAPL	AALFFMPH	TSWIFAT	LAIAILV	LLRHKS	NI
	130	140	150	160	170	
m313.pep	LI	KG	KESKIG	KERX		

a313.seq

1	ATGGACGACC	CGCGCACCTA	CGGATCGGGC	AATCCGGGGG	CAACCAATGT
51	TTTACGCAGC	GGCAAAAAAA	AGGCGGCCGC	GCTGACGCTC	TTGGGCGATG
101	CCGCGCAAAG	TTTGGTTGCG	GTTTGTGCTT	CACGCGTGCT	TCAAGAACCG
151	CTCGGTTTAT	CCGACGCGC	AATCGCGGCC	GTCCGACTCG	CCGCGCTGGT
201	CGGGCATATG	TGGCCGGTGT	TTTTCGGATT	TAAAGCCGCG	AAAGGCGTGG
251	CAACGGCATT	GGGCGTGCTT	CTGGCACTCT	CTCCACAAC	TGCCTTGCTC
301	TGCGCGTTGA	TTTGGCTTGT	GATGCGATT	GGCTTCAAG	TGTCTCTCCT
351	TGCCGCAAT	ACCGCCACAA	TCGCCGCCCC	CCTTGCCGCA	CTGTTTTTTA
401	TGCCGCATAC	TTCTTTGGATT	TTTCAACCC	TCGCAATCGC	CATATTGGTG
451	TGTGTCGCCG	ATAAGAGCAA	CATCTCAAC	CTGATTAAAG	GCAAAGAAAG
501	CAAAATCGGC	GAAAAACGCT	GA		

a313.pep

1 MDDPRTYGSG NPGATNVLRSG KKKKAAALTL LGDAAKGLVA VLLARVLQEP  
51 LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPTTALV  
101 CALIWLWMAF GFKVSSLAAL TATIAAPLAA LFFMPHTSWI FATLAIATLV  
151 LLRHKSNI LN LIKGESKIG EKR\*

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRS	GKKKAAALT	TL	LGDAAKGLVAVLLARVL	QEP	PLGLSDSAIAA
a313	MDDPRTYGSNPGATNVLRS	GKKKAAALT	TL	LGDAAKGLVAVLLARVL	QEP	PLGLSDSAIAA
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMPVVF	FGFKGGKGV	VAT	ALGVLLAL	SPAT	ALVCA
a313	VALAALVGHMPVVF	FGFKGGKGV	VAT	ALGVLLAL	SP	TALVCA
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVVAASFF	MPHVS	WVAT	VAIA	LLVLF	FRHKS
a313	TATIAAPVVAASFF	MPHVS	WVAT	VAIA	LLVLF	FRHKS
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```

g401.seq
1   atgaaattac aacaattggc tgaagaaaaa atcggcggtc tgattgtgtt
51  cacgctgctt gtagtcagtg tcggtctgtt gattgaagtt gtgcccttgg
101 cctttaccac ggccggcaaca cagccggcgc cgggctgtaa gccttacaat
151 gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
201 ctgccactct caaatgattc gtccgttccg tgcggaaacc gagcgctacg
251 gtcattactc tgttgccgga gagtcggttt acgaccatcc gttccaatgg
301 ggttccaaac gtaccggtcc tgatttggca cgtgtgggeg gccgctattc
351 cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgctg
401 agtccaatat gccggcattc ccgtggcttg cacgcaataa agtcgatgtc
451 gatgaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501 cagtgatgag gaaattgcca aagcgctga ggctttggca aacaaatccg
551 agctggatgc ttagtcgcc tatctgcaag gattgggtct ggctttgaaa
601 aacgtaaggt aa

```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```

g401.pep
1   MKLQQLAEK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVAVV YLQGLGLALK
201 NVR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```

m401.seq
1   ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GGCGGCAACA CAGCCGGCGC CGGGCTGAA GCCTTACAA
151 GCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCG TGCggAAACC GAGCGTTACG
251 GTCATTACTC TGTGCGGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGCG GTCCGTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGCGATC CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```

m401.pep
1   MKLQQLAEK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVAVV YLQGLGLALK
201 NVR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

```

m401/g401
      10      20      30      40      50      60
m401.pep  MKLQQLAEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g401      MKLQQLAEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          10      20      30      40      50      60

      70      80      90     100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW

```

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```

g401      |||||
          IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSDEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVVPESNMPAFPPWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
g401      HRIHLLNPRDVVPESNMPAFPPWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
g401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1  ATGAAATTAC AACAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GGC GGCAACA CAGCCGCGT CGGGCGTGAA GCCTTACAAT
151 GCCCTGCAGG TTGCCGACG CGATATTTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCCG TCGGGAACCG GAGCGTTACG
251 GTCATTACTC TGTGCCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATT CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
1  MKLQQLAE EK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGRYSDEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

          10      20      30      40      50      60
m401.pep  MKLQQLAE EK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN ALQVAGRDIY
          |||||
a401      MKLQQLAE EK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN ALQVAGRDIY
          10      20      30      40      50      60

          70      80      90      100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSDEW
          |||||
a401      IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSDEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVVPESNMPAFPPWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
a401      HRIHLLNPRDVVPESNMPAFPPWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
a401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

```

g402.seq
1  ATGGATATGG  TGAACACTAA  Accgaatact  agtgtgatta  atatgctttc
51  tttccttacc  ggatTATTGA  GCTTGGGTat  agaagtCtTg  tGGGTAAGGA
101 TGtttttcgTT CGCagcAcag  tccgtgcctc  aggCATTtTC  atttattctt
151 gcctGtttttc tgACCGgtat  cgccgtcggc  gCgTATTTTG  GCAAACGGAT
201 TTGCCGCAGC  CGCTTGTGTG  ATATTCcctT  TATCGGGCAG  TgcttcttgT
251 GGGCGGGTAT  TgccaTttt  ttgatTTTGG  GTGCTGCGTG  GTTGTGACG
301 GGTtTTTccg  gtttcGTCCA  CCACGCCGGT  AtttTCATTA  CCCTgtctgc
351 CGtcGTCAGG  GGGTTGATTt  TCCCACTTGT  ACACCAgtg  GGTACGGATG
401 GCAACAAATC  CGGACGACAG  GTTCCAATG  TTTATTTGCG  CAACGTGACC
451 GGCAGTGCAT  TGGGTCCGGT  CCTATCGGC  TTTGTGATAC  TTGATttgtt
501 gTCCACCCAA  CAGATTtacc  tgctcatCTG  TTTGATTtCT  GCTGctgtcc
551 cTTTGTtTTg  tacaCTGtTC  CAAAAAGTC  TCCGACTGAA  TGCAGTGTcG
601 GTAGCAGTTT  CCCTAATGTT  CGGCATCCTC  ATGTTCTTAC  TGCCGGATTc
651 TGTCTTTCAA  AATATTGCTG  GCCGTCCGGA  TAGGTTGATT  GAAAACAAAC
701 ACGGCATTGT  TGCGGTTTAC  CATAGAGATG  GTGATAAGGT  TGTtTATGGG
751 GCGAATGTAT  ACGACGGCGC  ATACAATACC  GATATATTCA  ATAGTGTCAA
801 CGGCATCGAA  CGTGCTATC  TGCTACCCTC  CCTGAAGTCC  GGCATACGCC
851 GCATTTTCGT  CGTTGGATTG  AGTACAGGTT  CGTGGGCGCG  CGTCTTGTCT
901 GCCATTCCGG  AAATGCAGTC  GATGATCGTT  GCGGAAATCA  ATCCGGCATA
951 CCGTAGCCTT  ATCGCGGAcg  agccgcAAAT  CGCACCgCTT  TTGCAGGACA
1001 AACGTGTTGA  AATTGTATTG  GATGACGGTA  GGAAATGGCT  GCGTCGCCAT
1051 CCTGATGAAA  AATTCGACCT  GATTTTGATG  AATTCGACTT  GGTACTGGCG
1101 TGCCTATTCC  ACTAACCTGT  TGAGTGCGGA  ATTTTAAAA  CAGGTGCAAA
1151 GCCACCTTAC  CCCGGATGGT  ATTGTAATGT  TTAATACCAC  GCACAGCCCG
1201 CATgctTTTG  CTACCGCCGT  ACACAGTATT  CCCTATGCAT  ACCGCTACGG
1251 GCATATGGTA  GTCGGCTCGG  CAACCCCGGT  AGTTTTcct  AATAAAGAAC
1301 TGCTCaagca  aCGCCTTtcc  cgGTTGATTt  GGCCGGAAG  CGGCAGgcac
1351 gtATTGACA  GCAGACCGT  GGATGCTGCA  GCACAAAAG  TTGtctctCG
1401 TATGCTGATT  CGGATGACGG  AAcctTCGGC  TGGGGCGGAA  GTCATTACTG
1451 ACGATAATAT  GATTGTAGAA  TACAAATACG  GCAGAGGGAT  TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

```

g402.pep
1  MDMVNTKPNt  SVINMLSFLt  GLLSLGIEVL  WVRMFsFAAQ  SVPQAFsFIL
51  ACFLtGtIAGV  AYFGKRICRS  RFVDIPFIQ  CFLWAGtADf  LILGAAWLLT
101 GFSGFVHHAG  IPITLSAVVR  GLIFPLVHHV  GTDGNKSGRQ  VSNVYFANVA
151 GSALGPVLIG  FVILDLLStQ  QIYLLICLIS  AAVPLFCTLF  QKSLRLNAVS
201 VAVSLMFGIL  MFLLPDSVFQ  NIAGRPDRLI  ENKHGtIVAVY  HRDGDkVVYg
251 ANVYDGAYNT  DIFNSVNGIE  RAYLLPSLKS  GIRRIfVVGL  STGSWARVLS
301 AIPEMQSMIV  AEINPAYRSL  IADEPQIAPL  LQDKRVEIVL  DDGRKWLRRH
351 PDEKFDLILM  NSTWYWRAYS  TNLLSAEFLK  QVQSHLTPDG  IVMFNtTHSP
401 HAFATAVHSI  PYAYRYGHMV  VGSATPVVFP  NKELLKQRLS  RLIWPESGRH
451 VFDSStVDAA  AQKVVSRLI  RMTEPSAGAE  VITDDNMIVE  YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

```

m402.seq
1  ATGGATATAG  TGAACACTAA  ACCGAATACT  AGTTTGATTt  ATATGcNtTC
51  TTTCTTtAGC  GGCTTATTGA  GCTTGGGTAT  AGAAGTCTTG  TGGGTGAGGA
101 TGTTTTCGTT  CGCAGCACAG  TCCGTGCCTC  AGGCATTtTC  ATTTACCCTT
151 GCCTGTTTTc  TGACCGGTAT  CGCCGTcGGC  GCGTATTTTG  GCAAACGGAT
201 TTGCCGCAGC  CGCTTGTGTG  ATATTCcCTT  TATCGGGCAG  TGCTTCTTGT
251 GGGCGGGTAT  TGCCGACTTt  TTGATTTTGG  GTGCTGCGTG  GTTGTGACG
301 GGTtTTTCCG  GTTCTGTCCA  CCACGCCGGT  ATCTTCATTA  CCCTGTCTGC
351 CGTCGTcAsA  sGGTTGATTt  TCCGCTCGT  ACACCATGTG  GGTACGGATG
401 GCAACAAATC  CGGACGACAG  GTTCCAATG  TTTATTTGCG  CAACGTGACC
451 GGCAGTGCAT  TGGGTCCGGT  CCTATCGGC  TTTGTGATAC  TTGATTtCTT
501 GTCCACCCAA  CAGATTtACC  TGCTCATCTG  TwTGATTtCT  GCTGCTGTCC
551 CTTTGTtTTG  TACACTGTTC  CAAAAAGTC  TCCGACTGAA  TGCAGTGTcG
601 GTAGCAGTTT  CCCTAATGTT  CGGCATCCTC  ATGTTcYtAC  TGCCGGATTc

```



	:
g402	HRDGDGVVYGANVDGAYNTDIFNSVNGIERAYLLPSLKSGIRRIFFVVGLSTGSWARVLVS
	250        260        270        280        290        300
m402.pep	310        320        330        340        350        360
	AIPQMQSMIVAEPINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDFLIIM
g402	AIPQMQSMIVAEPINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDFLIIM
	310        320        330        340        350        360
m402.pep	370        380        390        400        410        420
	NTTWYWRAYSTNLLSAEFLKVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
	:
g402	NSTWYWRAYSTNLLSAEFLKVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
	370        380        390        400        410        420
m402.pep	430        440        450        460        470        480
	VGSATPVVFPPNKELLQRLSRLIWPESEGRHVFDSSSTDAAAQKVSRMLIQMTEPSAGAE
	:
g402	VGSATPVVFPPNKELLQRLSRLIWPESEGRHVFDSSSTDAAAQKVSRMLIRMTEPSAGAE
	430        440        450        460        470        480
m402.pep	490
	VITDDNMIVEYKYGRGIX
g402	VITDDNMIVEYKYGRGI
	490

```

a402.seq
1  ATGGATATAG  TGAACACTAA  ACCGAATACT  AGTTTGATT  ATATGCTTTC
51  TTTCTTATAG  GGCTTTATAG  TCTTGGGTAT  AGAAGTCTTG  TGGGTAAAGA
101 TGTTTTCGTT  CGCAGCACAG  GCCGTGCCCT  AGGCATTTTC  ATTACTCTTT
151 GCCTGTTTTT  TGACCCGGTAT  CGCCGTCGGC  GCGTATTTTG  GCAAACGGAT
201 TTGCCGCAGC  CGCTTTGTGT  ATATTCCCTT  TATCGGGCAT  TGCTTCTGTG
251 GGGCGGGTAT  TGCCGACTTT  TTGATTTTGG  GTGCTGCGTG  GTTGTTGACG
301 GTTTTTTCCG  GCTTTCGTCCA  CCACGCCGTG  ATCTTCATTA  CCTGTCTGCG
351 CGTCGTGAGA  GGGTTGATTT  TCCCGCTCGT  ACACCATGTG  GGTACGGATG
401 GCAACAAATC  CGGACGACAG  GTTCCAATG  TTTATTTGCG  CAACGTTGCC
451 GGCAGTGCAT  TGGGTCCGGT  CCTTATCGGC  TTTGTGATAC  TTGATTTCTT
501 GTCCACCCAA  CAGATTTACC  TGCTCATCTG  TTTGATTTCT  GCTGCTGTCC
551 CTTTGTTTTG  TACACTGTTC  CAAAAAAGTC  TCCGACTGAA  TCGAGTGTGC
601 GTAGCAGTTT  CCCTAATGTT  CGGCATCCTC  ATGTTCTTAC  TGCCGGATTC
651 TGCTTTTCAA  AATATTGCTG  ACCGTCCGGA  TAGGCTGATT  GAAAACAAAC
701 ACGGCAATTG  TGCGGTTTAC  CATAGAGATG  GTGATAAGGT  TGTTTATGGG
751 GCGAATGTAT  ACAGCCGCGC  ATACAATACC  GATGTATTCA  ATAGTGTCAA
801 CGGCATCGAA  CGTGCCCTAT  TGCTACCCTC  CCTGAAGTCT  GGCATACGCC
851 GCATTTTCGT  CGTTGGATTG  AGTACAGGTT  CGTGGGCGCG  CGTCTTGCTT
901 GCCATTCGGG  AAATCGAGTC  GATGATCGTT  GCGGAAATCA  ATCCGGGCAT
951 CCGTAGCCTT  ATCGCGGACG  AGCCGCAAT  GCGCCCGCTT  TTGCAGGACA
1001 AACGTGTTGA  AATTGTATTG  GATGACGGTA  GGAATGGCT  GCGTCGCCAT
1051 CCTGATGAAA  AATTCGACCT  GATTTTGATG  AATACGACTT  GGTACTGGCG
1101 TGCTATTTC  ACCAACCTGT  TGAGTGCGGA  ATTTTTAAAA  CAGGTGCAAA
1151 GCCACCTTAC  CCCGGATGGT  ATGTGAATGT  TTAATACCAC  GCACAGCCCG
1201 CAGCTTTTTC  CTACCGCGGT  ACACAGATT  CCTATGAT  ACCGCTATGG
1251 GCATATGGTA  GTCGGCTCGG  CAACCCCGGT  AGTTTTCCCT  AATAAAGAAC
1301 TGCTCAAGCA  ACGTCTCTCC  CGTTTGATTT  GGCCGAAAG  CGGCAGGCAC
1351 GTATTTGACA  CGAGCACCGT  GGATGCTGCA  GCACAAAGAT  TTGTCTCTCG
1401 TATGCTGATT  CAGATGACGG  AACCTTCGGC  TGGTGCGGAA  GTCATTACCG
1451 ACGATAATAT  GATTGTAGAA  TACAATACG  CGCAGGGGAT  TTA

```

a402.pep  
1 MDIVNTKPNT SLIYMLSFLS GLLSLGIEVL WVRMFSAQAQ SVPOAFSETL

```

51 ACFLTGI AVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGFPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLQRLS RLIWPESGRH
451 VFDSSSTDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

## m402/a402 99.0% identity in 497 aa overlap

```

              10      20      30      40      50      60
m402.pep      MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSAAQSVPAFSTLACFLTGI AVG
              |||||
a402           MDIVNTKPNTSLIYMLSFLSGLLSLGIEVLWVRMFSAAQSVPAFSTLACFLTGI AVG
              10      20      30      40      50      60

              70      80      90      100     110     120
m402.pep      AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX
              |||||
a402           AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR
              70      80      90      100     110     120

              130     140     150     160     170     180
m402.pep      XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQIYLLICXIS
              |||||
a402           GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQIYLLICLIS
              130     140     150     160     170     180

              190     200     210     220     230     240
m402.pep      AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY
              |||||
a402           AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY
              190     200     210     220     230     240

              250     260     270     280     290     300
m402.pep      HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS
              |||||
a402           HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS
              250     260     270     280     290     300

              310     320     330     340     350     360
m402.pep      AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHHPDEKFDLILM
              |||||
a402           AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHHPDEKFDLILM
              310     320     330     340     350     360

              370     380     390     400     410     420
m402.pep      NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
              |||||
a402           NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
              370     380     390     400     410     420

              430     440     450     460     470     480
m402.pep      VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSSTDAA AQKVSRMLIQMTEPSAGAE
              |||||
a402           VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSSTDAA AQKVSRMLIQMTEPSAGAE
              430     440     450     460     470     480

              490
m402.pep      VITDDNMIVEYKYGRGIX
              |||||
a402           VITDDNMIVEYKYGRGIX
              490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACAC TGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCTGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGCGG GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAGC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRIYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGRSSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSXGKIK PTEGLMVDPS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACAC TGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TCGCGGTCTGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAGC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK

```

729

```

51  DMDLQALHGR  KVALYIATMG  DQSGSGLTGG  RYSIDALIRG  EYINSPAVRT
101 DYTYPREYET  AETTSGLTGG  LTSLSTLNA  PALSRTQSDG  SGSKSSLGLN
151 IGGMGDYRNE  TLTTNPRDTA  FLSHLVQTVF  FLRGIDVVSP  ANADTDVFIN
201 IDVFGTIRNR  TEMHLYNAET  LKAQTKLEYF  AVDRNTKKLL  IKPKTNAFEA
251 AYKENYALWM  GPYKVSIGIK  PTEGLMVDFS  DIRPYGNHTG  NSAPSVEADN
301 SHEGYGYSDE  VVRQHRQGPX  *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from

*N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA	AVKMDLQALHGR				
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA	AVKMDLQALHGR				
	10	20	30	40	50	60
g406.pep	KVALYIATMGDQSGSGLTGG	RYSIDALIRGEYINSPAVRTDY	TYPREYET	AETTSGLTGG		
m406	KVALYIATMGDQSGSGLTGG	RYSIDALIRGEYINSPAVRTDY	TYPREYET	AETTSGLTGG		
	70	80	90	100	110	120
g406.pep						
m406						
	70	80	90	100	110	120
g406.pep	LTSLSTLNAPALSRTQSDGSGSRSS	LGLNIGMGDYRNETLTTNPRDTA	FLSHLVQTVF			
m406	LTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTTNPRDTA	FLSHLVQTVF				
	130	140	150	160	170	180
g406.pep						
m406						
	130	140	150	160	170	180
g406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNR	TEMHLYNAETLKAQTKLEYFAVDRTNKKLL				
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNR	TEMHLYNAETLKAQTKLEYFAVDRTNKKLL				
	190	200	210	220	230	240
g406.pep						
m406						
	190	200	210	220	230	240
g406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS	DIQPYGNHTGNSAPSVEADN				
m406	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS	DIRPYGNHTGNSAPSVEADN				
	250	260	270	280	290	300
g406.pep						
m406						
	250	260	270	280	290	300
g406.pep	SHEGYGYSDEAVRQHRQGPX					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406.seq

```

1  ATGCAAGCAC  GGCTGCTGAT  ACCTATTCCT  TTTTCAGTTT  TTATTTTATC
51  CGCTGCGGG  ACACTGACAG  GTATTCCATC  GCATGGCGGA  GGTAACGCT
101 TC GCGGTCGA  ACAAGAACTT  GTGGCCGCTT  CTGCCAGAGC  TGCCGTTAAA
151 GACATGGATT  TACAGGCATT  ACACGGACGA  AAAGTTGCAT  TGTACATTGC
201 AACTATGGGC  GACCAAGGTT  CAGGCAGTTT  GACAGGGGGT  CGCTACTCCA
251 TTGATGCACT  GATTCGTGGC  GAATACATAA  ACAGCCCTGC  CGTCCGTACC
301 GATTACACCT  ATCCACGTTA  CGAAACCACC  GCTGAAACAA  CATCAGGCGG
351 TTTGACAGGT  TTAACCACTT  CTTTATCTAC  ACTTAATGCC  CCTGCACCTC
401 CGCGCACCCA  ATCAGACGGT  AGCGGAAGTA  AAAGCAGTCT  GGGCTTAAAT
451 ATTGGCGGGA  TGGGGGATTA  TCGAAATGAA  ACCTTGACGA  CTAACCGCGG

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730

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501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGGCAG GACATAGACA
951 AGGGCAACCT TGA

```

-- This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAANK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVD FS DIQPYGNHMG NSAPSVEADN
301 SHEGYGSDE AVRRHRQGQP *

m406/a406 98.8% identity in 320 aa overlap

          10      20      30      40      50      60
m406.pep  MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAANKDMDLQALHGR
          |||
a406       MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAANKDMDLQALHGR
          10      20      30      40      50      60

          70      80      90      100     110     120
m406.pep  KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPREYET AETTSGLTGT
          |||
a406       KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPREYET AETTSGLTGT
          70      80      90      100     110     120

          130     140     150     160     170     180
m406.pep  LTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF
          |||
a406       LTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF
          130     140     150     160     170     180

          190     200     210     220     230     240
m406.pep  FLRGIDVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
          |||
a406       FLRGIDVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
          190     200     210     220     230     240

          250     260     270     280     290     300
m406.pep  IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVD FS DIRPYGNHTGNSAPSVEADN
          |||
a406       IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVD FS DIQPYGNHMGNSAPSVEADN
          250     260     270     280     290     300

          310     320
m406.pep  SHEGYGSDEAVRRHRQGQPX
          |||
a406       SHEGYGSDEAVRRHRQGQPX
          310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
1  atggtcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
51  ggcaggcggga gatggcaaga tgcagcatca ctttgacggc aggggttcgt

```

```

101  tcgtcaaacy attcggacac caagccgctg tctcggtcga ggccgagggg
151  cagctgggtc atgtcggttc agccgatgga gaagccgctg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttcct tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggg cagaccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgctgccgc
501  cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggatgc gtaaccggcg atgcggcgga
651  taatttcgcg tttcagttcg tcgtcttgtt tgtcaaattc caacaaggct
701  ttcgggtgga tgcgatttgc gcggttgatg ataaattcca tacgcgcaa
751  gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801  tgcgcagctt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacattcg taatttgtac gtccagcagg ccggcataga taaagccggt
901  atcgccctcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggtcgcatt gccgcagccg acgacggcag gaatacccag ttcgcgcgcg
1001 atgatggcgg cgtggcaggt gcgtccgccg cggttggtca cgtggcgga
1051 agcacgtttc atcacgggtt cccaatccgg atcggctcat tcggttaacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatt tttaatcagg
1151 gcacacttgc cctgaccgac tttttgaccg atggcacgac cttcgacaaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttgagg tttgacggtt tcggggcggg cttgcaggat gtagagtttg
1301 ccgtccaggc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgcgt agtgtgcaa ctccgtgatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcttcgg ggacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 acccatggtc ttgcgcagga tggcggtttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLTA DT DIFVLLAAGG DGMQHHFDG RFAVVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAAADQV GVFGFVEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRCG VTGDAADNFR FQFVLFVKF QQGFVRDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDGDCFWH IVQGDIGNLY VQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDDG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHALTD FLTDGTTFAQ
401 DGFFAVDQVA AQVAAAFLLG FDGFGAGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQRVVCQ LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGF EHI KFRVRDRALY DVFAQTVRGG NKDDL VVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atggctcgac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51  ggcaggcgga gatggcagg tgcagcatca ctttgacggc agggttgcgt
101  tcgtcaaacy attcggatac caagccgctg tcgcggtcga gaccgagggg
151  cagttgggtc atgtcggttc agccgatgga gaagccgctg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttcct tcagggtctt
301  gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  caacgttggg caacccatt tcacgcgga cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgttgccgc
501  cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggccaat gtcgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcggg
651  taatttcgcg ttttaattcg tcgtcttgtt tgtcaaattc caacaargct

```



732

```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca gggtggcgaa gctgaatgcg agttcgggat
801 tgccgacgtt catcatgact tttacaggtg ctttaggcat attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgcccttcg gcacaggata cggttaacttc ttgaccgttt ttcagcaatt
951 cggttgcatc gccgcagccg acaacggcag gaatgcccga ttcacgcgcg
1001 atgatggcgg cgtggcaggt acggcgcccg cggttggtta cgatggcaga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgccgc cttcgcataa
1201 tacggttttg tcgcccgttg tggcgaagcg gcgcagggtg cggttgccct
1251 cttcttgga ttttacgggt tcgggacggg cttgcaggat gtagagtttg
1301 ccgtccaagc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgccc ctcagtaatt tcttcgctcg
1401 taatggagaa gcggttgccg tcttcctcgg ggacatcgac gttgggtacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtgttttga
1501 acccatggtt ttacgcagga tggcgggcgt gcccggttg agcgtgggtt
1551 tgaacacatr aaattcgtcc ggggtgaccg caccttgatc gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
  1  MVGXALTADA DIFVLLAAGG DGKVQHFDG RVAFVKRFGY QAAVAVETEG
 51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101  DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRR
151  TEAQHRVFFM RFVYVAADQV GVFGFVGVGH TDDGFTRINR CGQCRHAFGD
201  FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QQXFGVDTDL AVDDKFHTRQ
251  ADAFAGQVGE AECEFGIADV HHDIFYRCFRH IVXGDIGNLY VQQTGIDKAG
301  IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAAVGNDGR
351  STFHHGFPIR IGHVGVNEYVA GFDGIHLGSI FNQAHALTD FLTDGAAPAX
401  YGFVAVDGEA AQVAVALFLG FYGFTGLQD VEFVQAVAS PFDIHRAAVV
451  PFDGQCVMRQ LSNFFVGNGE AVAVFLGDD VGYFTGFCF VGKNHDFVFX
501  THGFTQDQGL ARFERGFEXH KFRVRDRTLY DVFAQTVRGG NKDDLIVXGF
551  GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

m501/g501

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
g501	MVGRTLTADTDIFVLLAAGGDGKMQHFDGRVAFVKRFGHQAQAVSVEAEGQLGHVVRADG					
	10	20	30	40	50	60
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
g501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQCLNHCFGFAQSADERNHDFDVG					
	70	80	90	100	110	120
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRITTEAQHRVFFMRVYVAADQGVFGFVGVGH					
g501	QTHFVTNAFQGFQGETVFEALGNITRRITTEAQHRVFFMRVYAAADQGVFGFVGVGH					
	130	140	150	160	170	180
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQXFGVDTDL					
g501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQXFGVDTDL					
	190	200	210	220	230	240

733

g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAADNFRFQFVVLVFKFQQGFRVDADL
	190 200 210 220 230 240
m501.pep	250 260 270 280 290 300
	AVDDKFHTRQADAFAGQVGEAECEFGIADVHDFYRCFRHIVXGDI GNLYVQQTGIDKAG
g501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHDFYRCFRHIVXGDI GNLYVQQAGIDKAG
	250 260 270 280 290 300
m501.pep	310 320 330 340 350 360
	IAFGTGYGNFLT V FQQFGC IAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPPIR
g501	IAFGTGYGNFLT V FQEFGR IAAADDGRNTQFARDDGGVAGASAAVGHGSGSTFHHGFPPIR
	310 320 330 340 350 360
m501.pep	370 380 390 400 410 420
	IGHVGNQYVAGFDGIHLGSI FNQAH LALTDFLTDGA AFXYG FVAVDGEAAQVAVALFLG
g501	IGHVGNQYVAGFDGIHLGSI FNQAH LALTDFLTDGTTFAQDGF FAVDGVAAQVA AAFVFLG
	370 380 390 400 410 420
m501.pep	430 440 450 460 470 480
	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDGGQVMRQLSNFFVGNGEAVAVFLGDID
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDGGQVVCQLGDF FVGNGEAVAVFFGDFD
	430 440 450 460 470 480
m501.pep	490 500 510 520 530 540
	VGYGFTGFCFVGKNHFDVFXTHGFTQDGG LARFERGF EHXK FVRVDR TLYDVFAQTVRGG
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGF EHIK FVRVDR ALYDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	550
	NKDDLIVXGFGVEGEHHT
g501	NKDDLIVVAGFGVEGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq (partial)

```

1  ATGGTCGGAC GGGCCTTGAC CGCAGATGCC GACATATTG TTCTGCTTGC
51  GGCAGGCGGA GATGGCAAGG TGCAGCATCA CTTTGACGGC AGGGTTGCGT
101 TCGTCAAACG ATTCGGATAC CAAGCCGCTG TCGCGGTCGA GACCGAGGGT
151 CAGTTGGGTC ATGTCGTTTC AGCCGATGGA GAAGCCGTCG AAGTATTGCA
201 GGAATTGTTC CGCCAATACC GCGTTGCTCG GCAGCTCGCA CATCATAATC
251 AGGCGCAGGC CGTTTTTGCC GCGTTCCAAG CCGTTTTCTT TCAGGGCTTT
301 GACAACGGCT TCGGCTTCGC CCAAAGTGCG GACGAACGGA ATCATGATTT
351 CAACGTTGGT CAACCCATT TCATCGCGGA CGCGTTTCAA GGCTTTGCAT
401 TCCAAGGCGA AACAGTCTTT GAAGTTGTCG GCGACATAAC GCGCCGCACC
451 ACGGAAGCCC AACATCGGGT TTTCTTCATG CGGTTTCGTAT ACGTTGCCGC
501 CGACCAGGTT GCGTATTTCG TTGGATTTGA AGTCGGACAT ACGGACGATG
551 GTTTTACGCG GATAAACCGA TCGCGCCAAT GTCGCCACGC CTTCCGGCAT
601 TTTATCGACG TAGAAGTCGA CAGGGGACGC GTAACGGCGG ATACGGCGGG
651 TAATTTCCGC TTTTAATTCG TCGTCTTGTT TGTCAAATTC CAACAAGGCT
701 TTGGGGTGGA TACCGATTTC GCGGTTGATG ATAAATTCCA TACGCGCCAA
751 GCCGATGCCT TCGCTGGGCA GGTGGCGGAA GCTGAATGCG AGTTCGGGAT
801 TGCCGACGTT CATCATGACT TTTACAGGTG CTTTAGGCAT GTTGTCAAA
851 GCAACATCGG TAATTTGTAC GTCCAGCAGG CCGGAGTAGA TGAAGCCGGT
901 ATCGCCTTCG GCACAGGATA CGGTAACCTC TTGACCGTTT TTCAGCAATT
951 CGGTTGCATT GCCGCAGCCG ACAACGGCAG GAATACCCAG TTCGCGCGCG

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734

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1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGTT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTGCGACAA
1201 GACGGTTTTT TCGCCGTGA TAGAAAAGCG GCGCAGGTG CGGCTGCCTT
1251 CTTCTGGGA TTTGACGGT TCGGGACGGG CTTGCAGGAT GTAGAGTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTCGATG TCCATCGGGC GGCCGTAGTG
1351 TTTTTCGATG GTCAGTGGT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGGTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGATC GACGTTTTCG
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGGTTCG AACCGGATTC
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

```

a501.pep
1 MVGRALTADA DIFVLLAAGG DGKVQHFDG RFAFVKRFGY QAAVAVETEG
51 QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFVGFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR F*FVVLVVKF QQGFVVDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH VVQSNIGNLY VQAGVDEAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHGDDG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAFAAQ
401 DGFFAVDRKA AQVAAFFLG FDGFGTGLQD VEFVQAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVNGE AVAVFFGDI VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFGIDCALY DVFAQTVG*S DKDDLVTGTG
551 GIEGEHH

```

m501/a501 90.3% identity in 557 aa overlap

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
a501	MVGRALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
a501	EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFVGH					
a501	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFVGH					
	130	140	150	160	170	180
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTDAGNFRFXFVVLVVKFQQGFVVDL					
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTDAGNFRFXFVVLVVKFQQGFVVDL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVVQSNIGNLYVQAGVDEAG					
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVVQSNIGNLYVQAGVDEAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m501.pep	IAFGTGYGNFLTIVFQQFGCIAAADNGRNTQFARDGGVAGTAAVGNDRSTFHHGFPPIR					
a501	IAFGTGYGNFLTIVFQQFGCIAAADNGRNTQFARDGGVAGTAAVGNDRSTFHHGFPPIR					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m501.pep	IGHVGN EYVAGFDGIHLGSI FNQAH LALTD FLTDGAA FAXYGFVAVDGEAAQVAVALFLG					
a501	VGHVGNQYVAGFDGIHLGSI FNQAYLALTD FLTDGAAFAQDGF FAVDRKAAQVAAAFFLG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m501.pep	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDGGCVMRQLSNFFVGNGEAVAVFLGDID					
a501	FDGFGTGLQDVEFAVQAVASPFVDHRAAVVFFDGGCVMRQLGDFVGNGEAVAVFFGDID					
	430	440	450	460	470	480
	490	500	510	520	530	540
m501.pep	VGYGFTGFCFVGKNHFDVFXTHGFTQDGLARFERGFENXKFVRVDRTLVDVFAQTVRGG					
a501	VGYRFAGFCFVGKNHFDVFXAHGFAQDGRFACFQRFGEHIEFVGIDCALYDVFAQTVGXS					
	490	500	510	520	530	540
	550	559				
m501.pep	NKDDLIVXGFGVEGEHHTX					
a501	DKDDLVTGFGIEGEHH					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

```

g502.seq
1  atgatgaaac cgcacaacct gttccaattc ctcgccgttt gctccctgac
51  cgtcgccgtc gcttcgcgac aggcggggcgc ggtggacgcg ctcaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca aaccgtccaa
151 agcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgccc
201 gggcctcttc aaatgggaat acactttgcc ctacagacag actattgtcg
251 gcgacgggtca aaccgtttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcggcggc agccccgccg ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcaacg cccaaacgca acaacgccgg
451 ctaccaatac atccgcatcg gcttcaaagg cggcaacctc gccgccatgc
501 agcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

```

g502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG IGSFTQTQVQ
51  SKKKKTQTAHG TFKILRPGLF KWEYTLPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RNAQTQQR
151 LPIHPHRLQR QPRRHAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

```

m502.seq
1  atgatgaaac cgcacaacct gttccaattc ctcgccgttt gctccctgac
51  cgtcgccgtc gcttcgcgac aggcggggcgc ggtagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca amccgtccaa
151 wgcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgacc
201 gggccttttc aaatgggaat acaccaaact t.acaggcaa accatcgctc
251 gcgacgggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc catagggcgc agccccgccg ccatcctgtc
351 gaacaaarcc gccctcgaaa gcagctacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgcccgtta
451 ccaatacatc cgcacgggct tcaaaaggcg caacctcgcc gccatgcagc
501 tyaa

```

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

```

m502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG IGSFTQXVQ
51  XXXKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGX SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQQRRL
151 PIHPHRLQR QPRRHAA

```

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLTPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502.seq

```

1  ATGATGAAAC CGCACAACT GTTCCAATC CTCGCCGTTT GCTCCCTGAC
51  CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCT AAGACCAGGC CATAGCGGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG GGCAACGCCC AAACGCAACA ACGCCGGCTA
451 CCAATACATC CGCATCGGCT TCAAAGGCGG CAACCTCGCC GCCATGCAGC
501 TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502.pep

```

1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51  SKKKKTQTAHG TFKILRPGLF KWEYTSPIYKQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV GNAQTQQRRL
151 PIHPHRLQRR QPRRHAA*

```

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSPIYKQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

## g502-1.seq

```

1 ATGatGAAAc cgcaCaacct gttccaaTtC CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGCGGGGCGC GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTC AAATGGGAAT ACACTTTGCC CTACAGACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATCGGCGGC AGCCCCGCGC CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGTTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CGGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

## g502-1.pep

```

1 MMKPHNLQFQ LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51 SKKKTQTAHG TFKILRPGLF KWEYTLPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

## m502-1.seq

```

1 ATGATGAAAC CGCACAACTT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGCGGGGCGC GGTAGACGCG CTTAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGACC
201 GGGCCTTTTC AAATGGGAAT ACACCAAACC TTACAGGCAA ACCATCGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATCTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCGC CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGTTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

## m502-1.pep

```

1 MMKPHNLQFQ LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51 SKKKTQTAHG TFKILRPGLF KWEYTKPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLQFQ	LAVCSLTVAV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVO	SKKKTQTAHG
g502-1	MMKPHNLQFQ	LAVCSLTVAV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVO	SKKKTQTAHG
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLF	KWEYTKPYRQ	TIVGDGQTVW	LYDVDLAQVT	KSSQDQAIGG	SPAAILSNKT
g502-1	TFKILRPGLF	KWEYTLPYRQ	TIVGDGQTVW	LYDVDLAQVT	KSSQDQAIGG	SPAAILSNKT
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKED	GSSNGIDYV	LATPKRNNAG	YQYIRIGFKG	GNLAAMQLKD	SFGNQTSISF
g502-1	ALESSYTLKED	GSSNGIDYV	VRATPKRNNAG	YQYIRIGFKG	GNLAAMQLKD	SFGNQTSISF
	130	140	150	160	170	180

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```

                190      200
m502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||||
g502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACT GTTCCAATC CTCGCCGTTT GCTCCCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCGAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCGC CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51 SKKKTQTAHG TFKILRPLGF KWEYTSFYKQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIIG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep    MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVOQSKKKTQTAHG
                |||||
m502-1        MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVOQSKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep    TFKILRPLGFKWEYTSFYKQTIVGDGQTVWLYDVDLAQVTKSSQDQAIIGGSPAAILSNKT
                |||||
m502-1        TFKILRPLGFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIIGGSPAAILSNKT
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep    ALESSYTLKEDGSSNGIDYVLTATPKRNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
                |||||
m502-1        ALESSYTLKEDGSSNGIDYVLTATPKRNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
                130     140     150     160     170     180

                190     200
a502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||||
m502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgctcgcatc ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaagggcgt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggaac cgtcttcgac atccaatttt
151 gccagagcgg cggaaatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggttag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSSTSNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

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m503.seq  
 1 atgtccgcac cgccggcatc ggcaaccatt ttgttccatg cgcgttcgat  
 51 ttcggcatcg agctgttcgg ggaaggcgt atccaaaatc cattggcgga  
 101 tttctttgcc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt  
 151 gccagtgcgg cggaatgcg ttcgctcaga ccgttgtgtg cgaggaatgc  
 201 gcggtag

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

m503.pep  
 1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNNF  
 51 ASAAEMRSLR PLCARNAR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

m503/q503

	10	20	30	40	50	60
m503.pep	MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNNFASAAEMRSLR					
	:  :					
g503	MSAPSASVILFHAASISASSCSGKGVSKIHWRIPLTRASSETSSTSNNFARAAEMRSFR					
	10	20	30	40	50	60

	69
m503.pep	PLCARNAR
g503	PLCARNAR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

a503.seq  
 1 ATGTCCGCGC CGCCGGCATC GGCAACCATT TTGTTCATG CCGCTTCGAT  
 51 TTCGGCATCG AGCTGTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA  
 101 TTTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT  
 151 GCCAGTGGCG CGGAAATGCG TTCGCTCAGA CCGTTGTGTG CGAGGAATGC  
 201 GCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

a503.pep  
 1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNNF  
 51 ASAAEMRSLR PLCARNAR\*

m503/a503 100.0% identity in 68 aa overlap

	10	20	30	40	50	60
m503.pep	MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNNFASAAEMRSLR					
	:  :					
a503	MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNNFASAAEMRSLR					
	10	20	30	40	50	60

	69
m503.pep	PLCARNARX
a503	PLCARNARX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

g503-1.seq  
 1 ATGGCGCGGT CGTTGTACAG GGAGCGGAAA ACGTGGCGCA TCGCTTTTTT  
 51 AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA  
 101 ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG  
 151 GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTGTTC ATGCCGCTTC  
 201 GATTTCCGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC  
 251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG AAACGCTCTC GACATCCAAT  
 301 TTTGCCAGAG CGGCGGAAAT GCGTTCGTTC AGACCGTTGT GTGCGAGAAA  
 351 TGCGCGGTAG



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This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

## g503-1.pep

```

1  MARSLYREAK TWRI AFLTSL KPLIFRKVSC WPANDASGRS SAVAERTAT
51  EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FARAAEMRSF RPLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

## m503-1.seq

```

1  ATGGCACGGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
51  AACGTTATCC AAGCCGTTGA TGTTCAGAA GGTTCCTGT TGTCCAGCGA
101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG
151 GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTGTGTTCC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

## m503-1.pep

```

1  MARSLYREAN TWCIASLTSL KPLMFKKVSC CPANDASGRS SAVAERTAT
51  EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRI	AFLTSLKPLIFRKVSCWPANDASGRSS	SAVAERTATE	MSAPSASVI		
m503-1	MARSLYREANTWCI	ASLTSLKPLMFKKVSCCPANDASGRSS	SAVAERTATE	MSAPPASAT		
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCS	GKGVSKIHWRISLPTRASSETSSSTN	FASAAEMRSLRPLCARNARX			
m503-1	ILFHAASISASSCS	GKGVSKIHWRISLPTRASSETSSSTN	FASAAEMRSLRPLCARNARX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

## a503-1.seq

```

1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT
51  AACGTTTTCC AAGCCGTTGA TATTCAGGAA GGTTCCTGT TGGCCGGCAA
101 ATGATGCGTC GGCAGGTCT TCGGCGTTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCCG CGCCGCCGGC ATCGGCAACC ATTTGTGTTCC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTGTCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

## a503-1.pep

```

1  MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAERTAT
51  EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRI	ASLTFSKPLIFRKVSCWPANDASGRSS	SAVAERTATE	MSAPPASAT		
m503-1	MARSLYREANTWCI	ASLTSLKPLMFKKVSCCPANDASGRSS	SAVAERTATE	MSAPPASAT		
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCS	GKGVSKIHWRISLPTRASSETSSSTN	FASAAEMRSLRPLCARNARX			
m503-1	ILFHAASISASSCS	GKGVSKIHWRISLPTRASSETSSSTN	FASAAEMRSLRPLCARNARX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

```

g504.seq
1  atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggg gagaaactcg agcgcacccat ccgcgtgaac
151 catcctttga ccttgcacgg catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttggaa
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaaac ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgtgta ccgcatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccggtttt gcaggacaaa gattatTTTT
551 ggctgaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagcgccacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatgta aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgacccggt cgccgggtgc gcttttggtc tatctcggct cggtatgtgt
1101 ggttttgggt acagtattta tgttttatgt gcccaaaaaa cgggctgggg
1151 tattgttttc aaacdgcaaa atccgttttg ctatgtcttc ggcccgcagc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

```

g504.pep
1  MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFAWNLK DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKES LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQODKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLHLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFVVPKK RAWVLFNSKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

```

m504.seq..
1  atatttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggg gagaaactcg agcgcacccat ccgcgtgaac
151 catcctttga ccttgcacgg catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttggaa
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaaac ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccggtttt gcaggacag gattatTTTT
551 ggattaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagcgccacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatgta aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgtc gggtttgcag

```

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```

1051 atgaccggtt ccccggtgc gcttttggtc tatctcggct cgggtgctgtt
1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtg99
1151 tattgttttc agacggcaaa atccggtttg ccatgtcttc ggcccgacg
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg
1251 gctcggcaag gacttgaatc atga

```

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

```

m504.pep..
1  ILVQDLPPFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLLS MDAYTGLTEY PAPMLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERDLQKEFPK HVESLQRLGK DLNHD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng)

from *N. gonorrhoeae*:

m504/g504

	10	20	30	40	50	60
m504.pep	ILVQDLPPFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERIRVNHPLTLHGITI					
	:					
g504	MLVQDLPPFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERIRVNHPLTLHGITI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m504.pep	YQASFADGGSDDLTFKAWNLGDASREPVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
g504	YQASFADGGSDDLTFKAWNLGDASREPVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
g504	MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPILQDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m504.pep	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI					
g504	DYFWLTGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKDAPAEI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m504.pep	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQDKMQGYFYEMLYGVMNAALDETIR					
g504	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKGQDKMQGYFYEMLYGVMNAALDETIR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m504.pep	RYGLPEWQQDEARNRFLLSMDAYTGLTEYPAPMLQLDGFSEVRSSGLQMTRSPGALLV					
g504	RYGLPEWQQDEARNRFLLSMDAYTGLTEYPAPMLQLDGFSEVRSSGLQMTRSPGALLV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m504.pep	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK					

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g504 YLGSVLLVLGTVFMFYVPKKRAWLFSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK  
 370 380 390 400 410

m504.pep DLNHD  
 |||||  
 g504 DLNHD  
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq  
 1 ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAAGTAAAA AATTCCATAT  
 51 CGATTTTAC AATACGGGTA TGCCGCGCGA TTTTGCCAGT GATATTGAAG  
 101 TAACGGATAA GGCAACCGGT GAGAACTCG AGCGCACCAT CCGCGTGAAC  
 151 CATCCTTTGA CCTTGCACGG CATCACGATT TATCAGGCGA GTTTTGCCGA  
 201 CGGCGGTTCG GATTGACAT TCAAGGCGTG GAATTTGGGT GATGCTTCGC  
 251 GCGAGCCTGT CGTGTGAAG GCAACATCCA TACACCAGTT TCCGTTGGAA  
 301 ATTGGCAAAC ACAATATATCG TCTGAGTTC GATCAGTTTA CTTCTATGAA  
 351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAAAAAGC CTGAAATCCA  
 401 CGCTGAACGA TGTCGCGGCC GTTACTCAGG AAGGTAAAAA ATACACCAAT  
 451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GGCAGGCGGT  
 501 CGAATATAAA AACTATATGC TGCCGGTTT GCAGGAACAG GATTATTTT  
 551 GGATTACCGG CACGCGCAGC GGCTTGACAG AGCAATACCG CTGGCTGCGT  
 601 ATCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCGTGA  
 651 GTTTTGAAGA GATGGGAAG GCGCAAACG TCTGGTTGCC GACGCAACCA  
 701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGTGGC TGCGGAAAAC  
 751 ACGCTGAACA TCTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT  
 801 TACGTCCAAT ATCCGAAAG AGCAGCAGGA TAAGATGCAG GGCTATTCT  
 851 ACGAAATGCT TTACGGCGTG ATGAACGCTG CTTGGATGA AACCATACGC  
 901 CCGTACGGCT TGCCGAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCCT  
 951 GCTGCACAGT ATGGATGCGT ACACGGGTT GACCGAATAT CCCGCGCCTA  
 1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TGCGTTCGTC GGGTTGTCAG  
 1051 ATGACCGGTT CCCCGGGTGC GCTTTGGTTC TATCTCGGCT CGGTGCTGTT  
 1101 GGTATTGGGT ACGGTATTGA TGTTTTATGT GCGCGAAAAA CGGGCGTGGG  
 1151 TATTGTTTTC AGACGGCAA ATCCGTTTTC CCATGTCTTC GGCCCGCAGC  
 1201 GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG  
 1251 GCTCGGCAAG GACTGAATC ATGACTGA

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep  
 1 ILVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN  
 51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE  
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKES LKSTLNDVRA VTQEGKKYTN  
 151 IGFSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR  
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMMLAEN  
 251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR  
 301 RYGLPEWQQD EARNRFLHS MDAYTGLTEY PAPMLQLDG FSEVRSSGLQ  
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWLFSQDGK IRFAMSSARS  
 401 ERDLQKEFPK HVESLQRLGK DLNHD\*

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
a504	ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
	10	20	30	40	50	60
m504.pep	YQASFADGGS DLTFKAWNLGDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
a504	YQASFADGGS DLTFKAWNLGDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
m504.pep	MSEGAREKES LKSTLNDVRAVTQEGKKYTNIGFSIVYRIRDAAGQAVEYK NYMLPVLQEQ					
a504	MSEGAREKES LKSTLNDVRAVTQEGKKYTNIGFSIVYRIRDAAGQAVEYK NYMLPVLQEQ					
	130	140	150	160	170	180
m504.pep						

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|||||
a504 MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ
      130      140      150      160      170      180

      190      200      210      220      230      240
m504.pep DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
      |||||||
a504 DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
      190      200      210      220      230      240

      250      260      270      280      290      300
m504.pep REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
      |||||||
a504 REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
      250      260      270      280      290      300

      310      320      330      340      350      360
m504.pep RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
      |||||||
a504 RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
      310      320      330      340      350      360

      370      380      390      400      410      420
m504.pep YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
      |||||||
a504 YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
      370      380      390      400      410      420

m504.pep DLNHDH
      |||||
a504 DLNHDH

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

```

g505.seq
1 atgtttcgtt tacaattcag gctgtttccc cctttgcgaa ccgccatgca
51 catcctgttg accgccctgc tcaaatgcct ctccctgctg tcgctttcct
101 gtctgcacac gctgggaaac cggctcggac atctggcgtt ttacctttta
151 aaggaaagacc gcgcgcgcat cgtcgccaat atgcggcagg cgggtttgaa
201 ccccgacacg cagacggtca aagccgtttt tgcggaaacg gcaaaatgcg
251 gtttgaact tgcccccgcg tttttcaaaa aaccggaaga catcgaaaca
301 atgttcaaa cggtacacgg ctgggaacac gtgcagcagg ctttggacaa
351 gggcgaaggg ctgctgttca tcacgcgcga catcggcagc tacgatttgg
401 gcggacgcta catcagccag cagcttccgt tccacctgac cgccatgtac
451 aagccgcca aaatcaaagc gatagacaaa atcatgcagg cgggcagggt
501 gcgcggcaaa ggcaaaaccg cgcccaccgg catacaaggg gtcaaaacaaa
551 tcatcaaggc cctgcgcgcg ggcgaggcaa ccatcatcct gcccgaaccac
601 gtcccttctc cgcaggaagg cggcggcgtg tgggcggatt ttttcggcaa
651 acctgcatac accatgacac tggcggcaaa attggcacac gtcaaaggcg
701 tgaaaaccct gtttttctgc tgcgaacgcc tgcccagcgg acaaggcttc
751 gtgttgaca tccgccccgt ccaaggggaa ttgaacggca acaaagccca
801 cgatgccgcc gtgttcaacc gcaataccga atattggata cgccgttttc
851 cgacgcagta tctgtttatg tacaaccgct ataaaacgcc gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

```

g505.pep
1 MFRLQFRLFP PLRTAMHILL TALLKCLSL SLSCLHTLGN RLGHlafyll
51 KEDRARIVAN MRQAGLNPD TQVKAVFAET AKCGLELAPA FFKKPEDIET
101 MFKAHVHWEH VQALDKGEG LLFITPHIGS YDLGGYISQ QLPFHLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTGIQG VKQIIKALRA GEATIILPDH
201 VPSPQEGGGV WADFFGKPAY TMTLAAKLAH VKGVKTLFFC CERLPDGQGF
251 VLHIRPVQGE LNGNKAHDAA VFNRTYEWI RRFTQYLFM YNRYKTP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

745

m505.seq (partial)

```

1  GGCATGTTTC GTTACAATT CAGGCTGTTT CCCCTTTGTC GAACCGCCAT
51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151 TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCCGAC CCCAAACGG TCAAAGCCGT TTTTGGGAA ACGGCAAAAG
251 GCGGTTTGA ACTTGCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTC AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTTGA
351 CAAACACGAA GGGCTGCTAT TCATCAGGCC GCACATCGGC AGCTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
451 TCAGAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTCGCGGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
601 ACGTCCCTC CCCTCAAGAA GCGGGGGAAG GCGTATGGGT GGATTTCTTC
651 GGCAACCTG CCTATACCAT GACGCTGGCG GCAAAATTGG CACACGTCAA
701 AGGCGTAAA ACCCTGTTTT TCTGTGCGA ACGCCTGCCT GGCGGACAA
751 GTTTCGATTT GCACATCCGC CCCGTCCAAG GGAATTGAA CGGCGACAAA
801 GCCCATGATG CCGCGTGTT CAACCGCAAT GCCGAATATT GGATACGCGC
851 TTTCCGACG CatATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCLHTLGN RLGHlafYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLAPA FFRKPEDIET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAI DKIMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGG EG VVWDFFGKPA YTMtLAAXLA HVKGvKTLFF CCERLPGGQG
251 FDLHIRPVQ G ELNGDKAHDA AVFNrNAEYW IRRFPthI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCLHTLGN	RLGHlafYLL	KEDRARIVAN
g505	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	SLSCLHTLGN	RLGHlafYLL	KEDRARIVAN
	10	20	30	40	50	60
m505.pep	MRQAGLNPD	P KTVKAVFAET	AKGGLLAPA	FFRKPEDIET	MFKAVHGW	EHVQQALDKHEG
g505	MRQAGLNPD	TQTVKAVFAET	AKGGLLAPA	FFRKPEDIET	MFKAVHGW	EHVQQALDKHEG
	70	80	90	100	110	120
m505.pep	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAI	DKIMQAGR	VRGKGKTAPTSIQG
g505	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAI	DKIMQAGR	VRGKGKTAPTSIQG
	130	140	150	160	170	180
m505.pep	VKQIIKALRS	GEATIVLPDH	VPSPQEGG	EG VVWDFFGK	PAYTMTLA	AXLAHVKGvKTLFF
g505	VKQIIKALRS	GEATIVLPDH	VPSPQEGG	-GVWDFFGK	PAYTMTLA	AKLAHVKGvKTLFF
	190	200	210	220	230	240
m505.pep	CCERLPGGQ	GFDLHIRPVQ	GELNGDKA	HDAVFNrNAEY	WIRRFthI	
g505	CCERLPGGQ	GFDLHIRPVQ	GELNGKHA	DAVFNrNTEY	WIRRFthI	QYLFMYNRYKTP
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

## a505.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTT TCGGAAACG GCAAAAGGCG
251 GTTTGGAAct TGCCCCGCG TTTTTCAGAA AACCAGGAAG CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGCG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAAACCG CGCCTACCAG CATACAAGGG GTCAAAACAAA
551 TCATCAAAGC CCTGCGTTTC GCGGAAGCAA CCATCGTCTT GCCCGACCAC
601 GTCCCTCTCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAGAC CTTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGTC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

## a505.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGHAFYLL
51  KEDRARIIVAN MRQAGMNPDP KTVKAVFAET AKGGLELAPA FFRKPEDIET
101 MFKAVHGEWH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTQYLF MYNRYKMP*

```

## m505/a505 99.0% identity in 287 aa overlap

	10	20	30	40	50	60
m505.pep	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTLGN	RLGHAFYLL	KEDRARIIVAN
a505	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTLGN	RLGHAFYLL	KEDRARIIVAN
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLNPD	KTVKAVFAET	AKGGLELAPA	FFRKPEDIET	MFKAVHGEWH	VQALDKHEG
a505	MRQAGMNPDP	KTVKAVFAET	AKGGLELAPA	FFRKPEDIET	MFKAVHGEWH	VQALDKHEG
	70	80	90	100	110	120
	130	140	150	160	170	180
m505.pep	LLFITPHIGS	YDLGGYISQ	QLPFPPLTAMY	KPPKIKAIK	IMQAGVRGK	GKTAPTSIQG
a505	LLFITPHIGS	YDLGGYISQ	QLPFPPLTAMY	KPPKIKAIK	IMQAGVRGK	GKTAPTSIQG
	130	140	150	160	170	180
	190	200	210	220	230	240
m505.pep	VKQIIKALRS	GEATIVLPDH	VPSPQEGGEG	VWVDFGKPA	YMTLAAXLAH	VKGVKTLFF
a505	VKQIIKALRS	GEATIVLPDH	VPSPQEGGEG	VWVDFGKPA	YMTLAAXLAH	VKGVKTLFF
	190	200	210	220	230	240
	250	260	270	280		
m505.pep	CCERLPGGQ	GFDLHIRPVQ	GELNGDKAHDA	AVFNRNAEYW	IRRFPTQYLF	MYNRYKMPX
a505	CCERLPGGQ	GFDLHIRPVQ	GELNGDKAHDA	AVFNRNAEYW	IRRFPTQYLF	MYNRYKMPX
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

747

## m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCGACCCC AAAACGGTCA AAGCCGTTT TGCGGAAACG GCAAAAGGCG
251 GTTTGGAAC TCCCCCGCG TTTTTCAGAA AACCAGGAAG CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCCGCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGCGAGGT
501 TCGCGGCAAA GGAACAAACC CGCCTACCAG CATAAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGGAAGCAA CCATCGTCTT GCCCGACCAC
601 GTCCCTCCCT CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CAGCTCAAAG
701 GCGTGAAAC CCTGTTTTTC TGCTGGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTCG ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

## m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGLHAFYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLELAPA FFRKPEDTET
101 MFKAVHGWHE VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIKDK IMQAGRVRGK GKTAFTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFFGKPA YMTLAAKLA HVKGVKTLFF CCELRPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRAEYV IRRFPTQYLF MYNRYKMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGLHAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGLHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFRRKPEDTETMPKAVHGWHEVQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKGGLLELAPAFRRKPEDTETMPKAVHGWHEVQALDKHEG					
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTSTIQQ					
g505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTSTIQQ					
	130	140	150	160	170	180
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYMTLAAKLAHVKGVKTLFF					
g505	VKQIIKALRAGEATIIIPDHVPSPQEGG-GVWADFFGKPAYMTLAAKLAHVKGVKTLFF					
	190	200	210	220	230	240
m505-1.pep	CCERLPGGQGFVHLIRPVQGEELNGDKAHDAVFNRAEYVIRRFPTQYLFMYNRYKMPX					
g505	CCERLPDGGQGFVHLIRPVQGEELNGDKAHDAVFNRAEYVIRRFPTQYLFMYNRYKTPX					
	240	250	260	270	280	290

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGLHAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGLHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120



748

m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAHVHGWEHVQQALDKHEG
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAHVHGWEHVQQALDKHEG
	70 80 90 100 110 120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPPLTAMYKPPKIKAIIDKIMQAGVRGKGKTAPTISIQQ
a505	LLFITPHIGSYDLGGYISQQLPFPPLTAMYKPPKIKAIIDKIMQAGVRGKGKTAPTISIQQ
	130 140 150 160 170 180
m505-1.pep	VKQIIKALRSGEATIVLPDHVSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
a505	VKQIIKALRSGEATIVLPDHVSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
	190 200 210 220 230 240
m505-1.pep	CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX
a505	CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX
	250 260 270 280 290 299

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

g506.seq

```

1  ATGGCGGTAT TTGATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
51  TGTCAAACAA AGCCTGTTTC TGCGCGTTCG TCATCAGGTT GAACAAGGCG
101 CGCGGTGGC TGAAGTAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GCGGAAGTCG GGTGTGTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGCGCG GGCCTTGTCG GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGATTG ACGGGGATTT GCGGAAGTT CACACCCAAG CGGTAACGTT
351 GCGCGTCGCG GTAATTGAAC AAACGGGCTT GCAACATTTT ATCCGGGCTC
401 GCGCCGATAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAAACGGA
551 TGATAAGGCA CTTTTTCGGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTT GGGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTGCGGCT
651 GATGGCTTTC GCGGTCGTCG GCGATGATTT TTGCAGCTTC TTCGTTGGTC
701 AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGGAATTTCA CCCAAAAACG
751 TTCGCCCGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGGG CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTGTTGGC
901 GGAACGCATA TTGGTGC GATCGCGTTT GACGGCTTTG TTCAGGTCGG
951 GGAATTTGCG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCACT TGCCTTCTTC GGTATAGAAT TTCAACGCAA AACC CGGAT
1051 GTCGCGTTC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAAAT TTTGGCGCGG
1151 GTGTATTGG TGATGTCGTG TGTTACGGTA AACGTACCGA ACGCGCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1301 CCGGCGGTCA GGCTGTTTTG ATTGTGCGCA ACGGGCGCGC CGTTGTTTCAT
1351 GGTCAGATGG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTTGTTCTCT
1401 TTCTCAGGTT GGTCAAATGG GGGGCAAACG GCTTACAGTA CGATTTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTGAATCG
1501 ACATTTTATT TTCCTTTTGC AAAAATATG GATGCGATTA TACGCCAAGA
1551 TTTTCGTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

g506.pep

```

1  MAVFDEVGRI AHGCGGVVKQ SLFLRVVHVQ EQGARLAEVV VIVLAVVPVC
51  RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGAALS VALVAVNRAT
101 RTIDGLAEV HTQAVTLRVG VIEQTGLQHF IRARADTGNE VARCEGGLFH
151 IGEEVFGLAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFG IGFRHDLVDH

```

m506.seq

1	ATGGCGGTA	TTGATGAAGT	CGGGCGCGTC	GCCCATTCGC	GCGGCGGTGT
51	TGCCGAACAA	TGCTGTTTTC	TGCGCGTCGT	TCATCAGGTT	GAACAGGGCG
101	CGCGGTTGGC	TGAAATAGTC	GTCATCGTCT	TGGCGGTA	CCCAGTGTGC
151	CGCGTCGCGC	TTGATTTTCA	AAGCGGTTTC	GGCGAAATCG	GGTGTGTGCT
201	GCCATTGGCC	GAAGCTGTyG	GGTTCGTAGT	GCGGCGAGGT	GCGCyAGTTG
251	CCGTGCGGCG	GGCCTTGCCC	GTyGCGsTgr	TtTgCTGTgAA	CAsgGCAACG
301	CGGACGATTG	ACGGGAATTT	GGCGGAAGTT	TACGCCCCAA	CGGTAGCGTT
351	GTGCGTCGGC	GTAATTGAAC	AAACGCGCTT	GCAGCATTTT	ATCTsGGCTG
401	GCGCCGACAC	CGGGAATCGG	GTTGCTCGGT	GCGAAGGCGG	ATTGTTCACG
451	ATCGGCGAAG	AAGTTTTCGG	GATTGCGGTT	CTCAACCGGA	TATGAAGGTA
501	CTTTTTCGCG	GTCGTCTTCA	GGCATGACTT	GGATGTACAT	CGTCAACTTC
551	GGAAACTCGC	CGCGTTCGAT	GGCTTCsTAT	AAGTCGCGCT	GATGGCTTTC
601	GCGGTGTCG	GCGATGATT	TGCGGCTTC	TTCGTTGGTC	AGGTTTTTAA
651	TGCCTTGTG	GGTGCGGAAA	TGGAATTTCA	CCCCAAAACG	CTCGGCTGCT
701	TCGTTCCAGA	AGCTGTAGGT	ATGCGAACCG	AAGCGCTGCA	TATGGCCGTGA
751	GCCGCGGGGG	ATGCGCGCGT	CGCTCATCAC	GATGTGAACT	TGGTGCAGTG
801	CTTCGGGCAG	CAGCGTCCAG	AAGTCCCAGT	TGTTTGTGGC	AGAGCGCATA
851	TTGGTGCGCG	GGTCGCGTTT	GACGGCTTTG	TTCAGGTCGG	GGAACCTACG
901	CGGGTCGCGC	AGGAAGAAC	CGGGCGTGT	GTTGCGGACC	ACATCCCAGT
951	TGCCTTCTTC	GGTATAAAAT	TTCAAGGCAA	AACCGCGGAT	GTCGCGTCTT
1001	GCATCGGCTG	GCGCGCGTTC	GCTTCGACAG	GTTGTGAAC	GTCGCAACAT
1051	CTCGGTTTTT	TTGCGCACTT	CGCTGAAGAT	TCCTTTGGCG	TGCATACGGC
1101	GTTCCGGGGAT	GACTTCGCGC	ACGAAGTCGG	CGAGTTTTTC	AGTCATCGCT
1151	CTTGTTCCCT	TTCTCAGGTT	GGTCAAATGG	GGGTAAACGG	CTTACAGTAC
1201	GATTTGGCGG	AAAGCGTATT	CGTAACCCGT	TTCTTGATTG	CAATAAATTT
1251	CTTGAATCGA	CATTTTATTT	CCCTTTTGTA	AAAACATATG	ATGCGACTAT
1301	ACGCGCAAGAT	TTTCGCTATT	AA		

m506, pep

1	MAVFDEVGRV	AHCGGVAAEQ	CLFLRVVHQV	EQGARLAEIV	VIVLAVVPVC
51	<u>RVAVDQRRF</u>	<u>GESGLLLPLA</u>	<u>EAVGFVVRQA</u>	<u>AXVAVGAALP</u>	<u>VAXXAVNXAT</u>
101	RTIDGNLAEV	YAQTVALCVG	VIEQTRLQHF	IXAGADTGNE	VARCEGGLPH
151	IGEEVFVGI	QLEFAHFNRF	IVFPRNFGQ	VKRMIRYFFR	VCFRHLDLVH
201	<u>RPRFKLAIAD</u>	<u>GFXFXALMFA</u>	<u>AVGDDDFGGF</u>	<u>DGNLVQFNALL</u>	<u>QAEEMFHPKT</u>
251	LACFVPEAVG	MRTAEVHMAV	AGDDAAVAHH	FVGLVQCQFGQ	GRPEVPVVCQ
301	RAHIGARVAF	DGFVQVGELT	RVAQEEHGRV	VADHIPVAFF	GIKPQGKTAD
351	VAFICGCAAF	ACHGETGEH	LGFFADPAED	FGAGVPGDVV	RYGKRTERAR
401	TFGVHTAFGD	DFAHEVSQFV	IQPQILRQQR	AARTGGQAVL	IVGNRRVVH
451	GQMGYRAFGG	SHRSCFSFGG	QQMGGKRLTV	RFGGKRIRNR	FLDCNKFLES
501	TFYFPEVKTM	DATIRODFRY	*		

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/q506

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDQRRF					
	:     :       :       :       :       :       :       :       :					
g506	MAVFDEVGRIAHCGGGVVKQSLFLRVVHQVEQGARLAEVVIVLAVVPVCRVAVDQRRF					
	10	20	30	40	50	60

	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGVFVRQAA	XVAVGAALPVAXXAVNXATRT	IDGNLAEVYAQTVALCVG			
g506	GEVGLLLPLAEAVGVFVRQAA	VAVGAALSVALVAVNRATRT	IDGDLAEVHTQAVTLRVG			
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFI	XAGADTGNEVARCEGGL	LFHIGEEVFGIAVQLEFA	HFNRQIRIVFFRPNFGQ		
g506	VIEQTGLQHFI	RARADTGNEVARCEGGL	LFHIGEEVFGIAVQLEFA	HFNRQIRIVFFRPNFGQ		
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVC	FRHDLDVHRPF	RKLAAFDGFX	XVALMAFAVVGDD	FGGFFVGQVFNALL	
g506	VKRMIRHFFGI	GRHDLDVHRPF	RELAAALDGF	VQVALMAFAVVGDD	FCSFFVGQVFNPLL	
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTL	ACFVPEAVGMRTEAVHMA	VAGGDAAVAHHDGNLV	QCFGQQRPEVPVVC		
g506	AAEMEFHPKTF	ARFVPEAVGMRTEAVHMA	VAGGNTAVAHHDGNLV	QCFGQQRPEVPVVC		
	250	260	270	280	290	300
	310	320	330	340	350	360
m506.pep	RAHIGARVAFD	GFVQVGELTRVAQEEH	GRVVADHIPVAFFG	IKFQGTADVAFCIG	CAAF	
g506	GTHIGARIAFD	GFVQVGEFARVAQEEH	GRVVADHIPVAFFG	IEFQRTADVAFRIG	CAAL	
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHL	GFFADFAEDFGAGV	FGDVVRYGKRTERART	FGVHTAFGDDFAHEV	GEFF	
g506	ACHGGETGEHL	GFFADFAENFGAGV	FGDVVVCYGKRTERART	FGVHTAFGDDFAHEV	GEFF	
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQQR	AARTGGQAVLIVGNRA	VVHGMGYRAFGGSHR	SCSFSQVGQMG	GKRLTV	
g506	IQPQILRQQGA	ARAGGQAVLIVGNRA	VVHGMGYGAFGGSHR	SCSFSQVGQMG	GKRLTV	
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNR	FLDCNKFLESTFYFP	FKTMDATIRQDFRY			
g506	RFGGKRIRNR	FLDCNKFLESTFYFP	FAKTMDAIRQDFRY			
	490	500	510	520		

a506.seq

1	ATGGCGGTAT	TTGATGAAGT	CGGGCCGCTC	GCCCATTGCG	GCGGCGGTGT
51	TGCCGAACAA	TGCGCTGTTT	TGCGCGTCTT	TCATCAGGTT	GAACAGGGCG
101	CGCGCTGGCG	TGAAATAGTC	TGCATCGTAGT	TGGCGGTAGT	CCCACTGCGC
151	CGCGTCCGCG	TTGATTTTCA	AAGGCGGTTC	GCGCAAGTCG	GCGTGCTGCT
201	GCCATTGGCC	GAAGCTGTTG	GGTTCGTAGT	GCGGCAGGCT	GCCGTAGTTG
251	CCGTCCGCGC	GTCTTTGTCC	TGCGCGCTAG	TTGCTGTGAA	CAGGGCAACG
301	CGGACGGTTG	ACAGGGATT	GGCGGAAGTT	TACGCCCCAG	CGGTAGCGTT
351	GCGCGTCCGC	GTAAATGAAC	AAACGCGCCT	GCAACATTTT	ATCTGGGCTT
401	GCGCCGACAC	CGGGAACGAG	GTTGCTCGGT	GCGAAGGCGG	ATTGTTCCAC
451	ATCGGCGAAG	AAGTTTTCGG	GATTGCGGTT	CAACTCGAAT	TCGCCCATT
501	CAATCAGCGG	ATAGTCTTTT	TTGCGCCAA	CTTTGGTCAA	GTCAAACGGA
551	TGATACGGCA	CTTTTTCCGC	ATCGGCTTCA	GGCATGACTT	GGATGTACAT
601	CGTCCATTT	GGAACTCGC	ATCGCTCGAT	GCGCTCGTAG	AGGTGCGGCT

751

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651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTGTG GGTGCGGAAA TGGAAATTTCA CCAAAAAACG
751 CTCGCCTGCT TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGTG CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTGTTGGC
901 AGAGCGCATA TTGGTGCAG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTACGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGCA ACAGGCGCGC CGTTGTTTCAT
1351 GGTACAGATGG GTTACAGGGC ATTGGAGGT ANTATCGCT CTTGTTCTCT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQGARLAEIV VIVLAVVPVR
51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTNE VARCEGGLFH
151 IGEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRHDLVDH
201 RPFRLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVCG
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICGAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVH
451 GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF					
a506	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVRRVAVDFQRRF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
a506	GEVGLLLPLAEAVGFVVRQAAXVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVALRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIWAGADTNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
a506	VIEQTRLQHFIWAGADTNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRHDLDVHRPFRKLAALDGFVQVALMAFAVVGDDFGGFFVGQVFNALL					
a506	VKRMIRHFFRIGFRHDLVHRPFRKLAALDGFVQVALMAFTTVVGDDFGGFFVGQVFNALL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
a506	GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
	250	260	270	280	290	300

752

	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGKIFQGKTADVAFICIGCAAF					
a506	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGKIFQGKTADVAFICIGCAAF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQQRARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFSQVGMGGKRLTV					
a506	IQPQILRQQRARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFSQVGMGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTM DATIRQDFRYX					
a506	RFGGKRIRNRFLDCNKFLESTFYFPFVKTM DATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTCCTCTG CTCAGACGG
101 CCTTTGCGCT CTTCTGTGCTT GGCAACGGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTGCT
201 GGGTTTGAA GGCAGCGTTG AGCGTGGCTT GGAATCTTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCGG CCAATTCGGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTC CTCAAGCTGC ACGCGGATT
351 GCTGCTGCTC CTGCGGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGCTTGGTG CAGGTTTTCG CCGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCGT
501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNGLFGMGKL
51  LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
101 LLFFDLQLVF LKLHADLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTAAAGGCTT GGTTCCTCTG TTTCAGACGA
101 CCTTTGCGCT CTTCTGTGCTT GGCAATCGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTGCT
201 GGGTTTGAA GGCAGCGTTG AGCGTGGCTT GGCCTTCTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCGG CCAGCTCGGT
301 TTGTTTTCCT TCGACCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATT
351 GCTGCTGCTC TTGATGAATG CGTTGTAAGT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGCTTGGTG CAGGTTTTCG TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGCTTGTG CTCAATTCAT
501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTQQGG CFLRGGGFGF VGQVXGLVFL FQTTFALFVL GNRLFGMGKL

```

753

51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLLVFG NLHRPFRQLG  
 101 LFFFDLQLVF FKLHADLLLL LMNALXLRLR CLLVAFDALV QVLLMADLFF  
 151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng)  
 from *N. gonorrhoeae*:

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGVXGLVFLFQTTFALFVLGNRLFGMGKLLLLQRQFAAD					
	:         :         :         :         :         :					
g507	MLLPALQQGGGFLSGGGFGLVGQVQLVFLQTAFALFVLGNLFGMGKLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m507.pep	AVCLVLLGLEGGVERGLGFFQFGQTLLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL					
	:         :         :         :         :         :					
g507	AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLLFFDLQLVFLKLHADLLLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m507.pep	LMNALXLRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG					
	:     :         :         :         :         :         :					
g507	LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLAQHAAFVAQFVYCLLLRLFGSLQG					
	130	140	150	160	170	180
m507.pep	VYFVV					
	:					
g507	VYFVI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

a507.seq  
 1 ATGCTCTTGC TGGCTTTGCA ACAAGGCGGC AGCTTCCTGC GCGGCGGGCG  
 51 TTTCGGCTTC GTCAGGCAGA TTCAGGGCTT GGTTTTCCTG TTTCAGACGA  
 101 CCTTTGCGCT CTTCTGTGCT GGCAACGGTT TGTTCCGCAT GGGCAAGCTG  
 151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTGCT  
 201 GGGTTTGGA GGGCGCATTG AGTGTGGCTT GGGTTTCTTC CAATTCGGGC  
 251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCGG CCAATTCGGT  
 301 TTGCTTTTCT TCCGCCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGATT  
 351 GCTGCTGCTC CTGATGGATG CGCTGCATCT GCGCCTGCGC CGCCTGCTTG  
 401 TCGCGTTCGA TCGTGTGGTG CAGGTTTTCG TGATGGCGGA TTTGTTCTTC  
 451 CAAACGGGCA ATCTGTTTCG CAAACACGCC GCGTTTGTG CCAATTCGT  
 501 GCACCGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG  
 551 TCGTTTAA

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep  
 1 MLLLALQQGG SFLRGGGFGF VRQIQGLVFL FQTTFALFVL GNLFMGKGL  
 51 LLLQRQFAAD AVCLVLLGLE GGIECGLGFF QFGQTLFVFG NLHRPFRQFG  
 101 LFFFDLQLVF FKLHADLLLL LMDALHLRLR RLLVAFDALV QVLLMADLFF  
 151 QTGNLFAQHA AFVAQFVHRL LLRLFGSLQG VYFVV\*

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGVXGLVFLFQTTFALFVLGNRLFGMGKLLLLQRQFAAD					
	:         :         :         :         :         :					
a507	MLLLALQQGGSFLRGGGFGFVRQIQGLVFLFQTTFALFVLGNLFGMGKLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

754

```

m507.pep  AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLHRPFRQLGFFFDLQLVFFKLHADLLLL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507       AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQFGLLFFRLQLVFFKLHADLLLL
          70      80      90      100     110     120

          130     140     150     160     170     180
m507.pep  LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
          ||:| ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||
a507       LMDALHLRLRRLVAFDALVQVLLMADLFFQTGNLFAQHAALVAQFVHRLLLRLFGSLQG
          130     140     150     160     170     180

m507.pep  VYFVVX
          |||||
a507       VYFVVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCCTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGAG GGTTCGTACG
101 CGGGCGTATT GCTCCCTGCC CTGTTCTCGA ATCTGCGCGA GTTTTCCTG
151 CACGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGG ACTCGGTTT ATAGCGGAGG
251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
301 GGCATTGTC TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1  MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLRFFLL
51  HGDVFFVQRV YGFGQLVELD VLLVVLELGF IGEGKLLPAF LPVQGLLFEP
101 GDLLPVVFL RVEFVDGDFG KPVLAGVFQK GKLRLFQTAL LLLAAVRGGL
151 LLVFEFGGGF LQSSDVV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGAG GGTTCGACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTCGA ATCTGCGCGA GTTCTCTTG
151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTGGG ACTCGGTTT ATAGCGGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCAAGCTG
301 GGCATTGTC TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLRFFLL
51  HNNIFFVQGL YGFAXFFKLD VLLVVLELGF IGEGKLLPAF LPVEGLLFKL
101 GDLLPVVFL LVEFVDGDFG KPVLAGVFQK GKLRLFQTAL LLLAAVRGGL
151 LLVFEFGGGF LQGNDDV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng)

from *N. gonorrhoeae*:

m508/g508

	10	20	30	40	50	60
m508.pep	MVAFGVDQGGFLLLQQGGLGGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
	:		:		:	:
g508	MVAFGVDQGGFLLLQQGGLGGGLKLRQLGLQGLYAGVLLPALFLNLREFFLHGDVFFVQRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLELGFIGEGKLLAPFLPVEGLLFKLGDLLPVVFLFLVEFVDGDFG					
	:	:		:		
g508	YGFQQLVELDVLVVLELGFIGEGKLLAPFLPVQGLLFEPGDLLPVVFLRVEFVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFGQGGKRLRFQTALLLLAAVRGGLLLVFEFGGFLQGNDDV					
				:		
g508	KPVLAVGFGQGGKRLRFQTALLLLAAVRGGLLLVFEFGGFLQSSDDV					
	130	140	150	160		

```
a508.seq
  1  ATGGTAGCGT  TTGGCGTTGA  TCAGGGCTTC  CTGCTGCTGC  AACAGGGCGG
  51  TTTGGGTGGC  GGCCTCAAGC  TCGCGCAGCT  TGTTTTCGAG  GTTTGTAGCT
101  CGGGCGTATT  GTTGTGCTACC  TGCTGCTGTA  ATCTGCGCGA  GTTTCTCTCG
151  TACGACAATA  TATTCTTCGT  CCAAACCTCTG  TACGGCTTCG  CTCAACTCTT
201  CGAGCTTGAT  GFGCTGCTCG  TCGTTTTGGA  ACTCGGTTTC  ATAGGCGAGG
251  GCAAGCTCTT  GCTGGCGTTC  CTGCCAATCG  AAGGTTTGTT  GTTCAAGCTG
301  GGC AATTTGC  TGTGTGTAGT  TTTGTTTTTG  CTGGTTGAGC  GTTGCGGACG
351  CGACTTCGGC  AAGCCCGTAT  TGGCGGTTGG  CTTCCAACAG  GGCAAGCTGC
401  GCCTGTTTCA  GACGACCTTG  CTGCTCTTGG  CGGCTGTGCG  CGGCGGTTTG
451  CTGCTGGTGT  TCGAGTTCGG  CGGCGGCTTC  CTGCAAAATG  GCGATGTCGT
501  CTGA
```

a508.pep

1	MVAFGVDQGF	LLLQGGGLGG	GLKLRQLGLQ	GLYAGVLFPT	LLLNLREFLL
51	YDNIFFVQTL	YGFAQLFDEL	VLLVLELGF	IGEGKLLAF	LPIEGLLFEL
101	GNLLLVLEFL	LVELVDGDFG	KPVLAVGFQQ	GKRLRFQTTL	LLLAARVGG
151	LLVFEFGGGF	LONGDVV*			

	10	20	30	40	50	60
m508.pep	MVAFGVDQGGFLLLQQGGLGGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
a508	MVAFGVDQGGFLLLQQGGLGGGLKLRQLGLQGLYAGVLFPTLLNLREFLLYDNIFFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAFFFKLDVLLVVLELGFIGEGLKLLAFLPVEGLLFKLGDLLPVVLELLVEFVDGDFG					
a508	YGFAQLFELDVLVVLELGFIGEGLKLLAFLPIEGLLFKLGNNLLVVLELLVELVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFQQGKLRLLFQTALLLLAAVRGGLLLVFEFGGGLQGNDDVVX					
a508	KPVLAVGFQQGKLRLLFQTLLLLAAVRGGLLLVFEFGGGLQGNDDVVX					
	130	140	150	160		

q509.seq



756

```

1  atggtcgctg tatgtgatga acgggctgta cagcggacgt tgggtggccca
51  attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgtttag
101 tcttccaagc ctgctgtgtg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgcaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgtcga taagggaacg ttgcaatttt ttcaaatacat cgagaaattt
301 ttgggcccga gcataaggct cgagaaagcc gaatttgag cccatgcccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggg aaggttcttc ggtgcgggcg atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac tttagcgcgg cgatggaaa
501 gcggcagttc gcggtaaagt ttgtcgagtt cgtgcggta aaaacggaac
551 acggcatcgg cgtggcggcg gaaggcaaag cgagggttt cgccagaaac
601 aaacggattg ccgtcgcggg cgccgcggat ccagccgcgg attttaagga
651 tattcggaac gcggacatcg ggataggccg tctgaaagtc gtgtccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg ggaagatgga
751 cacgcccgtt ttgatttcgt cgttgacgct gagtttgtgg cggcgcgttt
801 cgctggtctg ccacaagccc agaagcacgg tgcgatttc gcgcgcagc
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcgttcg gcagcagcg
901 gcggatgcgg cgttgaaat tcaaaacggg ttggcgttc acttcggtc
951 ggtgcgcggg caaaacggcg gtaacggacg tattgtccaa ctgccgctg
1001 accgatttgc cgtcggcttt ccccgctttg agcctgcgga cggtttccgt
1051 caggctgcct tctgctgctg tgtggccggc atcttcgtgg atttggcggc
1101 ggcgttcgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgtgtcgtc ggaagtggac aagagtttga
1251 ccgtttcgac aaccaacggc gaggtctctt cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtccgcccgc aaagccgcgt ccttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctcattgccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcc aaccgttcac actttaacca
1451 ctcattgtccc gaaatgccgt ctgaagtga acgccgccg acggcggcgt
1501 tacaatcgcc cgcaactgtt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctctgctgc ggtacagccg ccacatcctc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
1651 tttggtcgtc ggctcggcg gattgggcgc cgccgccctt gccctatctc
1701 gccgcctcgg gggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1  MVAVCDERAV QRTLVAQFAQ QGGLFLLFVQ AVVVFAQCVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAVAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDFVDA EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAFALRQOR
301 ADAAVEIQNG LALHFGRVRG QNGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVVAG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLRI
451 VQDMQLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVPKCR LKLNAAARRR
501 YNRPQLFFSE HHHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
551 FGRRLRRIGR RRPCFISPPR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1  ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTttttGCT CTTCGTTTCA GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTtt
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTCGGCAAG CAGACGGCTG
251 CCGTTGTGCA TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGCGGTT AGGTTCTTTC GCGCGGGCGC ATTTCTTCGT CGGGCGATTT
451 GTCGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGTT CGCCGCGATA GAAGCGGAAC

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757

```

551  ACGGCATCGG CGTGGCGGCG GAAGGCAAAG CGCAGGGTTT CGGCAGAAAC
601  AAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
651  TGTCGGGAAC GCGGACGCCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701  TTGCGGTAGA GCTTGGGCAG GGCTTCGAAA AAGCTCATCG GGAAGATGGA
751  CACGCCGTTG TTGATTTCTG CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801  CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTGATTtC GCgGCGCAGC
851  CGTGCCAGCG CGTCGGCATT GGTGCAGCGT TCgCGTTGCG GCAACAGTGC
901  GCGGATGCGG CGGTTGAAGC TTAAGACGGT TTGGCGTTGC ACTTCGGTCG
951  GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTGC CGTCGGCTTT CCCCCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGGTTCTGT GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCTGCCA ATTGCGGCAA
1201 TACTTTTTC AATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CTGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAAGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCGCG GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAATTGCA TGATTTTCTT CTCTCGTCTG CCGTAAATAT
1401 TGTAAATGTA CCCCAAATGC CGCATCCGTG CCAAACCGTT CACACTTTAA
1451 CCGCCCGTGT CCCGAAATGC CGTCTGAAGT TGAACGCCGC CCGACGGCAG
1501 CGTTACAATC GCCCGCAACT GTTTTtTtCC GAACATCATC ATGACCACGA
1551 CCGAACACGA CAACGACGAT GCATTCTTGC TGCGGTACAG CCGCCACATC
1601 CTCTTGGACG AAATCGGCAT CGAAGGGCAG CAGAACTTT CCGCCGCGCA
1651 TATTTTGGTC GTCGGCTGCG GCGGTTTGGG TGCCGCCGCA CT.GCCCTAC
1701 CTTGCCGCTT CGGGTGTCGG CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

m509.pep

```

1  MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVFAQCVL EKLGNHIGVF
51  ACVLAQVERH HVKAEHGYGT DEVCQTAFGK QTAAVVDKGT LQFFQIIQKL
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAVGFF GAGDFFVGRF
151 VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201 KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFEKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQDQSVDF AAQPCQRVGI GAAFALRQQC
301 ADAAVEAXDG LALHFGRVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQGXI VGLLFVQLRQ
401 YFFNQCRAVV GSGQEFDCFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNAARRQ
501 RYNRPQLFFS EHHHDHRT RRCIPAAVQ PPHPLGRNRH RRAAETFRRA
551 YFGRRLRRFG CRRTXPTLPL RVSAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng)

from *N. gonorrhoeae*:

m509/g509

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFAQCVLEKLGNHIGVFACVLAQVERH					
g509	MVAVCDERAVQRTLVAQFAQQGGLFLLFVQAVVVFAQCVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m509.pep	HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAFAAHTQTER					
g509	HVEAEHGHGTDEVCQTAFGKQAAAVVDKGTLQFFQIIQKFLGRSIRLEKAFAAHTQTER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m509.pep	ARFAHSARHNVGDGAAVGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
g509	ARFAHSARHNVGNAAVRFFGAGDFFVRRGQCQHYVVVDFDAADGKRQFAVKFVEFAAV					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGFGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
g509	KTEHGIGVAAEGKAQGFARNKRIAVAVAADPAADFDIRNADIGIGRLKVVFHLAVEFGQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFKAHREDGHAVVDFVVDAEFVAARFAGLPQAQDSDVFAAQPQVRVIGAAAFALRQQC					
g509	GFKKAHREDGHAVVDFVVDAEFVAARFAGLPQAQKHGVDFAAQPQVRVIGAAAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m509.pep	ADAAVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFRAAASG					
g509	ADAAVEIQNLALHFGRVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFCCVVAG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m509.pep	FFVDLAAAFVHVFGDVQNLGEQAAGQGXIVGLLFVQLRQYFFNQCRVVVSGQEFDCFD					
g509	IFVDLAAAFVHVFGDIQNLGEQPAKQRQIVGLPFVQLRQYFFNQCRVVVSGQEFDRFD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m509.pep	NQRGFFVQVEVQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNIVNVPQMPHPCQTV					
g509	NQRGFFVQVEVQGLFQKFRVRRQSRVLRIQDMQLHDFPLI-AVNTVNVPQMPHPCQTV					
	430	440	450	460	470	
	490	500	510	520	530	540
m509.pep	HTLTARVPKCRCLKLNAARRQRYNRPQLFFSEHHHDHTRQRRCPAAVQPPHPLGRNRH					
g509	HTLTTHVPKCRCLKLNAARRRRYNRPQLFFSEHHHDDRTRQRRRTPAAVQPPHPLGRNRH					
	480	490	500	510	520	530
	550	560	570			
m509.pep	RRAAETFRRAYFGRRLRRFGCRRTCPTLPLRV SAR					
g509	RRAAEAFRRAYFGRRLRRIGRRRRCPCISPGR SAR					
	540	550	560	570		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1397>:

a509.seq

```

1  ATGGTCGCTG TATGTGATGA ACGGACTGTA CAGTGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGCT TGTTTTGTCT CTTCTGTTGAG GCTGTTGTAG
101 TCTTCCAAGC CTGCGTGTTC GAAAAGCTCG GCAACCACAT CGGCGTGTTC
151 GCCTGCGTGT TGGCGCAGGT CGAGCGGCAT CATGTGGAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTCCGCAAG CAGGCGGCTG
251 CCGTTGTCTGA TAAGGGAATG TTGCAATTTT TTCAAATCAT CGAGAAATTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCAATG
401 GCGCGACGGT AGGGTTCTTC GCGCGGGCGG GTTCTTCTCT CGGCGGATTT
451 GTCGGACAAC GCCATCATAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGTT CGCCACGGTA AAAACGGAAC
551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAA CGCAAGGTTT CGGCAGAAAC
601 GAACGGATTG CCGTCGCGGT CGCCGCGGAT CCAGCCGCCG ATTTTGAGGA
651 TGTCGGGAAC GCGGACATCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCAAAA AAGCTCATCG GAAAGATGGA
751 CACGCCGTTG TTGATTTCGT CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTGATTTTC GCGGCGCAGC
851 CGTGCCAGCG CGTCGGCATT GGTACAGCGT TCGCGTTGCG GCAGCAGCGC

```

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```
901 GCGGATGCGG CGGTTGAAAT TCAAGACGGT CTGGCGTTGC ACTTCGGTCG
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTCG CGTCCGCTTT CCCCCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTGGCGCGC
1101 GCGGTTTCGT GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTTCGTCCA ATTGCGGCAA
1201 TACTTTTTC AATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CCGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCCGC GTCCGCGGCC AAAGCCGCGT CCTTGGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCATTGCCG TAAATACTGT
1401 AAATGTACCT CAAATGCCGC ATCCGTGCCA AACCGTTCAC ACTTTAACCG
1451 CCCGTGTCCC GAAATGCCGT CTGAAGTTGA ACGCCGCCCG ACGGCAGCGT
1501 TACAATCGCC CACAACGTGT TTT.TCCGAA CATCATCATG ACCACGACCG
1551 AACACGACAA CGACGATGCA TTCCTGCTGC GGTACAGCCG CCACATCCTC
1601 TTGGACGAAA TTGGCATCGA AGGGCAGCAG AAACCTTCCG CCGCGCATAT
1651 TTTGGTCGTC GGCTGCGGCG GTTTGGGTGC CGCCG.CCCT GCCCTATCTC
1701 GCCGCTCCG GCATCGGCAC GCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

```
a509.pep
1  MVAVCDERTV QWTLMAQFAQ QGGLFLLFVE AVVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGYGT DEVCQTAFGK QAAAVVDKGM LQFFQIIIEKF
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGNGATVGGF GAGGFFVGRF
151 VGQRHHIAVD FDAADGERQF AVEFVEFATV KTEHGIGVAA EGKTQGFGRN
201 ERIAVAVAAD PAADFEDVRN ADIGIGRLKV VFHLAVELGQ GFKAHRKDG
251 HAVVDFVDA EFVAARFAGL PQAQDSVDF AAQPCQRVGI GTAFALRQQR
301 ADAAVEIQDG LALHFGRVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQG*I VGLLFVQLRQ
401 YFFNQCRVAV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LIAVNTVNVP QMPHPCQTVH TLTARVPKCR LKLNAARRQR
501 YNRPQLFXSE HHDHDRTRQ RRCIPAAVQP PHPLGRNWHR RAAETFRRAY
551 FGRRLRRFGC RXPCPISPLP ASAR*
```

m509/a509 93.0% identity in 575 aa overlap

```

      10      20      30      40      50      60
m509.pep  MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVVFQACVLEKLGNHIGVFACVLAQVERH
          |||||::|:| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a509      MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVVFQACVLEKLGNHIGVFACVLAQVERH
          10      20      30      40      50      60

      70      80      90     100     110     120
m509.pep  HVKAEHGYGTDEVCTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAEFAAHTQTER
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a509      HVEAEHGYGTDEVCTAFGKQAAAVVDKGM LQFFQIIIEKFLCRSIRLEKAEFAAHTQTER
          70      80      90     100     110     120

      130     140     150     160     170     180
m509.pep  ARFAHSARHNVDGAAVGGFAGDFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a509      ARFAHSARHNVGNGATVGGFAGGFFVGRFVGQRHHIAVDFDAADGERQFAVEFVEFATV
          130     140     150     160     170     180

      190     200     210     220     230     240
m509.pep  EAEHGIGVAAEGKAQGFGGRNKRIAVAVAADPAADFEDVRNADIGIGRLKVVFHLAVELGQ
          ::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a509      KTEHGIGVAAEGKTQGFGRNERIAVAVAADPAADFEDVRNADIGIGRLKVVFHLAVELGQ
          190     200     210     220     230     240

      250     260     270     280     290     300
m509.pep  GFKAHREDGHAVVDFVDAEFVAARFAGLPQAQDSVDFAAQPCQRVGIGAAAFALRQQC
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a509      GFKAHREDGHAVVDFVDAEFVAARFAGLPQAQDSVDFAAQPCQRVGIGTAFALRQQR
          250     260     270     280     290     300

      310     320     330     340     350     360
```

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m509.pep	ADA	AVE	AXD	GLA	LHF	GRV	RQNG	NGN	GRIV	QLP	LHR	FAV	GFPR	FEP	PAD	GFR	QAA	FRAA	ASG	
a509	ADA	AVE	I	QD	GLA	LHF	GRV	RQNG	NGN	GRIV	QLP	LHR	FAV	GFPR	FEP	PAD	GFR	QAA	FRAA	ASG
			310			320			330			340			350			360		
m509.pep	FFV	DLAA	AFV	VHV	FGD	VQNL	GEQA	AGQ	GXIV	GLLF	VQLR	QYFF	NQC	RAV	VGS	GQEF	DFCFD			
a509	FFV	DLAA	AFV	VHV	FGD	VQNL	GEQA	AGQ	GXIV	GLLF	VQLR	QYFF	NQC	RAV	VGS	GQEF	DFDRFD			
			370			380			390			400			410			420		
m509.pep	NQR	RGFF	VQ	VE	QGL	FQK	FRV	RQSR	VLW	IVQN	MLHD	FSLS	SAVN	IVNV	PPH	PCQ	TV			
a509	NQR	RGFF	VQ	VE	QGL	FQK	FRV	RQSR	VLW	IVQN	MLHD	FSLI	-AV	NTV	NV	PPH	PCQ	TV		
			430			440			450			460			470			480		
m509.pep	HTL	TAR	VPK	CR	LKL	NAAR	RQRY	NR	PQL	FF	SEH	HH	DH	DR	TRQ	RCIP	AAV	QPPH	PLGR	NRH
a509	HTL	TAR	VPK	CR	LKL	NAAR	RQRY	NR	PQL	FX	SEH	HH	DH	DR	TRQ	RCIP	AAV	QPPH	PLGR	NWH
			490			500			510			520			530			540		
m509.pep																				
a509																				
			480			490			500			510			520			530		
m509.pep	RRA	AE	TFR	RAY	FGR	RLRR	FG	CR	TX	PTL	PL	RV	SAR	X						
a509	RRA	AE	TFR	RAY	FGR	RLRR	FG	CR	XPC	PIS	PL	PAS	AR	X						
			540			550			560			570								

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1  atgccttcgc ggacaccgca gggaaaaagg ggattattcct gcccgaagcg
51  ggatagtgcc ttttggcagg cgttggtccat atcggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggagggttt caataggctcg
151 tggacgacgt tgagcgcggc cataatgacg attttttcgc tgcgcgcgac
201 ggggccgcct tcgcgatgg cttcggcttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcgtgatg acttcgatgt agacttggtc gatgttcac ctttaatcct
351 tattgctgcg tttcctgccg ttgggggagg cgcgctgccg gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1  MPSRTPOGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTTCCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTC AAGGAGGTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGC TGTCCGCGAC
201 GCGTCCGCT TCGCGATGG CTTCCGCTT GCCGTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301 GCGGTGCAwG ACTTCsAtGT GGA CTGTGTC GATGTTTCATC CTTTAATCCT
351 TATTGCTGCG TTTCTGCCA TTGGGGGAGG CGCGTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1  MPSRTPOGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA FQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
g510	MPSRTPQGKRGYSCPKRDSA FQALSISVILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
g510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

```

1  ATGCCTTCGC GGACACCGCA GGGAAAAAGG GGTATTTCCT GCGCCAAGCG
51 GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTC A GGGAGGTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGC TGTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTTGAGC ATCCGACTG
251 CCTGCAACAG TGTGTCTTT TCTTCTGCCG GCGTGTGAC GGTCAGCCGG
301 G.CGTGCATG ACTTCGATGT GGACTTGTTG GATGTTGATC CTTAATCCT
351 TATTGCTGCG TTCCTGCCG TTGGGGGAGG CGCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

```

1  MPSRTPQGKR GYSCAKRDSA FQALSISAI LRAKSPIAKS PPFREVFNR
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 XVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA FQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
a510	MPSRTPQGKRGYSCAKRDSA FQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
a510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRXVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

```

1  atgaaagtgc ttgttttagg tgcgggtggt gccggcgat cctccgtgtg

```

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```

51  gtatctggca gaggccggac atgaagtaac ggtcatcgac cgcaccgagg
101  gtgtggcgat ggaaaccagt tttgccaatg caggccagct ttcttacggc
151  tataccacgc cttgggctgc acccggtatt ccgaccaaag cactgaaacg
201  gctgtttaaa agccatccgc ctttactgtt ccgccctgac ggccggcctgt
251  atcaaatcga atggctgtgg cggatgctgc aaaactgcac ggcaacgcgc
301  tatcaaatca ataaagagcg catggtcagg atttccgaat acagccgtga
351  aatgttccgc cgttttgaag cgcaaacga catgaatttt gagggacgca
401  aaaaaggac gttgcagatt ttccgcaaaa ccgaagaagt cgaagcggca
451  aaacaagaca ttgccgtttt ggaacgctac ggcgtgccgt accgccgtct
501  gaagcccgaa gaatgcgcag aattcgagcc tgcgtggca cgcgttaccg
551  ccaaaattgt cggcggtctg cacctgcctg cggatgcgac cggcgactgc
601  cgcctcttca ccgaaaacct gtacaaattg tgtcaagaga agggggtacg
651  gttctacttc aaccaacca tcagccgcat cgaccacaac gggctgcgca
701  tcaaagccgt tgaaacgaaa caggcggtt tgaacagat gccgttgtct
751  gcgcgctcgg ctgcttcagc aggactgtgt tggcgagtt ggatctcaat
801  ctgccattt atcccgtaa aggcatttcc ttga

```

This corresponds to the amino acid sequence <SEQ ID 1406; ORF 512.ng>:

```

g512.pep
1  MKVLVLGAGV AGVSSVWYLA EAGHEVTVID RTEGVAMETS FANAGQLSYG
51  YTPWAAFGI PTKALKRLFK SHPLLFRPD GGLYQIEWLW RMLQNCTATR
101  YQINKERMVR ISEYSREMF RFEAQTDMNF EGRKKGTLLQI FRQTEVEAA
151  KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIVGGL HLPADATGDC
201  RLFTENLYKL CQEKGVRFYF NQTISRIDHN GLRIKAVETK QGGLKQMPLS
251  ARSAASAGLC WRSWISICPF IPSKAIP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1407>:

```

m512.seq (partial)
1  ..GTTTGGAAAC GCTACGGCGT GCCGTACCGC CGTCTGAAAC CCGAAGAATG
51  TGCAGAATTT GAGCCTGCGC TGGCAGCGT TACCGCCAAA ATTGCCGGCG
101  GCCTGCACCT GCCTGCAGAT GCGACCGGCG ACTggCGCCT CTTCCTGAA
151  AACCTATACA AATTGTGTCA GGAAAAGGGC GTACGGTTTC ATTTCAACCA
201  AAACATCAGC CGCATCGACC ACAACGGGCT GCGCATCAAA ACCGTTGAAA
251  CCAAACAGGG CGGTTTGAAG CAGATGCCGT TGTCTGCGCG CTCGGTTGCT
301  TCAGCAGGAC GGTTTTGGCG CAGTTGGATC TCAATCTGCC CATTTATCCC
351  GTCAAAGGCT ATTCCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1408; ORF 512>:

```

m512.pep (partial)
1  ..VLERYGVPYR RLKPEECAEF EPALARVTAK IAGGLHLPAD ATGDWRLFTE
51  NLYKLCQEK GVRHFHFNQIS RIDHNLRIK TVETKQGGK QMPLSARVA
101  SAGRFRWSWI SICPFIPSKA IP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 512 shows 93.4% identity over a 122 aa overlap with a predicted ORF (ORF 512.ng) from *N. gonorrhoeae*:

```

m512/g512

m512.pep                                10      20      30
                                VLERYGVPYRRLKPEECAEFEPALARVTAK
                                |||
g512      TDMNFEGRKKGTLLQIFRQTEVEAAKQDIAVLERYGVPYRRLKPEECAEFEPALARVTAK
              130      140      150      160      170      180

              40      50      60      70      80      90
m512.pep    IAGGLHLPADATGDWRLFTEENLYKLKQEKGVRFHFNQISRIDHNLRIKTVETKQGGK
              :|||
g512      IVGGLHLPADATGDCRLFTENLYKLKQEKGVRFYFNQTISRIDHNLRIKAVETKQGGK
              190      200      210      220      230      240

              100      110      120
m512.pep    QMPLSARSVASAGRFRWSWISICPFIPSKAIP
              |||
g512      QMPLSARSAASAGLCWRSWISICPFIPSKAIP

```

250                      260                      270

```
a512.seq
1 ATGAAAGTGC TTGTTTTAGG TGCTGGTGTT GCCGGCGTAT CTTCCGCGTG
51 GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCACTGAC CGCGCCGAGG
101 GCGTGGCGAT GGAAACCAGT TTTGCCAACG CAGCCGACCT TTTCTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCCGCG
301 TATCAAAATCA ATAAAGAGCG CATGTCGAGG ATGTCGGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAT GGCGTGCCGT ACCCGCCTCT
501 GAAGCCCGAA GAATGCGCAG AATTGCGAGC TGCGCTGGCA CGCGTTACCG
551 CCAAATTGC CGCGCGCTCG CACCTGCCCC CAGACGCGAC CGCGCACTGC
601 CCGCTCTTCA CTGAAACCTT GTACAAATTG TGTCAAGAAA AGGGCGTACG
651 GTTTCATTTT AACCAAACCA TCAGCGCGAT CGACCACAA CAGGCTGCGCA
701 TCAAAACCGT TGAAACGAAA CAGGCGCGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGCGCGAAGT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

a512.pep

1	MKVLVLGAGV	AGVSSAWYLA	EAGHEVTVID	RAEGVAMETS	FANAGQLSYG
51	YTPWPAAPGI	PTKALKWLFK	SHPPLLFRPD	GSLYQIEWLW	QMLQHCTAAR
101	YQINKERMVR	MSEYSREMFR	RFEAQTGMNF	EGRKKGTLQI	FRQTKEVEAA
151	KQDIADVLER	GVPPYRRKFE	ECAEFEPALA	RVTAKIAGGL	HLPADATGDC
201	RLFTENLYKL	CQEKGVRFHF	NQTISRIDHN	GLRIKTVETK	QGGCLKQMPLS
251	ARSAASAGRF	WGWKISICRF	IPSKAIP*		

```

                                10      20      30
m512.pep                      VLERYGVPYRRLKPEECAEFEPALARVTAK
                                |||
a512      TGMNFEGRKKGTLQIFRQTKEVEAAKQDIAVLERYGVPYRRLKPEECAEFEPALARVTAK
            130      140      150      160      170      180

                                40      50      60      70      80      90
m512.pep    IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGGLK
            |||
a512      IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQITSRIDHNGLRIKTVETKQGGGLK
            190      200      210      220      230      240

                                100      110      120
m512.pep    QMFLSARSVASAGRFWRKSWISICPFIPSKAIPX
            |||
a512      QMFLSARSAASAGRFWRKSWISICRFIPSKAIPX
            250      260      270

```

```
g513.seq
  1  ATGGGTTCGG  CGCCGAACGC  CGCCGCCGCC  GCCGAAGTGA  AACACCCTGT
51  TTCGCAAGGT  ATGATTCAAA  TGCTGGGCGT  GTTTGTCTGA  ACCATCATCG
101 TTTGTTCTTG  CACCGCCTTC  ATCATCTTGA  TTTACCAACA  GCCTTATGGC
151 GATTTTAGCG  GTGCGGCGCT  GAcgcAGGCG  GCGATGTGTA  GCCAAGTGGG
201 GCAATGGGGC  GCGGGTTTCC  TCGCCGTGTA  CCTGTTTATG  TTTGCCTTTT
251 CCACCGTTAT  CGGCAACTAT  GCCTATGCCG  AGTCCAACGT  CCAATTATC
301 AAAAGCCATT  GGCTGATTAC  CGCCGTTTTC  CGTATGCTGG  TTTTGGCGTG
351 GGTCTATTTC  GGCGCGGGTG  CCAATGTGCC  TTTGGTCTGG  GATATGGCGG
401 ATATGGCGAT  GGGCGATCAT  CGGTGGATCA  ACCTCGTCGC  CATCTCGCTG
451 CTCTCGCCat  TGCGTTTAT  GCTCGTGC  GATTACACCG  CCAAGCTGAA
```



501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC  
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep  
 1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQOPYG  
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILEM FAFSTVIGNY AYAESNVQFI  
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL  
 151 LSPLAFMLLR DYTAKLMGK DPEFKLSEHP GLKRRIKSDV W\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq  
 1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCCTGT  
 51 TTCGAAGGT ATGATTCAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG  
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC  
 151 GATTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG  
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT  
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC  
 301 AAAAGCCATT GGCTGATTAC CGCGGTTTTT CGTATGCTGG TTTTGGCGTG  
 351 GGTCTATTTC GCGCGGTTG CCAATGTGCC TTGGTCTGG GATATGGCGG  
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCTGCTG  
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCCG GATTACACCG CCAAGCTGAA  
 501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC  
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep  
 1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQOPYG  
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILEM FAFSTVIGNY AYAESNVQFI  
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL  
 151 LSPLAFMLLR DYTAKLMGK DPEFKLSEHP GLKRRIKSDV W\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

	10	20	30	40	50	60
m513.pep	MGSAPNAAAAAEVKHPVSQGMQMLGVFVDTIIVCSCTAFIILIYQOPYGDLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGMQMLGVFVDTIIVCSCTAFIILIYQOPYGDLSGAALTQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m513.pep	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLRDTAKLMGKDPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLRDTAKLMGKDPEFKLSEHP					
	130	140	150	160	170	180
	190					
m513.pep	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

765

```
1 ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51 CGATCCGATG TGGTCATACT TGGTTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACACCGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTG TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTGGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCAAGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTGTTTCGC CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTTGGGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAAATCGT
651 CGTCCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTAGAT TTTTTCGGGG
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTAAGTCGGG GTCTGATTTC
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CTGTATTCC AACGAGGCGG
851 GTATGGGTTC CGCGCCGAAC GCCGCCGCCG CCGCCGAAGT GAAACACCTT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTG ATACCATCAT
951 CGTTTGTCT TGCACCGCCT TCATCATCTT GATTTACCAA CAGCCTTACG
1001 GCGATTAG CGGTGCGGCG CTGACGAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCCGTC ATCCTGTTTA TGTTCGCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CTTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```
a513.pep
1 MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLEFTVTTG FVQFRLFGRS
51 IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGGPGA
101 VFWMWVTALI GMSSAFVESS LAQLEKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFALSL IFCFGFVFEA VQTNTIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNIPII PDVFQGIFSG
251 AFKFDAAAGG LLGGLISQTM MMGIKRGlys NEAGMGSAPN AAAAAEVKHP
301 VSGQMIQMLG VEVDTIIVCS CTAFLILIYQ QPYGDLGSGA LTQAAIVSQV
351 GQWAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYTAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*
```

m513/a513 100.0% identity in 191 aa overlap

```

                                     10      20      30
m513.pep                               MGSAPNAAAAAEVKHPVSQGMIOQLGVFVD
                                     |||
a513      DAAAGLLGGLISQTM MMGIKRGlysNEAGMGSAPNAAAAAEVKHPVSQGMIOQLGVFVD
          260      270      280      290      300      310

          40      50      60      70      80      90
m513.pep      TIIVCSCTAFIILIYQ QPYGDLGSGAALTQAAIVSQVQWAGFLAVILFMFAFSTVIGNY
          |||
a513      TIIVCSCTAFIILIYQ QPYGDLGSGAALTQAAIVSQVQWAGFLAVILFMFAFSTVIGNY
          320      330      340      350      360      370

          100      110      120      130      140      150
m513.pep      AYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMADMAMGIMAWINLVAILL
          |||
a513      AYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMADMAMGIMAWINLVAILL
          380      390      400      410      420      430

          160      170      180      190
m513.pep      LSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX
          |||
```

a513                      LSPLAFMLLRDYTA KLKMGKDPEFKLSEHPGLKRRIKSDVWX  
                               440                      450                      460                      470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq  
 1 atggttcaaa tacaggttgt gcgcgcgcgc ggcggtgccc gtggtctgca  
 51 ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttcgacaatg  
 101 ccgttttgaa tcacgaagcg cggcgcggtg gcaacacctt ccgcatcaaa  
 151 atagctgctg cggaaagagc gggggatgtg cggttcttcg cgcaggttga  
 201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt  
 251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag  
 301 cccgcccga acggtggtat cgaagaggac ggggtagctg cctgtcggga  
 351 tgctgcggtt gccgagtcgg cgcaaatgac ggcgggcggc ggtttgaccg  
 401 atggtttcgg ggctgtccat atccggatgg cggcagggcg aatcgtaacca  
 451 gtagtcgcgc tgcattccgt ttctgcggc ggcgacgacg ctgcaggaaa  
 501 tgctgtggtg cgtgctttgc cgggtgtcgg caaaaccgtg ggtgttgccg  
 551 taaacgtatt ggtactgtcc ggtttgcacc gccgcgcctt cggagttttc  
 601 gatgcggctg tccgtgtcca acgctgcctg ttcgcattgt ttgccaagc  
 651 cgacggcggc ttccgtatcc aaatccatt cgtggtaaag gtcggggtcg  
 701 ccgatgtgtt gcgccatcaa ctcggggtcg gcaagtccgg cgcaaccgtc  
 751 ttccgcggtg tggcgggcga tgcgcgcggc ggcgcgacg gtgtcgcgca  
 801 gggcttggtt ggagaagtcg cgggtgccgg cgcggccttt gcgtttgccg  
 851 acgtaaacgg taatgtccag cgatttgtcc tgctggaact cgatttgttc  
 901 gatttcgccc aagcgacgc tgacgctttg tccgagcgat tcgctgaagt  
 951 cggttcggc ggcggtcgg cccgctgctt ttgccaagtc gagegtgcgg  
 1001 cggcagaggt cgaggagttc ggaagcgggt tggttgaaca gcataacaat  
 1051 cttctctggt ggagcgttgt ggcattttaa

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep  
 1 MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGNTFRIK  
 51 IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDQ  
 101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP  
 151 VVALHSVFGV GDDAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF  
 201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV  
 251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLELDLF  
 301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEEVEF GSGVVEQHNN  
 351 LSWWSVVF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)  
 1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA  
 51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC  
 101 GCGCCGCCCG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCCGAAAC  
 151 GGTGGTATCG AAGAGGACGG GGTAGCTGCC TGTCGGGATG CTGCGGCTGC  
 201 CGAGTCGGCG CAAAGTGC GGCGCGCGG TTTGACCGAT GGTTCGGGG  
 251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG  
 301 CATGCCGTTT TCGTCGGCG CAACGACGCT GCAGGAAATG CTGTGGTGCG  
 351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTGCGGTA AACGTATTGG  
 401 TAATGGCCCG TTTGCACCGC CGCGCCTTCG GAGTTTTCGA TCGCTCATC  
 451 CTCGTTGAGG GCGGCTGTGT CGCATGTGTT TGCCAAGCCG ACGGCGGCTK  
 501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CGGGGTCGCC GATGTGTTTT  
 551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CGGCGGTGTG  
 601 GCGGGCGATG TCGATGGCG CTTTGACGGT GTCTTGACAG GCTTTTTCGG  
 651 AGAAGTCGGC AGTACTGGCG CGGCCTTTCG GTTTGCCGAC GTAAACGGTA  
 701 ATGTCCAGCG ACTTGTCTCT CTGGAACGCG ATTTGTTsGA TTTsGCCCCAG  
 751 CCGCACGCTG ACGCTTGTG CCAATGATTC GCTGAAATCG GCTTCGGCGG  
 801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGGCGCG GCAGAGGTCTG  
 851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA  
 901 TGCTTTGCGG CATTTTAA

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

767

```

1  ..GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51  GGIEEDGVAA CRDAAAESA QSAAGGGLTD GFGAVHIRMA AGGIVPVVAL
101 HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151 LVQGGLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201 AGDVGDFG VLQGFGEVG STGAAFAD VNGNVQRLVL LELDLXDAQ
251 PHADALSQXF AEIGFGGCA RRFCQVERAA AEVEEFGSGV VEQHRNLSXX
301 CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

m515/g515

```

m515.pep          10      20      30
                  GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                  ::| | | | | | | | | | | | | | | | | |
g515              30      40      50      60      70      80
AEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA

m515.pep          40      50      60      70      80      90
VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
| | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
g515              90     100     110     120     130     140
VERAAGECADEVSDQPARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA

m515.pep          100     110     120     130     140     150
GGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRRAFGVFDALIL
| | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
g515              150     160     170     180     190     200
GGIVPVVALHSVFVGGDDAAGNAVVRALPVCCKTVGVAVNVLVLSGLHRRRAFGVFDAAVR

m515.pep          160     170     180     190     200     210
VQGGFLFALFCQADGGXRIQIPFVVKVGADVDFCHQTGIGKSGATVFGGVAGDVGDFG
| | | | | | | | | | | | | | | | | | : | | : | | | | | | | | | |
g515              210     220     230     240     250     260
VQRCFLFALFCQADGGFRIQIPFVVKVGADVLRHQLGVGKSGATVFGGVAGDVGGGADGV

m515.pep          220     230     240     250     260     270
LQGFGEVVGSTGAFAFADVNGNVQRLVLELDLXDAQPHADALSQXFAEIGFGGCGAR
| | : | | | | : | | | | | | | | | | | | | | | | | : | | : | | |
g515              270     280     290     300     310     320
AQGLFGEVGGAGAAFAFADVNGNVQRFVLELDLFDFAQAHADALSERFAEVGFGGGRAR

m515.pep          280     290     300
RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAF
| | | | | | | | | | | | | | | | | | : | |
g515              330     340     350
CFCQVERAAAEVEEFGSGVVEQHNNLSWWSVAF

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

a515.seq

```

1  ATGGTTCAAA TAAAGTTGT GCGCGCCGCC GCGTTGCCG GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGC CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTCG CCGTGTGCGG CAAAACCGTA GGTGTTGCCG

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551	TAAACGTATT	GGTAATGGCC	GGTTTGCACC	GCCGCGCCTT	CGGAGTTTTC
601	GATGCGCTCA	TCCTCGTTCA	GGCGGCGTTG	TTTCGATTGT	TTTGCCAAGC
651	CGACGGCGGC	TTCGTATACC	AAATCCCAT	CGTGGTAAAG	GTCTGGGGTCG
701	CCGATGTGTT	GCGCCATCAA	CTCGGGGTCG	GCAAGTCCGG	CGCAATCCGC
751	TTCGGGCGTG	TGGCGGCGCA	TGTCNNNNGC	GGGCGGACAG	GTGTCGCGCA
801	GGGCTTGTTT	CGAGAAATCG	GCGGTGCCGG	GCGGCGCTTT	GCGTTTGCCG
851	ACGTAAACGG	TAATGTCCAG	CGACTGTGCC	TGCTGAAACT	CGATTTGTTC
901	GATTTCGCCC	AGCCGCACGC	TGACGGTTTG	TCCCAATGAT	TCGCTGAAAT
951	CGGCTTCGGC	GCGCGTTGCG	CCCCTCGCTT	TTGCCAAGTC	GAGCGTGCGG
1001	CGGCACAGGT	CGAGGATGTC	GGAAGCGGTG	TGGTTGAACA	GCATAGAAAT
1051	CTTTCTTGAT	GATGCTTTGC	GGCATTTTAA		

a515.pep

```

1  MVQIKVVRAA  GVARGLHSEF  ARAVTAEEIA  FDNAVLNHEA  RCGGNAFRIK
51  IAAAERAGDV  RFFAQVEEIG  QDFFADAVDQ  ETALAVEGSA  GCEADVESDK
101  TARNGGIEED  GVVACRDAAA  AESAQSAAGG  GLTDGFGAVH  IRMAAGGIVP
151  VVALHAFVFG  GNDAAAGNAV  RALPVCCKTV  GVAVNVLVMA  GLHRRAGFVF
201  DALILVQGGL  FALFCQADGG  FRIQIPFVVK  VGADVLRHQ  LGVGKSGATV
251  FGGVAGDVXX  GADGVAQGLF  GEIGGAGAAF  AFADVNGNVQ  RLVLKLDLF
301  DFAQPHADAL  SQ*FAEIGFG  GGCARRFCQV  ERAAAEVEEF  GSGVVEQHRN
351  LS**CAAAF*

```

[illegible]

g515-1.seq

1 ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GGC GTTGCCC GTGGTCTGCA

769

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51  TTCGAGTTT  GCGCGCGCTG  TAACTGCCGA  GGAAATAGCC  TTCGACAATG
101 CCGTTTTTGA  TCACGAAGCG  CGGCGCGGTG  GCAACACCTT  CCGCATCAAA
151 ATAGCTGCTG  CGGAAAGAGC  GGGGGATGTG  CGGTTCTTCG  CGCAGGTTGA
201 GGAATCGGG  CAGGACTTTT  TTGCCGATGC  TGTCGATCAG  GAAACTGCTT
251 TGGCGGTAGA  GCGCGCCGCC  GGAGAGTGTG  CCGACGAGGT  GTCCGATCAG
301 CCCGCCGAA  ACGGTGGTAT  CGAAGAGGAC  GGGGTAGCTG  CCTGTGCGGA
351 TGCTGCGGCT  GCCGAGTCGG  CGCAAAGTGC  GCGGGCGCGC  GGTTTGACCG
401 ATGGTTTCGG  GGCTGTCCAT  ATCCGGATGG  CGGCAGGCGG  AATCGTACCA
451 GTAGTCGCGC  TGCATTCCGT  TTTCTGTCGG  GGCAACGACG  CTGCAGGAAA
501 TGCTGTGGTG  CGTGCTTTGC  CGGTGTGCGG  CAAAACCGTG  GGTGTTGCCG
551 TAAACGTATT  GGTAGTGTCC  GGTGTGCACC  GCCGCGCCTT  CGGAGTTTTC
601 GATGCGGCTG  TCCGTGTCCA  ACGCTGCCTG  TTCGATTGTG  TTTGCCAAGC
651 CGACGGCGGC  TTCCGTATCC  AAATCCCAT  CGTGGTAAAG  GTCGGGGTCG
701 CCGATGTGTT  GCGCCATCAA  CTCGGGGTCG  GCAAGTCCGG  CGCAACCGTC
751 TTCGGCGGTG  TGGCGGGCGA  TGTGCGCGGC  GCGCGCGGAC  GTGTCGCGCA
801 GGGCTTGTTC  GGAGAAGTCG  GCGGTGCGCG  CGCGGCCTTT  GCGTTTGCCG
851 ACGTAAACGG  TAATGTCCAG  CGATTGTGCC  TGCTGGAAGT  CGATTGTGTC
901 GATTTGCGCC  AAGCGCACGC  TGACGCTTTG  TCCGAGCGAT  TCGCTGAAGT
951 CGGCTTCGGC  GCGGTGCGCG  CCCGCTGCTT  TTGCCAAGTC  GAGCGTGCGG
1001 CGGCAGAGGT  CGAGGAGTTC  GGAAGCGGTG  TGGTTGAACA  GCATAACAAT
1051 CTTTCTTGGT  GGAGCGTTGT  GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA  GVARGLHSEF  ARAVTAEEIA  FDNVNLNHEA  RRGNTFRK
51  IAAAERAGDV  RFFAQVEEIG  QDFFADAVDQ  ETALAVERAA  GECADSVSDQ
101 PARNGGIEED  GVAACRDAAA  AESAQAAGG  GLTDGFGAVH  IRMAAGGIVP
151 VVALHSVFVG  GNDAAAGNAV  RALPVCCKTV  GVAVNVLVVS  GLHRRAFGVF
201 DAAVRVQRCL  FALFCQADGG  FRIQIPFVVK  VGVADVLRHQ  LGVGKSGATV
251 FGGVAGDVGG  GADGVAQGLF  GEVGGAGAAF  AFADVNGNVQ  RVLLELDLF
301 DFAQAHADAL  SERFAEVGFG  GGRARCFQV  ERAAAVEEF  GSGVVEQHNN
351 LSWWSVVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA  TACAGTTGT  GCGCGCCGCC  GCGGTTGCCC  GTGGTCTGCA
51  TACCGAGTTT  GCGCGCGCTG  TAACTGCTGA  GGAAATAGCC  TTCGACAATG
101 CCGTTTTTGA  TCACGAAGCG  CGGTGCGGTG  GCAACGCCTT  CCGCATCAAA
151 ATAGCTGCTG  CGGAAAGAGC  GGGGGATGTG  CGGTTCTTCG  CGCAGGTTGA
201 GGAATCGGG  CAGGACTTTT  TTGCCGATGC  TGTCGATCAG  GAAACTGCTT
251 TGGCGGTAGA  GCGCGCCGCC  GGAGAGTGTG  CCGACGAGGT  GTCCGATAAG
301 ACCGCCGAA  ACGGTGGTAT  CGAAGAGGAC  GGGGTAGCTG  CCTGTGCGGA
351 TGCTGCGGCT  GCCGAGTCGG  CGCAAAGTGC  GCGGGCGCGC  GGTTTGACCG
401 ATGGTTTCGG  GGCTGTCCAT  ATCCGGATGG  CGGCAGGCGG  AATCGTACCA
451 GTAGTCGCGC  TGCATGCCGT  TTTCTGTCGG  GGCAACGACG  CTGCAGGAAA
501 TGCTGTGGTG  CGTGCTTTGC  CGGTGTGCGG  CAAAACCGTG  GGTGTTGCCG
551 TAAACGTATT  GGTAATGGCC  GGTTTGCACC  GCCGCGCCTT  CGGAGTTTTC
601 GATGCGCTCA  TCCTCGTTCA  GGGCGGCTTG  TTCGATTGTG  TTTGCCAAGC
651 CGACGGCGGC  TTCCGTATCC  AAATCCCAT  CGTGGTAAAG  GTCGGGGTCG
701 CGATGTGTT  TTGCCATCAG  ACAGGCATCG  GCAAGTCCGG  CGCAACCGTC
751 TTCGGCGGTG  TGGCGGGCGA  TGTCGATGCG  GGCTTTGACG  GTGCTTTGCA
801 GGGCTTTTTC  GGAGAAGTCG  GCAGTACTGG  CGCGGCCTTT  GCGTTTGCCG
851 ACGTAAACGG  TAATGTCCAG  CGACTTGTC  TGCTGGAAGT  CGATTGTGTC
901 GATTTCGCCC  AGCCGCACGC  TGACGCTTTG  TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA  GVARGLHTEF  ARAVTAEEIA  FDNVNLNHEA  RCGNNAFRK
51  IAAAERAGDV  RFFAQVEEIG  QDFFADAVDQ  ETALAVERAA  GECADSVSDK
101 TARNGGIEED  GVAACRDAAA  AESAQAAGG  GLTDGFGAVH  IRMAAGGIVP
151 VVALHVFVVG  GNDAAAGNAV  RALPVCCKTV  GVAVNVLVMA  GLHRRAFGVF
201 DALILVQGL  FALFCQADGG  FRIQIPFVVK  VGVADVFCQ  TGIGKSGATV
251 FGGVAGDVGG  GFDGVLQGF  GEVSGTAAAF  AFADVNGNVQ  RVLLELDLF
301 DFAQPHADAL  SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

```

          10      20      30      40      50      60
g515-1.pep  MVQIQVVRAAGVARGLHSEFARAVTAEEIAFDNAVNLNHEARRGGNTFRIKIAAAERAGDV
          10      20      30      40      50      60
m515-1      MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVNLNHEARRCGNNAFRKIAAAERAGDV
          10      20      30      40      50      60

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	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSHVFGGNDAAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSHVFGGNDAAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
	190	200	210	220	230	240
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGVADVLRHQ					
m515-1	GVAVNVLVVSGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGVADVLRHQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
g515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFVLELDLF					
m515-1	TGIGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFVLELDLF					
	250	260	270	280	290	300
	310	320	330	340	350	360
g515-1.pep	DFAQAHADALSERFAEVGFGGGRARCFQVERAAAEVEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

1	ATGGTTCAAA	TAAAGTTGT	GCGCGCCGCC	GGCGTTGCCC	GTGGTCTGCA
51	TTCCGAGTTT	GCGCGCGCTG	TAACTGCTGA	GGAAATAGCC	TTCCGACAATG
101	CCGTTTTGAA	TCACGAAGCG	CGGTGCGGTG	GCAACGCCTT	CCGCATCAAA
151	ATAGCTGCTG	CGGAAAGAGC	GGGGGATGTG	CGGTTCTTCG	CGCAGGTGTA
201	GGAAATCGGG	CAGGACTTTT	TTGCCGATGC	TGTCGATCAG	GAAACTGCTT
251	TGGCGGTAGA	GCGCTCCGCC	GGAGAGTGCG	CCGACGAGGT	GTCCGATAAG
301	ACCGCCCGAA	ACGGTGGTAT	CGAAGAGGAC	GGGGTAGTTG	CCTGTCCGGA
351	TGCTGCGGCT	GCGAGTCCG	CGCAAAGTGC	GGCGGGCGGC	GGTTTGACCG
401	ATGGTTTCGG	GGCTGTCCAT	ATCCGGATGG	CGGCAGGCGG	AATCGTACCA
451	GTAGTCGCGC	TGCATGCCGT	TTTCGTCCGC	GGCAACGACG	CTGCAGGAAA
501	TGCTGTGGTG	CGTGTCTTGC	CGGTGTGCGG	CAAAACCGTA	GGTGTGCGG
551	TAAACGTATT	GGTAATGGCC	GGTTTGACCC	GCCGCGCCTT	CGGAGTTTTC
601	GATGCGCTCA	TCCTCGTTCA	GGCGGCGTTG	TTCGCATTGT	TTTGCCCAAGC
651	CGACGGCGGC	TTCCGTATCC	AAATCCCAT	CGTGGTAAAG	GTGCGGGTCG
701	CCGATGTGTT	GCGCCATCAA	CTCGGGGTGC	GCAAGTCCGG	CGCAACCGTC
751	TTCCGGCGGTG	TGGCGGGCGA	TGTCGGCGGC	GGCGCGGACG	GTGTCGCGCA
801	GGGCTTGTTT	GGAGAAATCG	GCGGTGCCGG	CGCGGCCTTT	CGGTTTGCCG
851	ACGTAACCGG	TAATGTCCAG	CGACTTGTC	TGCTGAAACT	CGATTTGTTT
901	GATTTCGCCC	AGCCGCACGC	TGACGCTTTG	TCCCAATGA	

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

1	MVQIKVVRAA	GVARGLHSEF	ARAVTAEIEA	FDNAVLNHEA	RCGGNAFRIK
51	IAAAERAGDV	RFFAQVEEIG	QDFFADAVDQ	ETALAVERSA	GECADEVSDK
101	TARNGGIEED	GVVACRDAAA	AESAQSAAGG	GLTDGFGAVH	IRMAAGGIVP
151	VVALHAVFVG	GNDAAAGNAV	RALPVCCKTV	GVAVNVLVMA	GLHRRAFGVF
201	DALILVQGG	FALFCQADGG	FRIQIPFVVK	VGVDVLRHQ	LGVGKSGATV
251	FGGVAGDVGG	GADGVAQGLF	GEIGGAGAAF	AFADVNGNVQ	RLVLLKLDLF
301	DFAQPHADAL	SQ*			

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEIEAFDVAVLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEIEAFDVAVLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNGGIEEDGVVACRDAAA					

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m515-1      RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
              70      80      90      100     110     120

              130     140     150     160     170     180
a515-1.pep  AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              |||||
m515-1      AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              130     140     150     160     170     180

              190     200     210     220     230     240
a515-1.pep  GVAVNVLVMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVLRHQ
              |||||
m515-1      GVAVNVLVMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVLRHQ
              190     200     210     220     230     240

              250     260     270     280     290     300
a515-1.pep  LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKDLF
              |::|
m515-1      TGIGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLELDF
              250     260     270     280     290     300

              310
a515-1.pep  DFAQPHADALSQX
              |||||
m515-1      DFAQPHADALSQX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

g516.seq

```

1  atgttggtcc gtaaacgac cgccgccgtt ttggcggcaa ccttgatact
51  gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacgtt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgccca attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgccg tcaatccga agattcggcg aagctgacgg
251 gccttttgaa ggccgggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccg gtcaaattcg aagcggccgg
351 cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcggtcaaa
451 ctcgacaatc ggaccattta cacgcgctgc gtatccgcc aaggcaata
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcathtt gagcaaagt
551 tgcccgccga tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctgtttg gaaatatctt atatacgccc cccttggtga tattggatgc
651 ggcggccgcg gtgctgttct tgcctatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

g516.pep

```

1  MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNILYTP PLLILDAAA VLVLPMALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

m516.seq

```

1  ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGCGC CTTCCGTTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCGGCG AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCCT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAAAT

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501 CTACGCCACA CCGCAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG  
 551 TGCCTGCCGA TATTTATTAC ACGTTACTG AAGAACATAC CGACAAATCC  
 601 AAGCTGTTTG CAAATATCTT ATATACGCC CCCTTTTGA TACTGGATGC  
 651 GCGGGCGCG GTACTGGCCT TGCCTGCGG GGTCTGGGT GCGGTCGTGG  
 701 ATGCCGCCG CAAATGA

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

m516.pep  
 1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV  
 51 VAEDNAQLEK GSLVMMGGKY WVVNPEDSA KLTGILKAGL DKPFQIVEDT  
 101 PSYARHQALP VKLESPGSON FSTEGLCRLY DTDKPADIAP LKQLGFEAVK  
 151 LDNRTIYTRC VSAKGYYAT PQKLNADYHF EQSVPADIYY TVTEHTDKS  
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

m516/g516

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDQIRAFGVVAEDNAQLEK					
g516	MLFRKTTAAVLAATLILNGCTMLLRGMNPNVSQTITRKHVDKDQIRAFGVVAEDNAQLEK					
	10	20	30	40	50	60
m516.pep	GSLVMMGGKYWVVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSON					
g516	GSLVMMGGKYWFAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSON					
	70	80	90	100	110	120
m516.pep	GSLVMMGGKYWVVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSON					
g516	GSLVMMGGKYWFAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSON					
	70	80	90	100	110	120
m516.pep	FSTEGLCRLYDTDKPADIAPKQLGFEAVKLDNRTIYTRCVSAKGYYATPQKLNADYHF					
g516	FSTGGLCLRYDTGRPDDIAKLQLEFKAVKLDNRTIYTRCVSAKGYYATPQKLNADYHF					
	130	140	150	160	170	180
m516.pep	FSTEGLCRLYDTDKPADIAPKQLGFEAVKLDNRTIYTRCVSAKGYYATPQKLNADYHF					
g516	FSTGGLCLRYDTGRPDDIAKLQLEFKAVKLDNRTIYTRCVSAKGYYATPQKLNADYHF					
	130	140	150	160	170	180
m516.pep	EQSVPADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
g516	EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLLILDAAGAVLALPAAALGAVVDAARK					
	190	200	210	220	230	239
m516.pep	EQSVPADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
g516	EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLLILDAAGAVLALPAAALGAVVDAARK					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

a516.seq  
 1 ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGTT  
 51 GAACGGCTGT ACGGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA  
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTCGGTGTG  
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAGAG GGCAGCCTGG TGATGATGGG  
 201 CGGGAAATAC TGGTTCGTCT TCAATCCTGA AGATTCGGCG AAGCTGACGG  
 251 GCATTTTGAA GGCCGGGTTG GACAAGCAGT TTCAATGGT TGAGCCCAAC  
 301 CCGCGCTTTG CCTACCAAGC CCTGCCGGTC AAATCGAAT CGCCCGCCAG  
 351 CCAGAATTC AGTACCGAAG GCCTTTGCCT GCGCTACGAT ACCGACAGAC  
 401 CTGCCGACAT CGCCAAGCTG AAACAGCTTG AGTTTGAGC GGTGCGAATC  
 451 GACAATCGGA CCATTACAC GCGCTGCGTC TCCGCCAAG GCAAATACTA  
 501 CGCCACACCG CAAAACTGA ACGCCGATTA TCATTTTGAG CAAAGTGTGC  
 551 CTGCCGATAT TTATTACACG GTTACGAAA AACATACCGA CAAATCCAAG  
 601 TTGTTGAAA ATATTGCATA TACGCCACC ACGTTGATAC TGGATGCGGT  
 651 GGGCGCGGTG CTGGCCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT  
 701 CCTCAGACAA ATGA

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

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```

1  MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFFVNPEDSA KLTGILKAGL DKQFQMVPEP
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIACL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVPADIIYT VTKKHTDKSK
201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHV	DKDQIRAFGVVAEDNAQLEK				
a516	MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHV	DKDQIRAFGVVAEDNAQLEK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m516.pep	GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKPFQIVEDT	PSYARHQALPVKLESPGSQN				
a516	GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKQFQMVPEP	NPRFA-YQALPVKLESPASQN				
	70	80	90	100	110	
	130	140	150	160	170	180
m516.pep	FSTEGCLCLRYDTPADIAKLQKLGFEAVKLDNRTIYTRCV	SAKGKYATPQKLNADYHF				
a516	FSTEGCLCLRYDTPADIAKLQKLEFEAVELDNRTIYTRCV	SAKGKYATPQKLNADYHF				
	120	130	140	150	160	170
	190	200	210	220	230	239
m516.pep	EQSVPADIIYTVTEEHTDKSKLFANILYTPPFLILDAAG	AVLALPAAALGAVVDAARKX				
a516	EQSVPADIIYTVTKKHTDKSKLFENIAYTPTTLILDAVG	AVLALPVAALIAATNSSDKX				
	180	190	200	210	220	230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

g517.seq

```

1  atgcatcggg tttcagacgg cattggagtg tcagtcgtgt tctgccgatt
51  cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 cgggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcacg
151 tgcgtctttc aatcccgaatt tgatgttttt gggcaggctg atttggctgg
201 tgtcgccggt aatgacggct ttcgcgccga agccgatgag ggtcaggaac
251 attttcattt gttcgggctt ggtgttttgc gcttcgtcga ggatgatgta
301 tgcgccgttg agcgtcctgc cgcgcataa ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagagggcat cataaagcgg acggaggtag gggctgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence &lt;SEQ ID 1436; ORF 517.ng&gt;:

g517.pep

```

1  MHRVSDGIGV SVVFCRFVGF DDFLHQRMPD NVFAGEGMEI QSCHAVQFLT
51  CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAHI GERGFNQAF FNQLGYTVKA HQVIEGLIKR TEVGVDPLGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

m517.seq

```

1  ATGCATCGGG TTTCCAGACGG CATTTGGAATG TCAGTCGTGT TCTGCCGATT
51  CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGAAATA CAGCCCTTCC ACGTTGTGCA GTTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCGATTTCOA
351 TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

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451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA  
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep  
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT  
51 RIFXSRFDVF GOVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV  
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ  
151 VSGQEAQFLA GFDGWAH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	:     :     :     :     :     :					
g517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGEGMEIQSCHAVQFLTCVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	:     :     :     :     :     :					
g517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAH					
	:     :     :     :     :					
g517	FNQLGYTVKAHQVIEGIIKRTGVDFLQVSGQEAQFLTGFDGRPN					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq

1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT  
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGCTTTCG  
101 CCGGTAAAGG TGTGAAATA CAGCCCTTCC ACGCCGTGCA GTTCTCAGC  
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG  
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTACGGAAC  
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA  
301 TCGCGCCGTT AGCGTCCTGC CGCGCATATA GGCAGAGCGG GCAATCTCAA  
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTGGAAGCC CATCAGGTCA  
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG  
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA  
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep

1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT  
51 RIF\*SRFDVF GOVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV  
101 CAVERPAAHI GERGNLQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ  
151 VTGQKTQFLA GFDGRPH\*

m517/a517 93.4% identity in 167 aa overlap

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	:     :     :     :     :     :					
a517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHAVQFLTRIFXSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	:     :     :     :     :     :					
a517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGNLQTF					

	70	80	90	100	110	120
m517.pep	130	140	150	160		
	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTVGQKTQFLAGFDGRPHX					
	130	140	150	160		

```
g518.seq
  1  atgacgtttt  cggcggcaaa  gctcaacatt  tcggcactga  tgttggtctt
51  ttcggcagga  atgacgttt  tactttccgc  ttttttactg  ctccgaccgg
101 aaggcagcat  ctatttaaac  cattttttca  gcataaatat  tctgaccgga
151 agagcggcat  ctccacgggc  aaccgtgttc  agactgcata  aggcggtacg
201 attccacaaa  atgccgaaaa  ccataagcaa  aatgcgtaga  aactacgccg
251 tcggaatcac  gccgcctctc  cgggcggcaa  cgcttcatta  taacagattg
301 ccccttaaaa  aatcagacct  tgctttttgt  cgcgagtctg  aaatttga
```

g518.pep  
1 MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR  
51 RAASPRATVR RLHQAVRFHK MPKTISKMRN NYAVRITPP RAATLHYNRL  
101 PLKKSDFPVF AESEI\*

```
m518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACGCTTT TACTTTCGCG TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCAC GCATAAATAT TCTGACCCGA
151 AGAGCGGCAT CTCCACAGGC AACCGTGTTC AGACGGCATC AGCGCGCGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCGC TAGAACTAC GCCGTCGGAA
251 TCACGCGGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTTT TGTGGCAGAG TCTGAAATTT
401 GA
```

m518.pep

1	MTFSAAKLNI	SARMLCLSAG	MTVLLSAFLL	LRPEGSILFN	HFFSINILTR
51	RAASPQATVF	RRHQARFARC	RTINKRRRNY	AVRITPPSXA	ATRHYNRLPS
101	AAGLVRRERR	RCAVILSNGR	KKSDPAFVAE	SEI*	

from *N. gonorrhoeae*:

```

m518/g518

m518.pep      MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF
                |||||
g518           MTFSAAKLNISALMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
                10      20      30      40      50      60

                70      80      90      100     110
m518.pep      RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRRRRCVILSN
                | ||| || : :||| ||||| ||| |||||
g518           RLHQAVRFHKMPKTISKMRNRNYAVRITPPPPAATLHYNRLPL-----
                70      80      90      100

                120     130
m518.pep      GRKKSDPAFVAESEI
                |||||
g518           --KKSDPAFVAESEI
                110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCAT GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCACGCC GTCCTCG.CG GCGGCAACGC GTCAATTATA CAGATTGCCC
301 TCC.....
351 ..... .AAAAAAT CAGACCCTGC TTTTGTGGCA GAGTCTGAAA
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*

m518/a518 79.9% identity in 134 aa overlap

          10      20      30      40      50      60
m518.pep  MTFSAAKLNI SARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
          ||||| || : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a518      MTFSAAKLNI SARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
          10      20      30      40      50      60

          70      80      90      100     110     119
m518.pep  RRHQ-RFARCRTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSNG
          ||||| || : ||||| ||||| ||||| ||||| ||||| ||||| |||||
a518      RRHQAVRFRKMPTINKRRRNYAVRITPSSXAATRHYNRLPS-----
          70      80      90      100

          120     130
m518.pep  RKKSDPAFVAESEIX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a518      -KKSDPAFVAESEIX
          110
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggcttcaa
51  atcctttgtc gtcattcccc agcaggaagt ccacgttgct gaaaggctcg
101 ggcgtttcca tcgcgccttg acggccggtt tgaatatttt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcctc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcggy ggcttggggt
451 gtgaaagtcc tcggttacga aatcaaggat ttggttcgcg cgaagaaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg cttaggctgc
651 ggtcaatgcy tccaatgccg agaaaaatcg ccgcatcaac cgcgccaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgccgccct tcaaacccaa agcggggcgg atcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaagg ttgccgaaat cgggaaccct
901 aattttcggc ggcataaaaa attttcgcca gaagcaaaaa cggccaataa
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```

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101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG  
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS  
 201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAEN  
 251 RQIAAALQTO SGADAVNLKI AGQYVTAFFN LAKEDNTRIK PAKVAEIGNP  
 301 NFRRHEKFSP EAKTAK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

m519.seq (partial)  
 1 ..TCCGTTATCG GCGGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA  
 51 AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGCTTgGG  
 101 GTGTGAAGGT TTTGCGTTAT GAGATTAAG ACTTGTTCC GCCGCAAGAA  
 151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC  
 201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA  
 251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT  
 301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA  
 351 AGGTGAAGCG GAATCCTTGC GCCTTGTTCG CGAAGCCAAT GCCGAAGCCA  
 401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC  
 451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA  
 501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC  
 551 TGATTCTGCG CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

m519.pep (partial)  
 1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE  
 51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLASGQREAE IQQSEGEAQA  
 101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV  
 151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng)

from *N. gonorrhoeae*:

m519/g519

				10	20	30
m519.pep				SVIGRMELDKTFEERDEINSTVVAALDEAA		
g519	YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
		40	50	60	70	80
m519.pep		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE				
g519		GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLASGQREAE				
		150	160	170	180	190
		100	110	120	130	140
m519.pep		IQQSEGEAQAQAVNASNAEKIARINRAKGEAESLRLVAEANA AEAIRQIAAALQTQGGADAV				
g519		IQQSEGEAQAQAVNASNAEKIARINRAKGEAESLRLVAEANA EANRQIAAALQTQSGADAV				
		210	220	230	240	250
		160	170	180	190	200
m519.pep		NLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK				
g519		NLKIAEQYVTAFFN LAKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK				
		270	280	290	300	310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

a519.seq  
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA  
 51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG  
 101 GCGGTTTCCA TCGCGCCCTG ACGGCCGCTT TGAATATTTT GATTCCCTTT  
 151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAAGAAATCC CTTAGACGT

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201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTACGCGCG AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATT CCGCCGCCCT TCAAACCCAA GCGGTTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTGCCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFGEKSFV VIPQGEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLSYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGRKIEQINLAS
201 GOREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAELAI
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDG SKTAK*

m519/a519 99.5% identity in 199 aa overlap

m519.pep
10 20 30
SVIGRMELDKTFEERDEINSTVVAALDEAA
|||||
a519 YFQVTPKLSYGSNNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
90 100 110 120 130 140

m519.pep
40 50 60 70 80 90
GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGQREAE
|||||
a519 GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGQREAE
150 160 170 180 190 200

m519.pep
100 110 120 130 140 150
IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAELAIQIAAALQTGGADAV
|||||
a519 IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAELAIQIAAALQTGGADAV
210 220 230 240 250 260

m519.pep
160 170 180 190 200
NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
|||||
a519 NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
270 280 290 300 310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCGCGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCGTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTC
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GTTCAGCGTG AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATT CCGCCGCCCT TCAAACCCAA GCGGGGCGG ATGCGGTCAA

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801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG  
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG  
 901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF  
 51 IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS  
 101 SNYIMAITQL AQTTILRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG  
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS  
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI  
 251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL  
 301 ISAGMKIIDS SKTAK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA  
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG  
 101 GCGGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT  
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTAGACGT  
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG  
 251 GCATCATCTA TTCCAAGTA ACCGACCCCA AACTCGCTC ATACGTTTCG  
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC  
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA  
 401 TCAACAGTAC TGTGTTGCG GCTTTGACG AGGCGGCCGG GGCTTGGGGT  
 451 GTGAAGGTTT TGCGTTATGA GATTAAAGAC TTGTTTCCGC CGCAAGAAAT  
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC  
 551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT  
 601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC  
 651 GGTCATGCG TCAATGCGC AGAAAATCG CCGCATCAAC CGCGCCAAAG  
 701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCG AAGCCAATGC CGAAGCCATC  
 751 CGTCAATATG CCGCCGCCCT TCAAAACCAA GCGGTGCGG ATGCGGTCAA  
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG  
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG  
 901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF  
 51 IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS  
 101 SNYIMAITQL AQTTILRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG  
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS  
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI  
 251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL  
 301 ISAGMKIIDS SKTAK\*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSI					
m519-1	MEFFIILLVAVAVFGFKSFVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSI					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTILRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTILRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEG RKIEQINLASGQREAEIQS EGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEG RKIEQINLASGQREAEIQS EGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240



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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51 ATCCTTTGTT GTCATCCCAC AGCAGGAAGT CCACGTGTGC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCGA GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCATTATGA GATTAAAGAC TTGGTTCGCG CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAATCAA CCTTGCCAGT
601 GGTGAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCC AGAAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTGCGG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATT CCGCCGCCCT TCAAACCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCGCG GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1  MEFFIILLAA VVVFQKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
51 IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESG RKIEQINLAS
201 GQREAEIQQS EGEAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

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m519-1/a519-1 99.0% identity in 315 aa overlap

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              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFQKSFVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              |||||
m519-1      MEFFIILLVAVAVFGKSFVVIQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              |||||

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKK
              |||||
m519-1      ISAGMKIIDSSKTAKK
              310

```

### Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in E.coli. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1  atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctggtgcc gttaataatg ccggcgatgg
101 atttaacctt gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt ttgttttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccg tgccgcccga caattcgacc aagacatcga cgtctttacg
351 cgcgaaacagt tcgaacggat cttttgacaa gggcggggcg cgggccgatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa ataccgattt
451 cgcgccccc aa gggcggggaa atttcctctg cgttgtcccg caacacggca
501 gccgcaccgc cgccgaccgt acctaagcct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1  MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1  ATGCCTGCGC TTCTTTTCA GT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTTCGGrK AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCC CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GGCAGCAGT TTTTGTGTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

```

301 GCAATGCCGG TACCGCCGaa CAATTCGACG ACGACATCGA CGTCTTCACG  
351 TGCGACCACT TCGAACGGAT CTTTGACAAA GGCTGc . CGG ACGGGCAGGT  
401 TTGTCCGGCT TTTTCTTCAC TCAATTCGCA CACGGCAGAA ATACGGATTT  
451 CGCGCCCCAA CGCGACGGGA ATTTCCTCCG CGTTGTcSg CACACCGCA  
501 GCCGTATCCG CGCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG  
551 CTTCACTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

m520.pap

```

1  MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDILFAA KPSRRALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCPL FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF
151 RAPSDGKFPP RCXATROPYR RRPYPNLKDR CLLASLCILV SRLKCKY*

```

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m520/g520

		10	20	30	40	50	60
m520.pep		MPALLSVHRANALPFSRISIXRMKLLVPLIMPAMDILFPAAKPSRRALMIGIPPATAASNW					
		::					
g520		MPALLSIRANALPFSRISERMKLLVPLIMPAMDILFPAAKPSRTALMIGIPPATAASNW					
		10	20	30	40	50	60
		70	80	90	100	110	120
m520.pep		TMTFCFSASGKISLPYSASSFLLAVTMCLPFMSAFNTASLAMPVPPNNSTTTSTSSRATS					
g520		TMTFCFSASGKISLPYSASSFLLAVTMCLPFMSAFNTASLAMPVPPNNSTKTSTSLRANS					
		70	80	90	100	110	120
		130	140	150	160	170	180
m520.pep		SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPFPRCXATROPYRRRYPYNLKDR					
		: :: :		: :			
g520		SNGSFDKGGRADFGGLFLRLSRTWQKYGFRAPSGGKFPLRCPATROPHRRRYPYLSLKDR					
		130	140	150	160	170	180
		190					
m520.pep		CLLASLCLLVSRLLKCKY					
g520		CLLASLCLLVSRLLKCKY					
		190					

a520.seq

1	ATGCCTGCGC	TTCTTTCAGT	ACATCGG.CA	AACGCGCTGC	CTTTTTCGCG
51	CATTTTCGGAG	AGGATGAAGT	TGCTGGTGCC	GTTAATAATG	CCGGCGATGG
101	ATTTAATCCT	GTTTGCCGCC	AAACCTTCGC	GCAGGGCTTT	GATGATTGGG
151	ATACCGCCCG	CTACTGCCGC	TTCAAATTGC	ACGATGACGT	TTTGTTTTTC
201	CGCCAGCGGG	AAGATTTCGT	TGCCGTATTC	GGCGAGCAGT	TTTTTGTTCG
251	CGGTAACGAT	GTGTTTGCCG	TTTCCAATGG	CTTTCAACAC	CGCATCTTTG
301	GCAATGCCGG	TACCGCCGAA	CAATTCGACG	ACGACATCGA	CGTCTTCACG
351	TGCGACCACT	TCGAACGGAT	CTTTGACAAA	GGCTG..CGG	ACGGGCAGGT
401	TTGTCCGGCT	TTTTCTTCAC	TCAAATCGCA	CACGGCAGAA	ATACGGATTT
451	CGCGCCCCAA	GCGACGGGAA	ATTTCTCTCG	CGTTGTCCCG	CAACACGGCA
501	CGCGTACCGC	GCGCCACCGT	ACCCAAACCT	AAAAGACCGA	TGTTTACTGG
551	CTTCATTGTG	TCTCCTTGTA	AGCCGACTGA	AATGTAAATA	TGA

a520.pep

```

1  MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDILILFAA KPSRRALMIG
51 IPPATAASNW TMTFCFSASG KISLPYSASS FLAVTMCCLP FSMAFNATSL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

```

783

151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY\*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNATSLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNATSLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCPATRQPYRRRPYPNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKYX					
a520	CLLASLCLLVSRKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTTCGTTG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTGGCA ATGCCCGTGC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGC GGGCTTTTTC
351 TTCCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTC CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCGC
451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1466; ORF 520-1.ng&gt;:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNATSLA MPVPPNNSTT TSTSLRATSS
101 NGSLTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPP
151 TVPKPRKPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTTCGTTG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTCG GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTG GGGCTTTTTC
351 TTTACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTC CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCGC
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1468; ORF 520-1&gt;:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNATSLA MPVPPNNSTT TSTSSRATSS

```

784

101 NGSLTAAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP  
151 TVPKPKRPMF TGFIVSPCKP TEM\*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASGK	ISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASGK	ISLPYSASSF	
	10	20	30	40	50	60
g520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSLR	ATSSNGSLTKA	ADGQIWRASF	SSLK
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAF	SSLK
	70	80	90	100	110	120
g520-1.pep	SHMAEIRISRPK	RREISSALSRNT	AAVPPPTVPK	PKRPMFTGFIV	SPCKPTEMX	
m520-1	SHTAEIRISRPK	RREISSALSRNT	AAVPPPTVPK	PKRPMFTGFIV	SPCKPTEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq

1 ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT  
51 TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA  
101 CTGCGCGTTC AATTGGACG ATGACGTTT GTTTTCCGC CAGCGGGAAG  
151 ATTTGCTTGC CGTATTCGGC GAGCAGTTT TTGTTGGCGG TAACGATGTG  
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC  
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTCACGTGC GACCAGTTCG  
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTG GGGCTTTTTC  
351 TTCACCTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC  
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGCAGCCGT ACCGCCGCCG  
451 ACCGTACCCA AACCTAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC  
501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep

1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK  
51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS  
101 NGSLTAAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP  
151 TVPKPKRPMF TGFIVSPCKP TEM\*

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASGK	ISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASGK	ISLPYSASSF	
	10	20	30	40	50	60
a520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAF	SSLK
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAF	SSLK
	70	80	90	100	110	120
a520-1.pep	SHMAEIRISRPK	RREISSALSRNT	AAVPPPTVPK	PKRPMFTGFIV	SPCKPTEMX	
m520-1	SHTAEIRISRPK	RREISSALSRNT	AAVPPPTVPK	PKRPMFTGFIV	SPCKPTEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq

1 ATGAAATCAA AACTCCCTT AATCCTAATC AACCTTTCCC TGATTTCAG  
51 CCCATTGGGT GCGAATGCGG CCAAAATCTA TACCTGCACA ATCAACGGAG  
101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTG

q521n.pep

1 MKSKLPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSchSTDL  
51 PPIGNYSSER YILPQTPEPA PSPSNGGQAV KYKAPVKTVS KPAKSNTPPQ  
101 QAPVNSRRS ILEAELSNER KALTEAQKML SQARLAKGGN INHQKINAL\*  
151 SNVLDRQQNI QALQRELGRM \*

m521.seq

ms21-189

1	ATGAAATCAA	AACCTCCTCT	AATCCTAATC	AACCTTTCCC	TGATTTCAAG
51	CCCATTTGGGT	GCGAATGCGG	CCAAAATCTA	sACCTGCACA	ATCAACGGAG
101	AAACCGTTTA	CACCAgCAAG	CCGTCCAAAA	GCTGCCACTC	AACCCGATTG
151	CCCCAATCG	GCAACTACAG	CAGCGAACGC	TATATCCCGC	CCCCAACGCC
201	CGCAACGGTA	TCATCACCGT	CAAAACGCGG	ACwGGTTGTc	AAATATAAAG
251	CCCCGGTCAA	AACAGTATCC	AAGCCGGCAA	AATCCAATAC	GCCGCCGCCG
301	CAACAAGCAC	CCTCAAACAA	CAGCAGACGC	TCCATTCTCG	AAACAGAATT
351	GAGCAACGAA	CGCAAAGCAT	TGGTTGAAGC	CCAAAAAATG	TTATCACAAG
401	CACGTCTGGC	AAAGGGCGGC	AACATCAACC	ATCAAGAAAT	AAATGCATTA
451	CAAGAGCAATG	TATTGGACAG	GCAGCAAAAT	ATTCAAGCCC	TGCAAAAGGA
501	ACTGGGGCGT	ATGTAA			

m521.pep

1 MKSKLLLLLI NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTDL  
51 PPTIGNYSSER YIPPQTPEPV SSPSNGGXVV KYKAPVKTVS KPAKSXTPPP  
101 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL  
151 QSNVLDROQN IQALQRELGR M\*

**Homology with a predicted ORF from *N. gonorrhoeae***

m521/q521

	10	20	30	40	50	60
m521.pep	MKS K L L L I L I N F S L I S S P L G A N A A K I X T C T I N G E T V Y T X K P S K S C H S T D L P P I G N Y S S E R					
	:           :           :           :					
g521	M K S K L P L I L I N L S L I S S P L G A N A A K I Y T C T I N G E T V Y T T K P S K S C H S T D L P P I G N Y S S E R					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	Y I P P Q T P E P V S S P S N G G X V V K Y K A P V K T V S K P A K S X T P P P Q Q A P S N N S R R S I L E T E L S N E					
	:           :           :           :					
g521	Y I L P Q T P E P A P S P S N G G Q A V K Y K A P V K T V S K P A K S N T P P - Q Q A P V N N S R R S I L E A E L S N E					
	70	80	90	100	110	
	130	140	150	160	170	
m521.pep	R K A L V E A Q K M L S Q A R L A K G G N I N H Q E I N A L Q S N V L D R Q N I Q A L Q R E L G R M X					
	:           :           :           :					
g521	R K A L T E A Q K M L S Q A R L A K G G N I N H Q K I N A L X S N V L D R Q N I Q A L Q R E L G R M X					
	120	130	140	150	160	170

a521.seq

1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTCAG

a521.pep

```

1  MKSKLPILIL NFSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCLSTDL
51  PPIGNYSSER YIPPQTSEPT PPSNGGQAV KYKAPVKTVS KPAKSNTPPP
101 QQAPSNRRSR SILETELSR KRALVEAQKM LSQARLAKGG NINHQEINAL
151 QSVLDRQON IQALQRELGR M*

```

	10	20	30	40	50	60
m521.pep	MKSKLLILINFSLISSPLGANA	AKIXTCTINGETVYTXKPSKSCHSTDLPP	IGNYSSER			
a521	MKSKLPLILINFSLISSPLGANA	AKIYTTCTINGETVYTTKPSKSLSTDLPP	IGNYSSER			
	10	20	30	40	50	60
m521.pep	70	80	90	100	110	120
	YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRS	ILETELSNE				
a521	YIPPQTSEPTSPSNGGQAVVKYKAPVKTVSKPAKSNTPPPQQAPSNNRRS	ILETELSNE				
	70	80	90	100	110	120
m521.pep	130	140	150	160	170	
	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLD	RQONIQALQRELGRMX				
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLD	RQONIQALQRELGRMX				
	130	140	150	160	170	

g522.seq

1	atgactgagc	cgaaacacga	aacgcccagc	gaagagcagg	ttgccgcgcg
51	caaaaaagca	aaagccaaaa	tccgacccat	ccgatttgg	gcgtgggtca
101	ttttggcggt	gctgccttca	acgcacctgc	tctcccaatg	cgcgatgtcc
151	aaaccgcgac	caaaacagaa	aattgtcgcg	tcttgcata	aaatatcc
201	gtttgtcgaa	aaatggcaga	acgatttgaa	agcgcgcggc	tgggatcgcg
251	acaatacccg	tctcgcgcgc	gactactgca	aatgtatgtg	ggagcagcct
301	ttggacggat	tgagcagata	acagatcagc	tccttcggca	aactcgggtg
351	acaagaacag	cttgacgtgc	tcggcggcgc	aaacgcggtt	gaaactcgag
401	acaaacaatq	tqtccgcgat	ttgaaagccq	attga	

q522.ppt

```

1  MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
51  KPQAKQKIVE SCMKNIPFAE KWQNDLKARG LDADNTRLAV DYCKCMWEQP
101 LDGLSEKOIS SFGKLGAEQ LDLLGGANAF ETRDKOCVAD LKAD*

```

m522.seq

1	ATGACTGAGC	CGAAACACGA	AATGCTGACG	AAAGAGCAGG	TTGCCGCGCG
51	CAAAAAAGCA	AAAGCCAAAA	TCCGCACCAT	CCGCATTGG	GGCTGGGTCA
101	TTTGTGCGTT	GCTCGCTTTA	ACCGCCTGC	TCTCCCAATG	CGCGATGTCC
151	AAACCGCAGG	CAAAACAGAA	AATTGTGCG	TCTTGCCTGA	AGAATATTCC
201	GTTTCCGGA	AAATGGCAAA	ACGATTTCG	GGCCCGCGGT	TTAGATTCAA
251	ACAATACCCG	CCTCGCCGTC	GACTACTGCA	AATGATATGG	GAGAGCGCCT

m522.ppt

```

1  MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWWILALLAL TALLSQCAMs
51 KPOAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKCMWEQP
101 LDRLSEKOIR SFGKLGAEQO LDLLGGANAF EARDKOCVAD LKSE*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m522/q522

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1481>:

a522.seq

1	ATGACTGAGC	CGAAACACGA	AATGCCGACG	GAAGAGCAGG	TTGCCGCGCG
51	CAAAAAAGCA	AAAGCCAAAA	TCCGACCATT	CCGATTTTGG	GCATGGGTCA
101	TTTTGGCGTT	GCTCGCTTCA	ACCGCCCTCG	TCCTCCAAATG	CGCGATGTCC
151	AAACCCGAGG	CAAAACACAA	AATGTGTCAG	CTTTCGTGA	AGAATATTTCA
201	GTTTGCCGAA	AAATGGCAAA	ACGATTTGCG	GGCCGCGCGT	TTAGATTTCAA
251	ACAATACCCG	CCTTACCGTC	GACTACTGCA	AATGTATGTG	GGAGCAGCCT
301	TTGGACAGAT	TGAGCGAGAA	TCAGGATAGT	TCCTTCGGCA	AACTCGGCGC
351	ACAAGAACAG	CTTGACCTGC	ACGCGGCGCG	AAATGCCTTT	GAAACGCGAG
401	ACAAGCAGTG	TGTTGCCGAT	TTGAAATCAG	AATAA	

This corresponds to the amino acid sequence <SEQ ID 1482: ORF 522.a>:

a522.pcp

```

1  MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
51  KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKCMWEQP
101 LDRLSEKQIS SFGKLGAEQ LDLLGGANAF ETRDKOCVAD LKSE*

```

**m522/a522 95.8% identity in 144 aa overlap**

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNI PF AEK W Q N D L R A R G L D S N N T R L A V D Y C K C M W E Q P L D R L S E K Q I R S F G K L G A Q E Q					
	:					
a522	SCVKNI PF AEK W Q N D L R A R G L D S N N T R L T V D Y C K C M W E Q P L D R L S E K Q I S S F G K L G A Q E Q					
	70	80	90	100	110	120



788

```

                130      140
m522.pep      LDLLGGANAFEARDKQCVADLKSEX
                |||||:|||||
a522          LDLLGGANAFETRDKQCVADLKSEX
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

```

g523.seq
1  atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
51 gacgggaacg gtttatcttt tggttgtcag cgcggtttg gcgggttcgg
101 gcattgccta cggggtgact ggcagcacgc ctgccgccgt cttgaccgcc
151 gcactgcttt ccgcgctggg catttggttc gtacatgcca aaaccgccgt
201 gggaaaaagt gaaacggatt catatcagga ttgggatacc ggaaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt tttttatcgc
301 ggtacgcact ggcaggcgca aaatacgggg caggaaagtgt ttgaaccggg
351 aacgcgcgcc ctcacgtcc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

```

g523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVVSAA LAGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKYEILRYT GGNRYEVFYR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

```

m523.seq (partial)
1  ..GCCGTCCTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGGTT CGGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCCTGCCGC CGTCTTGACC GncGCTCTGC TTTCCGCGCT GGGTATTnG
151 TTCGTACACG CCAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTTGGAT GCCGGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA
251 ACCGTTACGA AGTTTtTAT CGCGGTACGc ACTGGCAGGC TCAAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACTCGC GCCCTCAT TG TCCGCAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

```

m523.pep (partial)
1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDL D AGQYVEILRH TGNRYEVFY R GTHWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng) from *N. gonorrhoeae*:

m523/g523

```

                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLT XALLSALGIXF
                |||||:|||||:|||||:|||||:|||||:|||||:|||||
g523          MTVWFVAAVAVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTAALLSALGIWF
                10      20      30      40      50      60

                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDL D AGQYVEILRH TGNRYEVFYR GTHWQAQNTGQEELEPGTRA
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g523          VHAKTAVGKVETDSYQDLDTGKYAEILRYT GGNRYEVFYR GTHWQAQNTGQEVFEPGTRA
                70      80      90      100     110     120

                120
m523.pep      LIVRKEGNLLIITHP
                |||||:|||||:|

```

789

g523 LIVRKEGNLLIIANPX  
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

```
a523.seq
1  ATGACTGTAT GGTGTGTTGC CGCTGTTGCC GTCTTAATCA TCGAATTATT
51  GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CCGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTTGGTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

```
a523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVVSAAAL AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFYR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*
```

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTVWFVAAVAVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIITHPX				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

```
g525.seq
1  atgaagtacg tccggttatt ttctctcggc acggcactcg ccggcactca
51  agcggcggtt gccgaaatgg ttcaaatcga aggcggcagc tacggcccg
101 tttatctgaa aaaagatacc ggcctgatta aagtcaaacc gttcaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 cccccaatgg caaaaaggca ggatcggttc caaacaggca gaaccgctt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggcgaattga aacagccggt taccaatatt tcctgggttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttcgcc acgcagaaaa aacggctcaa acgaaccgg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaaaagca ccgcccgaac tactgggggtg tttatgatat
551 gcacgggctg a
```

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

```
g525.pep
1  MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDOT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKRLKRTR
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

```
m525.pep
  1  MKYVRLFXLG AAIAXTQXAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
 51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGRSRYPFKA
101  GELKQPVTNV SWXAAAYCA QAGKRLPTID EWEFAGLASA TQKXRLKRTR
151  LOPHYSLVLC RRRTERPARC RXKAARTTGA FMICTG*
```

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	60
m525.pep		MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLK KDTGLIKVKPFKLDKYPVTNAEF					
		:					
g525		MKYVRLFFLTALAGTQAAAAEMVQIEGGSYRPLYLK KDTGLIKVKPFKLDKYPVTNAEF					
		10	20	30	40	50	60
		70	80	90	100	110	120
m525.pep		AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVTVNSWXAAANAYCA					
		:					
g525		AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVTVNISWFAANAYCA					
		70	80	90	100	110	120
		130	140	150	160	170	180
m525.pep		AQGKRLPTIDEWEFAGLASATQKXRLKRTLQPHYSRLVCRRRTERPARCRXKAARTTGA					
		:					
g525		AQGKRLPTIDEWEFAGLASATQKXRLKRTLQPHYSRLVCRRRTERPARCQSTARTTGV					
		130	140	150	160	170	180
m525.pep		FMICTGX					
g525		FMICTGX					

```
a525.seq
1 ATGAAGTTTA CCCGGTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCCGCCCG
101 TTTATCTGAA AAAAGATAGG GTCCTGATTA AAGTCAAAAC GTTCAAATCG
151 GTATAATATC CCGTTACCAA TGCCGAGTTT GCGCAATTTC GTCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGCGAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGATTTAA AACAACCGGT AACCAATGTT TCCTGGTTTC CCGCGAACCG
351 CTATTGCGCC GCACAAGGCA AACGCTGCC GACCAATTGAC GAATGGGAAT
401 TTGCCGGACT TGCCTCCGCC ACGCAG.AAA AACGCTCAA ACGAACCCGG
451 CTACAACCCG ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
501 TGCACGATGT CGGCAAG.G TCGCCGAAC TACTGGGGCG TTTATGATAT
551 GACCGTCTG A
```

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
1  MKFTRLLEFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

	10	20	30	40	50	60
m525.pep	MKYVRLFXLGAALAXTQXAAA	AEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF				
a525	MKFTRLLEFLCAALAGTQAAA	AEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF				
	10	20	30	40	50	60
	70	80	90	100	110	120
m525.pep	AEFVNSHPQWQKGRIGSKQAE	PAYLKHHMKNGSRSYAPKAGELKQPVTNVSWXAANAYCA				
a525	AEFVNSHPQWQKGRIGSKQAE	PAYLKHHMKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA				
	70	80	90	100	110	120
	130	140	150	160	170	180
m525.pep	AQGKRLPTIDWEFAGLASATQ	XKRLKRTRLQPHYSRLV	CGRRTERPARC	CRXKAARTTGA		
a525	AQGKRLPTIDWEFAGLASATQ	XKRLKRTRLQPHYSRLV	CGWRPERPARC	RQXVARTTGA		
	130	140	150	160	170	180
m525.pep	FMICTGX					
a525	FMICTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
1  ATGAAGTACG TCCGGTTATT TTTCTCGGC ACGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGCAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351 CTATTGCCGC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAGAGACC GCCGAACTA CTGGGGTGGT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAACTATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAACT TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
1  MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKGLHDV GKDRPNYWG VYDMHGLIEWE TEDFNSLLS
201 SGNANAQMEC SGASVGASDS SNYAFLRYG IRTSLQSKYV LHNLFRCAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
1  ATGAAGTATG TCCGGTTATT TTTCTCGGC GCGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

792

```

151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGGGAATTAA AACCAACCGT AACCAATGTT TCCTGGTTTG CCGCAACGCG
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTCG AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAATATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```

1  MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK  NGSRSYAPKA
101 GELKQPVTNV SWFAANAYCA AQGRKLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV  GKGRPNYWG  YDMHGLIEW  TEDFNSLLS
201 SGNANAQMF  SGASIGSSD  SNYAAFLRY  IRTSLQSKY  LHNLFGRCTS
251  R*

```

m525-1/g525-1 97.6% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL DKYPVTNAEF					
g525-1	MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL DKYPVTNAEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKAGELKQPVTNV SWFAANAYCA					
g525-1	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKAGELKQPVTN ISWFAANAYCA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m525-1.pep	AQGRKLPTID EWEFAGLASAT QKNGSNEPG YNRTILDWYADGGKRLHDV GKGRPNYWG					
g525-1	AQGRKLPTID EWEFAGLASAT QKNGSNEPG YNRTILDWYADGGKRLHDV GKDRPNYWG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWE TEDFNSLLS SGNANAQMF CSGASIGSSD SNYAAFLRY GIRTSLQSKYV					
g525-1	YDMHGLIEWE TEDFNSLLS SGNANAQMF CSGASVGS DSNYAAFLRY GIRTSLQSKYV					
	190	200	210	220	230	240
	250					
m525-1.pep	LHNLFGRCTSRX					
g525-1	LHNLFGRCTSRX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

a525-1.seq

```

1  ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51  AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCGCG
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGGGAATTAA AACCAACCGT AACCAATGTT TCCTGGTTTG CCGCAACGCG
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA CTGGTATGCG GATGGCGACC GGAAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTCG AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAATATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKFTRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGRKDLHDV GKGRPNYWGV YDMHGLIEWE TEDFNSLLS
201 SGNANAQMFC SGASIGSSDS SNYAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVNTNAEF					
a525-1	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGELKQPVNTVSWFAANAYCA					
a525-1						
	70	80	90	100	110	120
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTIDEWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWGV					
a525-1						
	130	140	150	160	170	180
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWETEDFNSLLSSGNANAQMFCSGASIGSSDSSNYAFLRYGIRTSLSQSKYV					
a525-1						
	190	200	210	220	230	240
	250					
m525-1.pep	LHNLGFRCTSRX					
a525-1						
	LHNLGFRCTSRX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atgggttttac cagtctcctt ttttcagcct gtccagttgg cggcggtcgc
51  gcttggtcgg tctgccgtcg ggatgggcgg aagtgatgcg gctgaattgg
101 tcgagctggt tgcactcttc cctcaatgct gccgttttct cgtctctctc
151 atacagaagc cgcgcctcgg gtgccgggcg gcggttggtg ttcaaacctt
201 taaccttgat tttatgggga aggggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tgggtttact gtttttgact ttcgagccgt ttacttgaac
301 cctaccagct tcgatatgct tttgcgcaag ggaacgggtc ttgaaaaaac
351 gtgccgccca aagccatttg tccagccgca tggcgggaaga atcgtgcttg
401 tctttcatac gattttggtt gaaataattg aatttgtttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLPSVFFQP VQLAAVALGR SAVGMGGSDA AELVELFALF PQCCRFRVFF
51  IQKRLGCRA ALVVQTFNLD FMKGIERQV DNIADVYGFT VDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
51  GCTTGGTTCG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTWTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCYTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT

```

794

```

201 TAACCKTGAT TTTATAGGGA AGGG.AATtk AgCkTCaGty GrTwATaTCG
251 CsGATGTmTA TGGTTTTACT GTTTTtGACC TTCGAGCCGT TTACTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTTGTtT GAAATAATTG AATTTGTTTC GAGTTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

m527.pep

```

1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRVRVLF
51 IQKPRXGCRA ALVVQTFNxD FIGKXNXASV XXIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRVRVLF IQKPRXGCRA					
g527	MVLPSVFFQP VQLAAVALGR SAVGMGSDA AELVELFALF PQCCRFRVFFI QKPRLGCRA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m527.pep	ALVVQTFNxD FIGKXNXASV XXIADVYGFT VFDLRAVYLN PTQFDVLLRK GTGLEKTCRP					
g527	ALVVQTFNLD FMGKIERQVD NIADVYGFT VFDRAVYLN PTQFDMLLRK GTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGR IVLVFHTILF EIIEFVSSLA					
g527	KPFVQPHGGR IVLVFHTILF EIIEFVSSLA					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

a527.seq

```

1 ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCCG
51 GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCCTCTTTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
251 CCGATGTCTA TGGTTTTACT GTTTTtGACC TTCGAGCCGT TTACTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTTGTtT GAAATAATTG AATTTGTTTC GAGTTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

a527.pep

```

1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLF
51 IQKPRLGCRA ALVVQTFNLD FIGKIERQV DNIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

m527/a527 93.3% identity in 150 aa overlap

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRVRVLF IQKPRXGCRA					
a527	MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLF IQKPRLGCRA					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m527.pep	ALVVQTFNXXDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
			:			
a527	ALVVQTFNLDFIGKGIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaaattc gggtaataaa atatacggca acggctgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcggggtg gtatgagtgt ttgtccttgt
101 cgggctggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggcggcgaga gtccgctgtc ttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatctt
251 acttttatag gaaaataggg aagtttgaag cctgcgggtt ggattggcgt
301 acgctgacg gcaaaccttt ggttgagagg ttcaaacagg aaggtttcga
351 ctggttgaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQGGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTTGGGATATT
151 GCGGCGGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTTACA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGTA
351 CTGCTTGGAA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

m528/g528	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
g528	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPLSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
g528	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQGGFDCLE					
	70	80	90	100	110	120



796

```

m528.pep      K
               |
g528          KQGLRRNGLSERVRW

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

```

a528.seq
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT
151 GCGGCGGAGA GTCCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

```

a528.pep
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLK KQGLRRNGLS ERVRW*

```

m528/a528 95.0% identity in 121 aa overlap

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
a528	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
a528	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLK					
	70	80	90	100	110	120

```

m528.pep      K
               |
a528          KQGLRRNGLSERVRW
               130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

```

g528-1.seq
1  ATGGAAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT
51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCTTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT
151 GCGGCGGAGA GTCCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAATCTT
251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GGTGAGAGG TTCAAACAGG AAGGTTTCGA
351 CTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGCCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

```

g528-1.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLIVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

```

m528-1.seq
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

```

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```

51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

```

m528-1.pep..
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

          10      20      30      40      50      60
g528-1.pep MEIRV KYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
          |||:|||| |||:|||||||:|||||||:|||||||:|||||||: || |
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90      100     110     120
g528-1.pep YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
          |||:|||||||:|||||||:|||||||:|||||||: || | |||||
m528-1      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90      100     110     120

          130
g528-1.pep KQGLRRNGLSERVRWX
          |||:|||||||
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

```

a528-1.seq
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GGCGGCGAGA GTCCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

```

a528-1.pep
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

          10      20      30      40      50      60
a528-1.pep MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
          |||:|||||||:|||||||:|||||||:|||||||: |||: |||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90      100     110     120
a528-1.pep YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE
          |||:|||||||:|||||||:|||||||:|||||||: |||: |||
m528-1      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90      100     110     120

          130
a528-1.pep KQGLRRNGLSERVRWX
          |||:|||||||
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

g529.seq (partial)

```

1 atgacccata tcaaaccctg cattgccgcg ctgcactca tcgggcttgc
51 cgctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggctgcaccg cctgatcaaa ctggaagtcc cgctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc ggctcggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccagcggatg
251 ccggaagtat tgaaaagcgt caaaggcgtc cgcttcgagc ggagacggca
301 gccaacgcct ggcttgcgt tgacggcaaa tcccccgccg aaatctccgc
351 cgctttctg.

```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

g529.pep (partial)

```

1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAAF..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

m529.seq

```

1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTGCACTCA TCGGGCTTGC
51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTCGCACCG CCTGATCAAA CTTGAAGTCC CACCTGATT GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCTG CGGCAAGTCT CTGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
451 CCCCAAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 CTACTCCACC GCGGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCG
701 TTGACGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAAGC AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCGCACCGT GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACGAAC GCCACGCCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCCT CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTGCGCA ACGGCTCGCG CATCGTCTTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGCG AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

m529.pep

```

1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAEVLKSV KGVRLERDGS
101 QRWLVDGKS PAEIWPLLKA FWQENGFDIK SEEPALGQME TEWAENRAKI
151 PQDSLRLRFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGKDKDTTV WQPSPSDPNL EAAFLTRFMQ YLGVDDQQA NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRTVLAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

          10      20      30      40      50      60
g529.pep  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA

```

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```

|||||
m529  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPDQGNLYRLPA
      10      20      30      40      50      60
      70      80      90      100     110     120
g529.pep GSGAVRAGDLEKRRTPAVQQPADAGSIEKRQRRPLRAATAANAWLVVDGKSPAIESAAFX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m529  GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLER-DGSQRWLVDGKSPAIEWPLLK
      70      80      90      100     110
m529  AFWQENGFDIKSEEPaIGOMETEWAENRAKIPQDSLRLRLFDKVLGGIYSTGERDKFIVR
      120     130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1523>:

```

a529.seq
1  ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51  CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTGCGACCG CCTGATCAAA CTCGAAGTCC CACCTGATT GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTGCG CGGCAAGTCT CATGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG TGCCAAATC
451 CCCCAGACA GCTTGCGCCG CCTATTCGAC ACAGTCGGT TGGGCGGCAT
501 CTAATCCACC GGCGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCG
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAAC TACCCTTCCC
751 GCGCCCAACG AAATGGCGCG TATCGAAGG AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCGCACCGC GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTACC GAACAAAAC CCGCCTGT
951 CAAACGCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCCGAG CCGTGTGCGA ACGGCTCGCG CATGCTCCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAACTC CATTCCGAAC TCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1524; ORF 529.a>:

```

a529.pep
1  MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPN
51  DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAELVLSV KGVRLERDGS
101 QRWLVDGKS HAEIWPILLKA FWQENGFDIK SEEPaIGOME TEWAENRAKI
151 PQDSLRLRLFD TVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGKDKDITV WQSPSPDENL EAAFLTRFMQ YLGVDGQQA NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRALAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPGLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELR*

```

m529/a529 99.2% identity in 375 aa overlap

```

      10      20      30      40      50      60
m529.pep MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPDQGNLYRLPA
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a529  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPDQGNLYRLPA
      10      20      30      40      50      60
      70      80      90      100     110     120
m529.pep GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVDGKSPAIEWPLLK
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a529  GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVDGKSHAIEWPLLK
      70      80      90      100     110     120
      130     140     150     160     170     180

```

800

```

m529.pep    FWQENGFDIKSEEPaIGQMETEWAENRAKIPQDSLRRLLFDKVLGGIYSTGERDKFIVRI
             |||||
a529        FWQENGFDIKSEEPaIGQMETEWAENRAKIPQDSLRRLLFDTVLGGIYSTGERDKFIVRI
             130      140      150      160      170      180

             190      200      210      220      230      240
m529.pep    EQGKNGVSDIFFAHKAMKEVYGGKDKDITVWQSPSPDNLEAFLTRFMQYLGVDGQQAEE
             |||||
a529        EQGKNGVSDIFFAHKAMKEVYGGKDKDITVWQSPSPDNLEAFLTRFMQYLGVDGQQAEE
             190      200      210      220      230      240

             250      260      270      280      290      300
m529.pep    NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTVLALDRIGLTVVGQNTERHAFVLQ
             |||||
a529        NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTALALDRIGLTVVGQNTERHAFVLQ
             250      260      270      280      290      300

             310      320      330      340      350      360
m529.pep    KAPNESNAVTEQKPLFKRLLGKGAEKPAEQPELIVYAEFPVANGSRIVLLNKDGSAYAG
             |||||
a529        KAPNESNAVTEQKPLFKRLLGKGAEKPAEQPELIVYAEFPVANGSRIVLLNKDGSAYAG
             310      320      330      340      350      360

             370
m529.pep    KDASALLGKLHSELRX
             |||||
a529        KDASALLGKLHSELRX
             370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga gcgcggaat gacgggttg atatgggtca tctgtcatc
51  ctgtgtgatg gatattaaag tgtttgcatt gttatgccgt ccgaacggtt
101 cagacggcat ggctatatat aaagttgtcc tgaggcttcc agggcgccgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgccacg
201 tgcgggtccg atccgcccaa ggccgatacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgctgtaaat cggaatcagc cggtcggttg

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCVM DIKVFVMLCR PNGSDGMAIF KVVLRLSGRR
51  GLLXVRLPSA ERAAGRAVR IRPRRIPPIS VRRDWVRRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  WTGAGTGCGA GCGCGGCAAT GACGGGTYTG ATATGGGTCA TCGTGTATC
51  STGTGTGATG GATATTAAAG TGTYTGTTC GWTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTIONTGC WTGTCCGTTT YCCGTCAGCG GAACGAGCGG CAGGCGGACG
201 TCGGGTTCGC ATCTGCCCAg GCGGATACC GCCCATTTTC GTGCGGCGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CCGTCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL IWVIVSSCVM DIKVXVAXCR PNGSDGMXIF KVVLRLSGRR
51  GLLXVRFPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

m530/g530

```

m530.pep    XSASAAMTGLIWVIVSSCVM DIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA 60
             |||||

```

g530	MSASAAMTGLIWWIVSSCVMDIKVFVMLCRPNNGSDGMAIFKVVLRLSGRRGLLPVRLPSA	60
	10 20 30 40 50 60	
m530.pep	ERAAGGRAVIRICPGRIPPISVRRGWVRRTWCRKSESVGR	99
	:            :       :	
g530	ERAAGARAVRIRPRRIPPISVRDWRVTWCRKSESAGR	99

```
a530.seq
1      ATGAGTGC GA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTATC
51     CTGTGTGATG GATATTAAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
101    CGGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151    GGACTTTTGC CTGTCCGCCT TCCGTCAGCG GAACAGCGGG CAGGCGGAGC
201    TCGCGTTTCG ATCTGCCCAT GCGCGATACC GCCCATTTCG GTGCGGCGGG
251    GCTGGGTTTC GACAACATGG TGTCTAAAT CGGAATCAGC CGTGCGTTGA
```

a530.pep  
1 MSASAAMTGL IWVIVSSCVI DIKFVVALCR PNGSDGMAIF KVLRLSGRR  
51 GLLPVRLPSA ERAAGGRAVR ICPGRIPIIS VRRGWVRRTW CRKSESAGR\*

	10	20	30	40	50	60
m530.pep	XSASAAMTGLIWVIVSSCVM DIKVVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFP					
a530	MSASAAMTGLIWVIVSSCVM DIKVFALCRPNGSDGMAIFKVVLRLSGRRGLLPVRLP					
	10	20	30	40	50	60
	70	80	90	100		
m530.pep	ERAAGGRAVRI CPGRIPPISVRRGWVRRTWCRKSES VGRX					
a530	ERAAGGRAVRI CPGRIPPISVRRGWVRRTWCRKSESAGR					
	70	80	90	100		

```
g531.seq
  1  ATGACCGCCC  TACTCGTCAT  CCTCGCCCTC  GCCCTGATAG  CCGTCGGCAC
51  GGCAGGCATC  GTCTATCCCG  CCCTGCCCGG  CTTGGCATTG  ATGTTTGCCG
101 GAACATGGCT  GCTTGCCAT  GCCGGCGGCT  ATCAAATCTA  CGCGCGCAGC
151 ATCTTGTGGA  CGGTGCGACT  CATCAGCCTT  GCGGCATAC  TGGCGGACTA
201 TATGGCAGCG  ATGTTGGGG  TAAAATACAC  TGGGGCAGGC  AAACTCGCGC
251 TCCGAGGTGC  ATTGCCCGC  AGCATATCG  GCATATTTT  CTCCTTCCC
301 GGAATAATAC  TCGGCCCTT  TATCGGCGCG  GCGCGAGCG  AACTGATCGA
351 TCGGCGCAAT  ATGCTTCAG  CAGGTAAAG  GGGCTTGGT  ACGCTGTTGG
401 GCGTTGTGCT  CGGCACGGC  TTCAAATCG  GCTGCGCGT  ATCCATCTTG
451 TTTATCTGCT  TGGTGAATA  CATCGCATA  CTGTTTTAA
```

g531.pep

1	<u>MTALLVILAL</u>	<u>ALIAVGTAGI</u>	<u>VYPALPGLAL</u>	<u>MFACTWLLAY</u>	<u>AGGYQIYGAG</u>
51	<u>ILWTVGLISL</u>	<u>GGILADYMG</u>	<u>MLGVKYTGAG</u>	<u>KLAVRGALAG</u>	<u>SIIGIFFSLP</u>
101	<u>GLLLGPFIGA</u>	<u>AAGELIDRRN</u>	<u>MLQAGKAGLG</u>	<u>TLLGLVVGTA</u>	<u>FKIGCAVSIL</u>
151	<u>FLLLVKKIAY</u>	<u>LF</u>			

```
m531.seq
1  ATGACCGTAC TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
51  GGCGGGCATC GTTTaCCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
101 GAACATGGCT GCTTGCCATAT CGCGGCGGCT ACCAAATCTA CGCGCGCGGC
151 GTTTTGTGGA CGGTCCGACT CATCAGCCTT GCCGCATAC TGGCGGACTA
201 TGTGGCAGGC ATATGGGGGA CAAATATATC CGGAGCGGGC AAGCTCGCCG
251 TTCGCGCGCC ATTGGCCGGC AGCATCATCG GCATATTTTT CTCCCTTCCC
301 GGACTAATAC TCGGTCCCTT TATCGGCGCG CGCGCAGGCG AACTGATCGA
```

m531.pcp

1 MTVLTVILAL ALIavgTAGI VYPALPLAL MFAGTWLLAY AGGYQIYGAG  
51 VLWTVGLISL AGILADYVAG IWGTYKTGAG KLAVRGALAG SIIGIFFSLP  
101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL  
151 FILLVKYIAY LF\*

Homology with a predicted ORF from *N. gonorrhoeae*

m531/q531

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1535>:

a531.seq

1	ATGACCGCCT	TGCTCGTCAT	CCTCGCCCTC	GCCTGATAG	CCGCCGGTAC
51	GGCGGGCATC	GTTTACCCCG	CCCTGCCCGG	ATTGGCATTG	ATGTTTGCCG
101	GAACCTTGCT	GCTCGCCTAC	TCCGCGCGCT	ACCAAATCTA	CGCGCGGGGC
151	GTTTTGTGGA	CGGTGGACT	CATCAGCCTT	GCCGCGATAC	TGGCGGACTA
201	TGTGGCAGGC	ATATGGGGGA	CAAAATATAC	CGGAGCGGAC	AGGCTCGCCG
251	TTCGCGGCGC	ATTGGCCGGC	AGCATCATCG	GCATATTTTT	CTCCCTTCCC
301	GGACTAATAC	TCGGTCCCTT	TATCGGCGCG	GCGCGAGGCG	AACTGATCGA
351	ACGGTCAATC	ATGCTTCAGG	CAGGTAAGC	GGGCTTGGGT	ACGCTGTTGG
401	GGCTTACTCG	CGGTACGGCG	TTCAAAATCG	GCTGCGCGGT	ATCCATCTTG
451	TTTATCTCTG	TGGTGAATAA	CATCGCCTAC	CTGTTTTAA	

This corresponds to the amino acid sequence <SEQ ID 1536; ORF 531.a>:

a531.pep

```

1  MTALLVILAL ALIAAGTAGI VYPALPGLAL MFAGTWLLAY SGGYQIYGAG
51  VLWTVGLISL AGILADYVAG IWGTKYGTAG KLAVRGALAG SIIGIFFSLP
101 GLILPFIGA AAGELIERNR MLQAGKAGLG TLLGLIVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

```

m531/a531 96.9% identity in 162 aa overlap

	10	20	30	40	50	60
m531.pep	MTVLTVILALIALI	AVGTAGI	VYPALPGLAL	MFAGTWLLAY	AGGYQIYGAG	VLWTVGLISL
	:					
a531	MTALLVILALIALI	AAGTAGI	VYPALPGLAL	MFAGTWLLAY	SGGYQIYGAG	VLWTVGLISL
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADYVAGI	WGTKYT	GAGKLAVR	GALAGSII	GIFFLPGLIL	GPFGIAAAGELI
						ERRN

803

```

|||||
a531      AGILADYVAGIWGTYKTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERRN
              70      80      90      100      110      120

              130      140      150      160
m531.pep  MLQAGKAGLGTLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
|||||
a531      MLQAGKAGLGTLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
              130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acagggcggt tcgcctgatt tgggtgtacgg
51  tttggaagac aggccgccgt tcggtaatgc gctcttgagc gcgggtaccc
101 atcttttggc gattttcgtg ccgatgatta cggccgcgct gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgatctctg tgctgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggtcaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattcgctc
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGSVGSGML SIQRYRHDCA
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCCGT TCGTAATGCG GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GCGCGCGCTG AATTGCCCGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGTTGCGC TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTGCTT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GCGCGGTTTT
401 TGGTGTTGTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACCGGTC GCGGCGTGGT CGTGATGCTC ATTTGGTTGA GTTTGTTACA
501 CGTCGGCATT ACCGATTTCG GCGGCGGCTT CCGCGCGAAG GCGGACGGCA
551 CGTTCCGGCT GATGAAAAC TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCGC CTGTTGCGCA TGAGCGGCAT
651 TGCGGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCGCGTACCG
751 TTTAAATACG GTTTTGCTTT CCACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCCTG
901 CGCGGCGGCG TGTTGGCTGA CCGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTGCGCA AAACAACGGC GTGATTCAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTT GATGTTCCGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCAG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKQAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVF GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVVL IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```



804

201 VLVFNCKMNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLFPV  
 251 FKYGFADFWDH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEYTKRL  
 301 RGGLADGLV SVIATAGSL PLTTFAQNNQ VIQMTGVASR HVGKYIAVIL  
 351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA  
 401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT  
 451 EAIVKFDTH LEH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from *N. gonorrhoeae*:

g532/m532

	10	20	30	40	50	60
g532.pep	MAETMKQADSPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
m532	MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	
g532.pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLSIQRYRHDCARRGDERGRFEX					
m532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

a532.seq

```

1   ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAGGAT AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GCGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTGCGATGGC
201 GATGGTTGCG TCGGGTGTCG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT CTCGTTTCGTT
301 ACCGTCATGA TTGCGCTCGG CGCGGGGATG AAAGAGGGCG GTTTGATATAA
351 GATGCGCATG ATTTCCGACG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTTT
401 TGGTGTGTTT TTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGTGTGGT GGTGATGCTG ATCGGCTTGA GTTTGTGTACA
501 CGTCGGTATT ACCGATTTTCG GCGCGCGGCTT CGGCGCAAAG GCGGACGGCA
551 CGTTCGGCTC GATGGAAAAC TTGGGGCTGG CATCGCTGGT GCTGCTGATT
601 GTGCTGGTGT TCAATTGCAT GAAAAACCCG CTGCTGCCGA TGAGCGGCAT
651 TGCGGTTCGT CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC GGCACGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTAAATATG GTTTTGCTTT TGAATGGCAC GCATTTATTG TGGCGGGTGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTG ACGGCGACGG
851 CAATGGTGTC CGACGACCGG ATTGAAGGCG AGGAATACAC CAAACGCTTG
901 CGCGCGGCGG TGTGGCGGGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTGCACA AAACAACGGC GTGATTGAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGA CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTCCGG TTGATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGCCACG GCATCCGCAG GCGCGAAGCG
1201 GTAATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532.pep

```

1   MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV

```

805

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSEFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCMKNP LLRMSGIAGV LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
251 FKYGFADFWDH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
301 RGGVLADGLV SVIATAGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

```

      10      20      30      40      50      60
m532.pep MSGQLGKGADAPDLVYGLEDPRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
a532      MSGQLGKGADAPDLVYGLEDPRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
      10      20      30      40      50      60

      70      80      90     100     110     120
m532.pep AYLVSAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM
a532      AYLVSAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM
      70      80      90     100     110     120

      130     140     150     160     170     180
m532.pep ISTLLGVSEFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK
a532      ISTLLGVSEFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK
      130     140     150     160     170     180

      190     200     210     220     230     240
m532.pep ADGTFGSMENLGLASLVLLIVLVFNCKMKNPLLRMSGIAGVLIAGYIVALFLGKVDFSALQ
a532      ADGTFGSMENLGLASLVLLIVLVFNCKMKNPLLRMSGIAGVLIAGYIVALFLGKVDFSALQ
      190     200     210     220     230     240

      250     260     270     280     290     300
m532.pep NLPLVTLVPVPFKYGFADFWDHAFIVAGAIFLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL
a532      NLPLVTLVPVPFKYGFADFWDHAFIVAGAIFLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL
      250     260     270     280     290     300

      310     320     330     340     350     360
m532.pep RGGVLADGLVSVIATAGSLPLTTFAQNNGVIQMTGVASRHHVGKYIAVILVLLGLFPVVG
a532      RGGVLADGLVSVIATAGSLPLTTFAQNNGVIQMTGVASRHHVGKYIAVILVLLGLFPVVG
      310     320     330     340     350     360

      370     380     390     400     410     420
m532.pep RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF
a532      RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF
      370     380     390     400     410     420

      430     440     450     460
m532.pep KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX
a532      KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX
      430     440     450     460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

g535.seq

```

1   atgccctttc ccgttttcag acaantattt gcttngtcc tgcctacggtt
51  ttttgccgta ggctcgattc tcgaatccga catttccaac agcgggtttt
101 cggaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatctaca tcgcttccaa ttctgcaaac ttgggtatcca
201 gttctttcac gccctgtttg ccgaagttga tggcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttcggc tgtttgaagt

```

g535.pep

1	MPFPVFRQXF	AXSLLRFFAV	GRILESDISN	SGFSETINAS	NVFFVGYEYP
51	ACISNLHRFQ	FRKLGIQFFH	ALFAEVDGQS	GGFAFVCGID	NHAGAEEGVT
101	DVLSDEACV	GLRLFVIDD	FVPLYGGLAR	VAVAVEGGFF	DQGVVQYFWR
151	DFFDEAGCDA	ELGSLVQHAL	LCHGDVEAFA	GAGDGDVHEA	AFFFEAAALG
201	KAHFAGETPL	FLTGEEDGVE	FQAFGGVDGH	QLDGGFFACPC	LVFAGFEGGV
251	AOHEGDEGGG	IV*			

m535.seq

1	aTGCCCTTtc	CGGTTTTcAG	ACGGCCTTTT	GCTTTGCTCT	TACTtACGTT
51	TTTTGCCGTA	AGTCAGATTC	TTGTATCCGA	CATTTCCAAC	AGCGGTGTTT
101	CGGAACAAT	AGACGGCGTA	AATGTTTTTG	TCGGATACGA	ATATCCGACC
151	TACATTTCAA	ATTTACATCT	CTTCCAATTG	CGCAAACTTG	GTGTCCAAC
201	CTTTCACGCC	CTGTTTTGCCG	AAATGTATGG	TCAGTCGGGG	GGATTGCGCT
251	TTATCTGCGG	CATCGATAAT	CACGCCGGTG	CCGAATTGGG	CGTGGCGGAC
301	GTTTTGTCCG	ATACGGAAAC	CTGCGTAGGT	TTGGGGCTGT	TTGTAGTCGT
351	CGATGATTTT	ATCTTTGGAT	GCGGCGGTTT	GGCGCGTGTT	GCCGTAAC
401	TCGTAGGCAG	GCTTTTTGAC	GACAGAGTAG	TGCAATACTT	CGGGTGGGAT
451	CTCTTCGACG	AAGCGGGAGA	CGATGCCGAA	TTGGGTTTGT	CCGTGCAGCA
501	TGCGTTTGTG	GCCCATGGTG	ATGTAGAGGC	GTTTGGCGGG	CGGGGTGATG
551	GCGACGTACA	TGAGGCGGCG	TTCTTCTTCG	AGGCCGCCGC	GTTCGGCAAG
601	GCTCATTTCG	CTGGGGGAAG	GGCCTTCTTC	CATGCCGGTG	AGGAAGACGG
651	CGTTAAATTC	CAAGCCTTTG	GCGGCGTACG	CGGTCTATGAG	TTGGACGGCC
701	TTTTCGCCTG	CGGCTCGCTG	GCTTCCTGGA	GATTCGAGGG	CGGCATTGCT
751	TAGGAAGGCG	AGAATGGGGA	AGGCGGGGTC	GTCTGA	

m535.pep

```

1  MPFPVFRRPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
51  YISNLHLFQF RKLGVQLFHA LFAEIDGQSG GFAFICGIDN HAGAEEGVAD
101 VLSDTETCVG LGLFVVVDDF IFGCGGLARV AVTVVGRLFD QGVVQYFGWD
151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFFEEAAAFGK
201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
251 XEFGEGGVV V*

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

m535/q535

	10	20	30	40	50	59
m535.pep	MPFPVFRPPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEPTYISNLHLFQ					
	:            :              :            :					
g535	MPFPVFRQXFAXSLLRFFAVGRILESDISNSGFSETINASNVFFVGYEYPACISNLHRFQ					
	10	20	30	40	50	60
	60	70	80	90	100	119
m535.pep	FRKLGVLGFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDD					
	:  :     :      :      :      :      :      :      :					
g535	FRKLGIQFFHALFAEVDGQSGGFVFCGIDNHAGAEFGVTDVLSDAEACVGLRLFVIDD					
	70	80	90	100	110	120

807

	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGRLLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFA						
	:      :    :        :						
g535	FVPLYGGLARVAVAVEGGFFDGQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACAC						
	:        :          :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVFQAFGGVDGHLQDGFACPC						
	190	200	210	220	230	240	
	240	250	260				
m535.pep	LVFTGFEGGIAXEGENGEGGVV						
	:      :    :      :						
g535	LVFAGFEGGVAQEGEDGEGGIV						
	250	260					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1547>:

a535.seq (partial)

1	TTTCAGACGGC	CTTTTGCCCT	GTCCTTGCTA	CAGTTTTTTG	CCATAGGTGC
51	GATTCTCGAA	TCCGACATTT	CCAACAGCGG	TTTTTCGGAA	ACGATAGACG
101	CGTCAAATAT	TTTTGTCCGA	TACGAGTATC	CAGCCTGCAT	TTCAAATTTA
151	CATCGCTTCC	AATTTTCGAA	ACTTGGTGTC	CAACTCTTTC	ACGCCCTGTT
201	TGCCGAAATT	GATGGTCAGT	CGGGCGGATT	CGCCTTTATC	TGCGGCATCG
251	ATAATCACGC	CGGTGCCGAA	TTTGGCGTGG	CGGACGTTTT	GTCCGATACG
301	GAAACCTGCG	TAGGTTTGGG	GCTGTTTGTA	GTCGTCGATG	ATTTTGTCTT
351	TGGGCGCGGC	GGTTTGCGGC	GTGTTGCCAT	AGCGGTCGTA	GGCGGGTTTT
401	TTGACGGACA	GGTAGTGCAA	TACTTCGGGC	GGGATTTCTT	CGACGAAGCG
451	GGAGACGATG	CCGAATTGGG	TTTGTCCGTG	CAGCATGCGT	TGTGCGCCA
501	TGGTGATGTA	GAGGCGTTTG	CGGGCGCGGG	TGATGGCGAC	GTACATCAGG
551	CGGCGTTCTT	CTTCGAGGCC	GCCGCGTTCG	GCAAGGCTCA	TTTCGCTGGG
601	GAAGCGGCCT	TCTTCCATGC	CGGTGAGGAA	TACGGCGTTA	AATCCAAGC
651	CTTTGGCGGC	GTGCACGGTC	ATGAGTTGTA	CGGCTTTTTC	GCCGCGCCT
701	GCTTGGTTTT	CGCCGATTTC	GAGAGCAGCA	TTGCTTAGGA	AAGCGAGGAT
751	GGGAAGGCG	GGTCGCTCTG	A		

This corresponds to the amino acid sequence <SEQ ID 1548; ORF 535.a>:

a535.pep (partial)

1	FRRPFALSL	QFFAIGRILE	SDISNSGFSE	TIDASNIFVG	YEYPACISNL
51	HRFQFRKLG	VLFAHFAEI	DGQSGGFAFI	CGIDNHAGAE	FGVADVLSDT
101	ETCVGLGLF	VVDVDFVGRG	GLARVAIAVV	GGFFDGQVVQ	YFGRDFFDEA
151	GDDAELGLSV	QHALLRHGDV	EAFAGAGDGD	VHQAAFFFEA	AAFGKAHFAG
201	EAAFFHAGEE	YGVKFQAFGG	VHGHLYGFF	ARACLVFAGF	ESSIA*ESED
251	GEGGVV*				

m535/a535 88.7% identity in 256 aa overlap

	10	20	30	40	50	60
m535.pep	MPFPVFRPFALSLTFFAVSQILVSDISNSGVSETIDASNVFVGVEYPTYISNLHLFQF					
	:					
a535	FRRPFALSLQFFAIGRILESDISNSGFSETIDASNIFVGVEYYPACISNLHRFQF					
	10	20	30	40	50	
	70	80	90	100	110	120
m535.pep	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
a535	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	60	70	80	90	100	110
	130	140	150	160	170	180
m535.pep	IFGCGGLARVAVTVVGRLLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	:       :     :        :					
a535	VFGRGGLARVAIAVVGFFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	120	130	140	150	160	170

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          190      200      210      220      230      240
m535.pep  AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKQAFGGVDGHELDGLFACACL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a535      AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKQAFGGVHGHELYGFFARACL
          180      190      200      210      220      230

          250      260
m535.pep  VFTGFEGGIAXEGENGEGGVVX
          ||:||||:||||:|||||
a535      VFAGFESSIAXESEDGEGGVVX
          240      250

```

q537.seq

1	atgaaatccc	tttttatttg	gtcgtctcta	ttgggctcgg	cggcaggcgt
51	tttctaccat	acccaaaacc	aatccctgcc	cgcgggcgaa	cttgtctatc
101	cgtccgcacc	gcaaatcagg	gacggcgggc	atgcgctgca	ctaccccaac
151	cgcattccga	cacaaaatcg	tttgcacgcg	ctggcacacg	cgcgggtttt
201	ggaaaattcc	gccgcaggc	acgcacgcgt	tctcacgctc	aatcccggaag
251	acggacacgg	cgcacaccaat	cccgacaatc	cgcactacac	cgcacaaaag
301	ctgaccgaac	gcacacgcct	tgccgggtat	ctctacaacg	gcgtgcatga
351	aaacatcagc	acggaagagg	aagccgcgga	atcgtccgac	agcgacatcc
401	gcacgcagca	acgccaagtg	gacgctttga	tgagcgcaat	ctaccaccgc
451	ctttcgtctg	ttgaccgcga	taccagcgaa	gcaggtgcgg	ctatttgtcg
501	cgaaaacggc	aaaaccgtcc	tcgtattcaa	tcagggtcaac	ggcagcttcg
551	agcgcgcctg	tgcaaaagga	aggcggcagc	cggaaagcagg	acggaaatat
601	taccgcaacg	cttgccacaa	cggtcgggcc	gtttatgctg	acgaagccat
651	gcccgtaaag	gaattgtctt	ataccgccta	tcgggtttgc	ggcggtcgcc
701	tgccttattt	ttacggggaa	gctcccgacc	ccgtggtcgg	atattgaatc
751	acaggcaatc	ctgcgcagcat	tgatttttcc	gaggcggcag	gcaaaattgc
801	gatgaaaagt	ttcaagctgt	atcagggtaa	aaacgaaatc	cgccccgtca
851	gggttttaac	cgcgcggcaa	gacctaacg	gcaggctgac	cgcgcaccaaa
901	ttcgcccttt	tcccgctcaa	acctttggaa	ctcggcacgc	tttatacggc
951	ggtatccgac	tatgtccgca	acggacggca	cgcgcaggcg	aaatggcaat
1001	ttagaaccgg	aaaaccggat	tacctttatt	ttgaggtaaa	cggcggcgag
1051	acacttgctg	ttagaaaaag	cgaaaaatat	ttcatccact	ggcgcggacg
1101	ctggtgtctg	gaagcgtgta	cccgttatac	ctaccggcgg	cagttcgcca
1151	acagcctgtc	catactccgg	cacgaagcgg	gcggcattgt	cttcagcgtc
1201	agcggaatgg	cgggaagcgg	catcaggctt	acctcggaag	acagcccgga
1251	acqcqgtgta	accctttatt	tgcaggattg	a	

q537.pep

```

1    MKSLFIWLLL  LGSAGVFYH  TQNQSLPAGE  LVYSPAPQIR  DGGDALHYLN
51   RIRTQIGLHA  LAHAPVLENS  ARRHARYLTL  NPEDGHGEHH  PDNPHYTAQK
101  LTERLTRLAGY  LYNGVHENIS  TEEEAESSD  SDIRTQQRQV  DALMSATYHR
151  LSLLDRLRTHD  AGAASFVRENG  KTVLVFNQGN  GSFERACAKG  RROQEAGRKY
201  YRNACHNGAA  VYADEAMPVT  ELLYTAYPVG  GGALPYFYGE  RPDVPVEYEI
251  TGNPASIDFS  EAAGKIAMKS  FKLYQGKNEI  RPYRVLTAGN  DPNGRLTAHQ
301  FALFPLKPLE  YGTLTYAVFD  YVRNGRGAHA  KWQFPTRKPD  YPYFEVNGGE
351  TLAVRKGEKY  FIIHWRGNVCL  EACTRYTYRR  QFGNSLSILR  HEAGGIVFSV
401  SGMAGSRIRL  TPEDSPERG  TLYLOD  *

```

m537.seq (partial)

1	ATGAAATCCC	TTTTTATTCG	GCTGCTCCTG	TTGGGTTCGG	CGGCAGGCGT
51	TTTCTACCAT	ACCCAAAmCC	AATCCCTGCC	CGCGGGCGAA	CTTGCTCTATC
101	CGTCCGCGAC	GCCAAATCAGG	GACGCGCGGG	ATCGCGTGCA	TACTCTCAAC
151	CGCATCCGAG	CCCAAATCGG	TTTGACAAG	CTGGCACACG	CGCCGGTTTT
201	GGAAACTCC	GCCCGCAGGC	ACGCAAGCTA	CCTCAGCTCT	AATCCCGAAG
251	ACGGGACACGG	GCAACACCAT	CCGCAACAT	CGCACTACAC	CGACCAAAAG

809

301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA  
 351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC  
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC  
 451 CTTTCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)  
 1 MKSLFIRLLL LGSAAGVFYH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN  
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK  
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR  
 151 LSLDRHTDE SGAA...

-- Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng)

from *N. gonorrhoeae*:

m537/g537

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIR DGGDALHYLN RIRAQIGLHK					
	:					
g537	MKSLFIWLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIR DGGDALHYLN RIRTAQIGLHA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
g537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
	:					
g537	TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAVFRENGKTVLVFNQGN					
	130	140	150	160	170	180
	190	200	210	220	230	240
g537	GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq  
 1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT  
 51 TTTTATCAT ACCCAAAACC AATCCCTGCC CGCGGGCGAA CTGTGTATC  
 101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC  
 151 CGCATCCGCG CCCAAATCGG TTGACACAAG CTGGCACACG CGCCGGTTTT  
 201 GGAAATTC GCGCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG  
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG  
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA  
 351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC  
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC  
 451 CTTTCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGCG  
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG  
 551 AGCGGCATTG CGCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT  
 601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT  
 651 GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC  
 701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC  
 751 ACGGGCAATC CTGCCAGCAT TGATTTTCC GAGGCGGCAG GCAAAATTAC  
 801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCGTCA  
 851 GGGTTTAAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA  
 901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC  
 951 GGTATTCGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT  
 1001 TTAGAACCGG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGGCGAG  
 1051 ACACCTGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GGCGCGGACG  
 1101 CTGGTGTGTTG GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

810

1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTCAGCGTT  
 1201 GACGGAATGG CGGGCAGCCG CATCACGCTT GCACCGAAG GAGAAACGGA  
 1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

a537.pep  
 1 MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN  
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK  
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR  
 151 LSLLDRHTDE AGAAFVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY  
 201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPPEYEI  
 251 TGNPASIDFS EAAGKITMKS FKLYQCKNEI RPYRVLTAGN DPNGRLTAYQ  
 301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE  
 351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RFGSRLSISR HKAGGIVFSV  
 401 DGMAGSRITL APEGETERGV TLYLQD\*

m537/a537 98.2% identity in 164 aa overlap

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL	LGSAAGVFYHTQXQSLPAGE	LVYPSAPQIR	DGGDALHYLN	RIRAQIGLHK	
a537	MKSLFIRLLL	LGSAAGVFYHTQXQSLPAGE	LVYPSAPQIR	DGGDALHYLN	RIRAQIGLHK	
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHAS	YLTNPEDGHGEHH	PDNPHYTAQK	LTERTRLAGY	LYNGVHENIS	
a537	LAHAPVLENSARRHAS	YLTNPEDGHGEHH	PDNPHYTAQK	LTERTRLAGY	LYNGVHENIS	
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQ	QRQVDGLMSAIYH	RSLDRHTDE	SGAA		
a537	TEEEAESSDSDIRTQ	QRQVDGLMSAIYH	RSLDRHTDE	AGA	AFVRENGKTVLVFNQGN	
	170	180	190	200	210	220
a537	GRFERHCAQGRNQ	PEAGRKYR	NACHNGAVVYT	DEAMPAQ	ELLYTAYPV	NGALPYFHGE
	230	240				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

g538.seq  
 1 atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccggaacg  
 51 cgctcatgctg gtggcgctaa tgttgataa agatgatacg ggcagcaatg  
 101 ccgcccgctct gaacgggttt cagacggcat tggcggaagc cgtcgagctg  
 151 gtcaaagcgg cgggcggcga ttccgtacgc gtggagactg ccaaacgcga  
 201 ccgccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt  
 251 cggaaagcagt tgccgcagac ggcattgatt tggctgatt caaccacgaa  
 301 cttactccca cgcaggaacg caatttgaa aaaatcctcc aatgcccgct  
 351 attggacaga gtgggctga ttctggcgat ttccgccgc cgcgcccgca  
 401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttgccg  
 451 ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggtat  
 501 cggcatgaaa gggccgggcg aaaccaaact ggaaaccgac cgccgattaa  
 551 ccgcccatcg gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa  
 601 cagcgcgccc tgcgccgcaa gtcccgcgag tcgggcagaa tcaaaacgtt  
 651 tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc  
 701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac  
 751 acgacggcgc ggcggctgta catcagtcgc gcatgcagca ttatcctgac  
 801 cgataccgctc ggattcgtca gcatctgcc gcacaaactg atttccgcct  
 851 tttccgccac cttggaagaa accgtgcaag ccgatgtgct gctgcacgct  
 901 gtcgatgctg ccgcccgga cagcgggcag cagattgaag acgtggaaaa  
 951 cgtactgcaa gaaatccatg cccacgatat tccgtgcatc aaggtgtaca  
 1001 acaaaaaccga cctgctgccc tctgaagaac aaaacacggg catatggcgc  
 1051 gacgctgcgg gaaaaattgc cgccgtccgc atttccgttg ctgaaaatac

This corresponds to the amino acid sequence <SEQ ID 1556; ORF 538.ng>:

```

g538.pep
  1  MSGRTGRNSA TQAQPERVML VGVMLDKDDT GSNAARLNGF QTALAEAVEL
 51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLTVFNHE
101  LTPTQERNLE KILQCRVLDL VGLILAIFAR RARTQEGRLQ VELAQLSHLA
151  GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLTAHRINA LKKQLANLKK
201  QRALRRKSRE SGRIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
251  TTARRLYISP ACSIIITDTV GFVSDLPKHL ISAFSATLEE TVQADVLLHV
301  VDAAARNSGO QIEDVENVLQ EIHADHIPC I KVNKTDLLP SEEQNTGIWR
351  DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

```

-- The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

```

m538.seq
  1  ATGACAGGCA GAACAGGCGG CAACGGCAGT ACCCAAGCGC AACCCGAACG
 51  CGTCATGCTG GTGGGCGTAA TGTGGACAA AGATGGTACG GGCAGTAGTG
101  CCGCCCCTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151  GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201  CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251  CAGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301  CTCACGCCCA CGCAGGAACG CAACCTTGAA AAAGAACTsA AATGCCGCGT
351  ATTGGACAGG GTAGGGCTGA TTCTGGCGAT TTTCGCTCGC CGCGCCCGCA
401  CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CGCAATTGAG CCATTTGGCG
451  GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501  CGGCATGAAA GGGCCCGGCG AAACCAAACCT GGAAACCGAC CGCCGATTGA
551  TCGCCCATCG GATCAATGCC TTGATAAAAC AGCTTGCCAA CCTCAAAAAA
601  CAGCGCGCCC TCGCGCGCAA GTCnCGCGAA TCGGGCACAA TCAAAACGTT
651  TCGCTGGTGC GGCTATACAA ATGTCGGAAA ATCCAGCCTG TTCAACCGGC
701  TGACAAAGTC GGGCATATAT GCAAAGGACA AGCTTAGTCC CGAATGCAGC
751  ATTATCCTGA CCGATACCGT CGGATTCGTn AGCGATCTGC CGCacAAACT
801  GATTTCCGCC TTTTCGCC.A CGCTGGAAGA AACCGCGCAA GCCGATGTGC
851  TGCTGCACGT CGTCGATGCC GCCGCTCCGA ACAGCGGACA GCAGATTGAA
901  GACGTGGAAA ACGTACTGCA AGAAATCCAT GCCGCGGATA TTCCGTGCAT
951  cAAGGTGTAC AACAAAACCG ACCTGCTGCC GTCTGAAGAA CAAAACACGG
1001 GCATATGGCG CGACGCTGCG GAAAAAATTG CCGCCGTCCG CATTTCGGTT
1051 GCTGAAAATA CCGGTATAGA CGCACTGCGC GAAGCcATTG CCGAGTCTTG
1101 TGCCGCCGCA CCAAACACAG ACGAAACCGA AATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

```

m538.pep
  1  MTGRTGGNGS TQAQPERVML VGVMLDKDGT GSSAARLNGF QTALAEAVEL
 51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLTVFNHE
101  LTPTQERNLE KELKCRVLDL VGLILAIFAR RARTQEGRLQ VELAQLSHLA
151  GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LIKQLANLKK
201  QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDKLSPECS
251  IILTDTVGFV SDLPHKLISA FSXTLEETAQ ADVLLHVDA AAPNSGQQIE
301  DVENVLQEIH AGDIPCIKVY NKTDLLPSEE QNTGIWRDAA GKIAAVRISV
351  AENTGIDALR EAIAESCAAA PNTDETEMP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

m538/g538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
	:      :                   :					
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLTVFNHELTPTQERNLEKELKCRVLDL					
	:					
g538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLTVFNHELTPTQERNLEKILQCRVLDL					



812

	70	80	90	100	110	120
m538.pep	130	140	150	160	170	180
	VGLILAI	FARRARTQ	EGRLQVELA	QLSHLAGRL	IRGYGHLQ	SQRRGGIGMKGPGETKLETD
g538	VGLILAI	FARRARTQ	EGRLQVELA	QLSHLAGRL	IRGYGHLQ	SQRRGGIGMKGPGETKLETD
	130	140	150	160	170	180
m538.pep	190	200	210	220	230	240
	RRLIAHR	RINALIKQ	LANKQAL	RRKSRES	GTIKTFAL	VGYTNVGKSSLFNRLTKSGIY
g538	RRLTAHR	RINALIKQ	LANKQAL	RRKSRES	GRIKTFAL	VGYTNVGKSSLFNRLTKSGIY
	190	200	210	220	230	240
m538.pep	250	260	270	280		
	AKDKL----	SPECSIIL	TDTVGFV	SDLPKLI	SAFSXTL	EETAQADVLLHV
g538	AKDQLFAT	LDDTTARR	LYISPAC	SIILTDV	GFVSDLP	KLISAFSATLEETVQADVLLHV
	250	260	270	280	290	300
m538.pep	290	300	310	320	330	340
	VDAAAPNS	GQQIEDV	ENVLQEI	HAGDIPCI	KVYNKTD	LLPSEEQNTGIWRDAAGKIAAVR
g538	VDAAARN	SGQQIED	VENVLQEI	HAHDIPCI	KVYNKTD	LLPSEEQNTGIWRDAAGKIAAVR
	310	320	330	340	350	360
m538.pep	350	360	370	380		
	ISVAENT	GIDALRE	AIAESCA	AAAPNTD	ETEMPX	
g538	ISVAENT	GIDALRE	AIAEYCA	AAAPNTD	ETEMPX	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1  ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGGGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGTCT GAACGGTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCCA TTCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTGGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTCGCCCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAACT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TCGCCGCAA GTCCCGCGAA TCGGGCACA TCAAAACGTT
651 TGCGCTGGTC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC GGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCGTCA GCGATCTGCC GCACAACTG ATTTCCGCCT
851 TTTCCGCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAATA
951 CGTACTGCAA GAAATCCATG CCGCGGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGCA CCTGCTGCGG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCCGC ATTTCCGTTG CTGAAAATAC
1101 CGGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1  MTGRTGRNGS TQAQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVALD GIDLVVFNHE
101 LTPTQERNLE KILQCRVLDL VGLILAIFAR RARTQEGRLQ VELAQLSHLA
151 RLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

```

813

201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD  
 251 TTARRLYISP ECSIILDTV GFVSDLPKLI ISAFSATLEE TAQADVLLHV  
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR  
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP\*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVM LDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
a538	MTGRTGRNGSTQAQPERVMLVGVM LDKDGTGSSATRLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRV LDR					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKILQCRV LDR					
	70	80	90	100	110	120
m538.pep	VGLILAI FARRARTQEGRLQVELAQ LSHLAGRLIRGYGHLQSQ RGGIGMKGPGETKLETD					
a538	VGLILAI FARRARTQEGRLQVELAQ LSHLAGRLIRGYGHLQSQ RGGIGMKGPGETKLETD					
	130	140	150	160	170	180
m538.pep	RRLIAHRINALIKQLANLKKQ RALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
a538	RRLIAHRINALKKQLANLKKQ RALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
m538.pep	AKDKL-----SPEC SIILDTVGFVSDLPKLI SAFSXTLEETAQADVLLHV					
a538	AKDQLFATLDTTARRLYISP ECSIILDTVGFVSDLPKLI SAFSATLEETAQADVLLHV					
	250	260	270	280	290	300
m538.pep	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
a538	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
m538.pep	ISVAENTGIDALREAIAESCA AAPNTDETEMPX					
a538	ISVAENTGIDALREAIAEYCA AAPNTDETEMPX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

```

1  atggaggatc tgcaggaaat cgggttcgat gtcgccgccg taaaggtagg
51  tcggcagcgc gaacatcatc gtctgcatca tacccagtcc ggcaacggca
101 aggcggacga tgtattgttt gcgttccttt tggttgccgg cttcgatttt
151 ttgcgcgtca tagggtgcgg cgggttagcc tgtctgccgg attttcaaca
201 gaatgtcggg gaggcggatt ttgccgtcgt ccagacgac gcggcagcgg
251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaag
301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaatg ccgtgagca
351 tcagcactgc ttcgtgcgtg ccattatggg tttccacaaa gtcggattgg
401 acttcgggca ggtcgtacag gcggatttgg tcgaggattt cttggggcgg
451 cagttcgggt tttttcgcgt cggcgggtgc tcgtttgtaa taactgccca
501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
551 gtttcgcggt cttcgccttc gtagcggacg gtcagatgca ggttttcggg
601 aacgtccagc ccgcagtggg aacagggttt tttcatggca tttcgggttc

```

814

```

651 gtctgtgttt ggtgcgccgg cacaatactc ggcaatggct tcgcgagtg
701 cgtctatacc ggtattttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccggtgtt tgttcttcag acggcagcag
801 gtcggttttg ttgtacacct tgatgcacgg aatategttg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgtt gttccggcgg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgacagg tttcttccaa
951 ggtggcgga aagggcgaaa tcagtttgtg cggcagatcg ctgacgaatc
1001 cgacggtatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgccgtcg tgctcgagagt ggcgaaaagc tggctcttcg catatatgcc
1101 cgacttgggc agccggttga acaggttga tttgccgaca ttggtatag

```

-- This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

```

g539.pep
1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQONVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGFHK VGLDFGQVVO ADLVEDFLGR
151 QGFFFRVGGG SFVITAQAGI DDALCDCLTA DAAGFAVFAF VADGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCPLFRA
301 AASTTCSSTS ACTVSSKVAE KAEISLCGRS LTNPTVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

```

m539.seq (partial)
1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTCTTTT TGGTTGGCGG CTTGATTTT
151 TTGCGCGTCA TAGGGTGCAG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCGTCTGT CCCAGACGAC GCGGCaGcGg
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAACCGC CTCGCGCGTG CCGCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCTGACAG GCGGATTGCG TCGAGGATT CTGGGGCGG
451 CAGCTCGGTT TTTTGCCTGT CCGCGTGGC TTGTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaGcGg
551 GTTTCGCGGT CTTCGTTTTC GTAACGGACA GTCAGGTGGA GGTGTTCCGG
601 AACATCCAGA CCGCAGTGA AACAGGTTT TTTTCATGGA TTTGTTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTG GGCAATGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTT
751 CCCGACGCGT CGCGCCATAT GCCCGTGTG TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTGT TGTACACCT TgATGCACGG AATATCGCCG GCATGGATT
851 CTGCGATGAC GTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCAGCG TTTCTTCCAG
951 CGTGGcG.AA AAGGCGGAAA TCAGTTTgTG CCGCAGATCG CThACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

```

m539.pep (partial)
1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQONVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVO ADLVEDFLGR
151 QLGLFRVGGG LFVITAQARV NNALCDRLTA GAQGFVAVVF VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPLFGA
301 AASTTCSSTS ACAVSSSVAX KAEISLCGRS LTNPTVSVRI MLHSG....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

```

m539/g539
10 20 30 40 50 60
m539.pep MEDLQEIGFDVAAVKVGRQREHHRLHHPQPNGEADDVLEAFFLVGGFDFLRVIGCGGVA
|||||
g539 MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLEAFFLVGGFDFLRVIGCGGVA

```

815

	10	20	30	40	50	60
m539.pep	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDVCAQKLLFDQPDAGGAGNAAEHQHC					
	70	80	90	100	110	120
m539.pep	130	140	150	160	170	180
	LARAAGVGHKVGGLDFGQVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGVGHKVGGLDFGQVQADLVEDFLGRQFGFVRVGGASFVITAQAGIDDALCDCLTA					
	130	140	150	160	170	180
m539.pep	190	200	210	220	230	240
	GAQGFVAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
g539	DAAGFAVFAFVADGQMVFVGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
m539.pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHFVFCSSDGSRSVLLYTLMHGISPAWISCSSTFTSSICCPFLGA					
g539	ATEMRTAAIFPAASRHFVFCSSDGSRSVLLYTLMHGISPAWISCSSTFTFTSSICCPFLFA					
	250	260	270	280	290	300
m539.pep	310	320	330	340		
	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRRAVSVRAKS					
	310	320	330	340	350	360
g539	WSFAYMPDLVSRNLRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTCTCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGC GGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TCGGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTTG ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCTGTACG GCGGATTGCG TCGAGGATTT CTGGGGCGG
451 CAGCTCGGTT TTTTGC GCGT GCGCGGTGCG TTGTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GCGCAGCAG
551 GTTTCGCGGT CTCGTTTTC GTAACGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGA AACAGGTTTT TTTTATGGCA TTTGCGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTT
751 CCCGAGCGT CCGCCCATAT GCGCGTGTTC TGTCTTTCAG ACGGCAGCAG
801 GTCGGTTTGT TGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGC GCGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTGTG CGGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTGAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CCGCGCGTCG TGTCGAGTGT GCGGAAAAGC TGGTCTTTCG CATATATGCC
1101 CCACTTGGTC AGCCGGTTGA ACAGACTGGA TTGCGGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF

```

816

51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAVRAVIEV DADDAVCTQK  
 101 LLFDQPDAGG AGDAAEH\*NR LARAAGVGHK VGLDFGQVVQ ADLVEDFLGR  
 151 QLGLRVGGA LFVITAQARV NNALCDCLTT GAAGFAVFVF VTDGQMVFVG  
 201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF  
 251 PAASRHPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPLFGA  
 301 AASTTCSSTS ACAVSSVAE KAEISLCGRS LTNPVSVRI MLHSGLMYSR  
 351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV\*

m539/a539 97.1% identity in 345 aa overlap

	10	20	30	40	50	60
m539.pep	MEDLQEIGFDVA	AAVKVGRQREHRLHHPQ	PGNGEADDVLF	FAFFLVGGFDF	LRVIGCGGVA	
a539	MEDLQEIGFDVA	AAVKVGRQREHRLHHPQ	PGNGEADDVLF	FAFFLVGGFDF	LRVIGCGGVA	
	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADFAVVPDD	AAVRAVIEVDADDAVCTQKLL	FDQPDAGGAGDAAEHXNR			
a539	YLPDFQQNVGKADFAVVPDD	AAVRAVIEVDADDAVCTQKLL	FDQPDAGGAGDAAEHXNR			
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAGVGHKVGLDFGQVVQ	ADLVEDFLGRQLGLRVGGAL	FVITAQARVNNALCDRLTA			
a539	LARAAGVGHKVGLDFGQVVQ	ADLVEDFLGRQLGLRVGGAL	FVITAQARVNNALCDCLTT			
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGFVAVFVFTDSQVEVFG	NIQTAVETGFFHGISVSSV	FGAAQDSAMASRSASIPVFS			
a539	GAAGFAVAVFVFTDGMQVFG	NVQPAVETGFFHGISVSSV	FGAAQYSAMASRSASIPVFS			
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAASRHPVFC	SSDGSRSVLLYTLMHGISP	AWISCSTFSTSSICCPLFGA			
a539	ATEMRTAAIFPAASRHPVFC	SSDGSRSVLLYTLMHGISP	AWISCSTFSTSSICCPLFGA			
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTTCSSTSACAVSSSVAX	KAEISLCGRSLTNPTVSVRI	MLHSG			
a539	AASTTCSSTSACAVSSSVAX	KAEISLCGRSLTNPTVSVRI	MLHSGMLYSRRRAVVSSVAKS			
	310	320	330	340	350	360
a539	WSFAYMPDLVSRLNRLDLPTLVX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

g540.seq

1 atgccgccct cccgacgcgg caacgggggtg ttttatcaaa acggcaaact  
 51 tgccaatgcg gtttcgctt gccgattgcc aaaccggcaa acctttcccg  
 101 tgccggtgcc gaaccgatg cgtctgaac cttcagacgg catcggtgtg  
 151 ttatttgctc actcggacgg gtgcaggttc gtattgtgtc gattcgtcgc  
 201 cgtaatacag cagcgcgagt ttgacgggga tgcgtccctg cgatttgccg  
 251 tgggcggttg aatcgcgcaa ggaatacgcg cagccgcagt attcctgctg  
 301 gtagaagttt tcgcgtttgc tgatttcaat catacgcgcg ccgcccgcgc  
 351 ctttcgcgca gttgaagtcc caataggcca catcatcgta aggcgcggcg  
 401 gcacggtgtc cgcagtcgtt gatttgccc atatttttcc agcgtga

This corresponds to the amino acid sequence &lt;SEQ ID 1568; ORF 540.ng&gt;:

g540.pep

1 MPPSRRGNGV FYQNGKLANA VSACRLPNRQ TFPVPVNPMP PSEPSDGIGC

```
m540.seq (partial)
1 ..CCGACCCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTGT
51 CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTCTGC GCCGTAATAC
101 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTCG GGTGGGCATT
151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCTGTC TGGTAGAAGT
201 TTTACAGTTT GCTGATTTCA ATCATGCGCG CGCTGCCGCG GCCTTTGCGC
251 CAGTTGAATT CCCAATACAC CACATCATCG TAAGGCGCGG CGGCGCGGTG
301 TCCGCAAGTC TTGATTTTGG CCAATATTTT CAGCGTGA
```

```
m540.pep (partial)
1 ..PNMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEDFG DSAL*FAVGI
51 GIPOGIGTTA IFLLEVETFT ADFNHARAAA AFAPVEIPIH HIIVRRGGAV
101 SAVVDLRHIF PA*
```

```

m540/g540
                                     10      20      30
m540.pep                          PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
g540                               |||||
GNGVFYQNGKLANAVSACRLPNRQTFFVPVNPMPSEPSDGIGCLFVHSDGCRFVLCRFV
      10      20      30      40      50      60

                                     40      50      60      70      80      90
m540.pep                          AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNHARAAAAAFAPVEIPIH
g540                              |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
AVIQHAEFDGDASLRFVAVGVGIAQGIRAAAVFLLVEVFADFNFHTRAAAAAFAPVEVPIG
      70      80      90      100     110     120

                                     100     110
m540.pep                          HIIVRRGGAVSAVVDLRHIFPAX
g540                              |||||:|||||
HIIVRRGGTVSAVVDLRHIFPAX
      130     140

```

a540.seq

```
1 ATGCCGTCCT CCCGACGCGG CAACGGGGTG TTTTATCAA ACGGCAAAC
51 TGCCAAATGCG GTTTCGATT GCAGATTGCC AAACCGGCAA ACCTTTCCCG
101 TGCCGATGCC GAACCCGATG CCGCTGAAC CTTCAGACGG CATCGGGTGT
151 TTATTGTGCC AACCGGATGG GTGCAGGTTG GTATTGTGTC GATTCGTGTC
201 CGTAATACAG CACGCCGAGT TTGATGGGGA TTCTGCCCTG TGATTTCGGG
251 TGGGCGTTGG AATCCTCAG GGAATAGGCA CAACCGCAAT ATTCCTGCTG
301 GTAGAAGTTT TCACGTTTGC TGATTTCATC CATACGCGCG CGGCCGCCG
351 CTTTGCGCCA GTTGAATACC CAATACACCA CATCATCGTA AGCGCGGGCG
401 CGCGGGCGCG CGCAGTCGTT AATCTGGTTC ATGTTTTCC A
```

```
a540.pep (partial)
      1 MPSSRRNGV FYQNGKLANA VSDCLPNRQ TFPVMPNPM PSEPSDGIGC
     51 LFVHPDGCRF VLCRFVAVIQ HAEFDGDSAL *FAVGVGIPQ GIGTTAIFLL
    101 VEFTFADFN HTRAAAAFAP VEIPIHHIIV RRGGAAAAVV NLVHVFP
```

818

m540/a540 92.8% identity in 111 aa overlap

```

                                10      20      30
m540.pep                      PNPMPSEPSDGI GCLFVHPDGGRFVLCRFV
                                |||
a540      GNGVIFYQNGKLANAVSDCRLPNRQTFFVPMFNPMPSEPSDGI GCLFVHPDGGRFVLCRFV
              10      20      30      40      50      60

                                40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHARAAAFAFVEIPIH
              |||
a540      AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHTRAAAFAFVEIPIH
              70      80      90      100     110     120

                                100     110
m540.pep      HIIVRGGAVSAVVDLRHIFPAX
              |||
a540      HIIVRGGAAA VVNLVHVFP
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

```

g542.seq
1  atgccgaaat  ggtcgcgcat  acggcggttg  agcgctcttt  cgctgatgtt
51 cagcgcggt  gtcagccggt  tgacttggtg  tgcgccgccg  tcgaacgcgg
101 cattcaggt  gcggtgaag  tcttcagacg  gcatagcgtc  tgcttccgcc
151 gtttgcccc  ccgccggtc  gatgccgtct  gaaaccgtgt  cccacaaatc
201 cgacagcagc  cgcaacacgt  ccgcctcgcg  gcgcaatggt  tcgcccaaat
251 gcccctttg  gacggtttg  aggcaggatg  ccgccaagcc  gcgcaggttt
301 gggggcaaat  cccatatact  gaccggttcg  cggtaa

```

This corresponds to the amino acid sequence &lt;SEQ ID 1574; ORF 542.ng&gt;:

```

g542.pep
1  MPKWSRIRRC  SVLSLMFSAA  VSRLTWCAFP  SNAAFVRVLK  SSDGIASASA
51  VCPAAGSMPS  ETVSHKSDSS  RNTSASRRNV  SPKCPFGTVC  RQDAAKPRRF
101 GGKSHILTGS  R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

```

m542.seq
1  ATGCCGAAAT  GGTGCGCAT  ACGGCGTTGC  AGCGTCCTTT  CACTGATGTT
51  CAGCGCGTCT  GTCAGCCGCT  TGACTTGGTG  TCGCCGCTCG  GCAAACGCGG
101 CATTTAGGTT  GCGGTGAAG  TCTTCAGACG  GCATAGCGTC  TGCTTCCGCC
151 GTTTGCCCGC  CCGCCGCCCC  GATGCCGTCT  GAAACCGTGT  CCCACAAGTC
201 CGACAGCAGC  CGCAACACGT  CCGCCTCGCG  .CGCAATGTT  TCGCCCAAAT
251 GCCCCTTGG  GACGGCTTTC  AGGCAGGATG  CCGCCAAGCC  GCGCAGGTTC
301 GGGGGCAAAT  CCCATATCCT  GACCGGTTTC  CGGTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1576; ORF 542&gt;:

```

m542.pep
1  MPKWSRIRRC  SVLSLMFSAS  VSRLTWCAFP  ANAAFRVLK  SSDGIASASA
51  VCPAAGSMPS  ETVSHKSDSS  RNTSASRAMF  RPNAPLGRNV  SPKCPFGTAF
101 RQDAAKPRRF  GGKSHILTGS  R*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

m542/g542

```

                                10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSASVSRLTWCAFP SNAAFVRVLK SSDGIASASAVCPAAGPMPS
              |||
g542      MPKWSRIRRC SVLSLMFSAVVSRLTWCAFP SNAAFVRVLK SSDGIASASAVCPAAGSMPS
              10      20      30      40      50      60

                                70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASXRNVS PKCPFGTAF RQDAAKPRRF GGKSHILTGSRX

```

819

```

|||||
g542      ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100      110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```

a542.seq
1  ATGCCGAAAT  GGTCCGCGCAT  ACGGCGTTGC  AGCGTCCTTT  CGCTGATGTT
51  CAGCGTGTCT  GCCAGCCGGT  TGA CTTGATG  TGC GCCGCCG  GCAAACGCCG
101 CATTCAAGAT  GCGGCTGAAG  TCTTCAGACG  GCATAGCGTC  TGCTTCCGCC
151 GTTTGCCCCG  CCGCCGGCCC  GATGCCGTCT  GAAACCGTGT  CCCACAAGTC
201 CGACAGCAGC  CGCAACACGT  CCGCCTCGCG  GCGCAATGTT  TCGCCCAAAT
251 GCCCCTTTGG  GACGGCTTTC  AGGCAGGATG  CCGCCAAGCC  GCGCAGGTTC
301 GGGGGCAAAT  CCCATATCCT  GACCGGTTTC  CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

```

a542.pep
1  MPKWSRIRRC  SVLSLMFSVS  ASRLT*CAPP  ANAAFRMLK  SSDGIASASA
51  VCPAAGPMPS  ETVSHKSDSS  RNTSASRRNV  SPKCPGTAF  RQDAAKPRR
101 GGSKSHLTGS  R*

```

m542/a542 94.6% identity in 111 aa overlap

```

              10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSASVSRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
              |||||:|||||
a542           MPKWSRIRRC SVLSLMFSVSASRLTXCAPPANAAFRMLKSSDGIASASAVCPAAGPMPS
              10      20      30      40      50      60

              70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASXRNVS PKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              |||||:|||||
a542           ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

g543.seq
1  atggtttgtc  ggattattgc  cgccgttttt  ggctttcaac  tcggcaatca
51  gcccgtcgat  gcctttggct  ttgatgattt  cgccgaattg  gttgcggtac
101 acggttaacca  ggctcgtgcc  ttcgatggcg  acgttgtagg  tacggtattt
151 gccgcccgtt  tggtaggtgg  taaagtccat  attgacgggc  ttctgaccgg
201 ggatgccgac  ttcggcacgg  acgacgattt  ccttgccgcc  cttattgacg
251 atgggattgt  ctttgacgtt  gacggtcgcg  tttttgaatt  tcagcatcgt
301 gccggaatag  gtgcggatca  gcagggtttg  aaattctttg  gccaacgctt
351 gtttttgccg  gtcggacgcg  gtacgccaag  gggtgccgac  cgccaatgcg
401 gtcatacggt  ggaaatcgaa  atagggaacc  gcataggctt  cggcttttgg
451 gcgtgcagaa  gccgcgtcgc  cgcttttgag  gatggtcaaa  acctgtgtgg
501 cgttttggcg  gatttgtccc  actgcgtcgg  ccggggaggc  aaatgccatg
551 ccgatgtcta  aaataccgat  gcccaatgcg  ctgatgaagg  aggatttttt
601 cacgatgtct  ttcctgaaaa  tggatgtgta  tgtttattct  gcggtttttt
651 ccgcattgcc  gccctcagcg  tttttctcgg  cgaagctggt  catgaattta
701 ccgatcagg  tttccagaac  cattgcagaa  ctggttacgg  agatggtgtc
751 gccggcagca  aggttttccg  tatcgccgcc  ctgctgcagc  ccgatgtact
801 gttcgccc  aagtcgcc  gtcaggattt  gcgcggaaac  gtcactgctg
851 aactgatact  tgccgtccaa  atcaaggcgc  accctcgcct  gataggattt
901 cgggtcaagc  ccgatagcgc  cgacgcgccc  gaccaatacg  cctgcggatt
951 tgacgggggc  attgaccttc  aaaccgccga  tgcgcggaa  atcggcataa
1001 acggcgtaag  ttttgtccga  accgcggaa  gccgcggcgc  ccgccacgcg
1051 gaaagcgaga  aaggcaaccg  ccgcgcgccc  gatcaagacg  aacagtccga
1101 cccaaaattc  caatatgttc  tttttcatta  a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

```

g543.pep
1  MVCRLFAAVF  GFQLGNQPV  AFGDDFAEL  VAVHGNQARA  FDGDVVGTVF

```



```

51  AAALVGKGVH  IDGLLTGDAD  FGTDDDFLAA  LIDDGIVFDV  DGRVFEFQHR
101 AGIGADQQGL  KFFGQRLFLR  VGRGTPRVAD  RQCIGHTLEI  IGNRIGFGFW
151 ACRSRVAAFE  DGONLCGVLA  DLSHCVGRGG  KCHADAQNTD  AQCADEGGFF
201 HDVFPENGCV  CLFCGFFRIA  ALSVFLGEAG  HEFTDQVFQN  HCRTGYGDGV
251 RSKVVFRIAA  LLQPDVLFAG  KSRQSDLRGN  VTAEILAVQ  IKAHPRLIGF
301 RVKPDADAP  DQYACGFDGG  IDLQTDVAE  IGINGVSFVR  TAERRAARHA
351 ESEKGNRRRA  DQDEQSDPKF  QYVLFD*

```

m543.seq

1	ATGTTTGTGC	GGTTATTTCG	CGCCGTTTTT	GGCTTTCAAC	TCGGCAATCA
51	GTCCGTCCAC	GCCTTTGCGT	TTGATAATTT	CGCCGAATTG	GTTGCGGTAC
101	ACGGTAACCA	GGCTCGCGCC	TTCCATGGCG	ACGTTGTAGG	TACGGTATTT
151	ACC CGCGCTT	TGGTAGGTGG	TGAAGTCAT	GTTGACGGGT	TTTGGCCGG
201	GTACGCGCAG	TTCGGCGCGG	ACGATGATTT	CTTTGCCGCC	TTTATTGACG
251	ATGGGATTGT	CTTTGACGTT	GACGTTGGCG	TTTTTTAATT	TCAGCATCGT
301	GCCGGAATAG	GTGCGGATCA	GCAGGTTTTC	AAATTTCTTG	GCCAAACGCT
351	GTTTTTCGCG	GTGCGACGCG	GTGCGCCAAG	GGTTGCCGAC	CGCCCAATCG
401	GTCATACGTT	GGAAATCGAA	ATAGGGAATC	GCATAGGCTT	CGCGTTTTTG
451	GCGAGCGGTG	TTGGCATCGC	CGTTTTTTAA	GATGCTCAAT	ACTTGAGTGG
501	CGTTTTGACG	GATTTGGCTT	ACCGCGTCGG	CAGGGGCGGC	AAATGCCATG
551	CCGATGCTCA	AAATACCGAT	GCCCAATGCG	CTGATGAGGG	AGGATTTTTT
601	CATGATTAA	TGTCCTAGTT	TGAATATGAT	GGCATACGTT	TATTCGGCGG
651	CTTTTTCCGC	ATTGCCCGCG	TCGCGATTTT	TCTCGGCAAA	ACTCGTCATG
701	AATTTGCCGA	TAAGGTTTTC	CAGAACCATT	GCAGAACTGG	TTACGGAGAT
751	GGTGTGCGCG	GCAGCAAGGT	TTTCGTTGTC	GCCGCCCTGC	TGACGCCCGA
801	TGTACTGCTC	GACCAAAAGT	CCCCAAGTCA	GGATTTGCGC	GGAAACGTCG
851	CTGCTGAAC	GATACCTGCG	GTCCAAATCG	AGGCGCACCC	TCGCTGTATA
901	GGATTTGCGG	TCAAGTCCGA	TAGCGCCGAC	GCGCCCGACC	AATACGCGTG
951	CGGATTTGAC	GGGGGCATTG	ACCTTCAAAC	CGCCGATGTC	GCCGAAATCG
1001	GCATAAACGG	CGTAAGTTTT	GTCGCCAACG	CCGAAGCCGG	CACCGCCGGC
1051	CACGCGGAAA	CGGAGAAAGG	CAACCGCCCG	CGCGCAATC	AGGACGAACA
1101	GTCCGACCCA	AAATTTCAAT	ATGTTCTTCT	TCATTTAA	

m543 . pep

1	MVCRLFAAVF	GQGLGNQSVH	AFRFDNFAEL	VAVHGNQARA	FDGDVVGVTF
51	TAALVGGEVH	VDGFLPGYAD	FGADDFFFAA	FIDDGIVFDV	DVGVFXPQHR
101	ASIGADQQLG	KFFGQRLFLR	VGRGAPRVAD	RQCCHTLEIE	IGNRIGFGFL
151	ASGVGIAVFX	DAGQLSLGVL	DLAYRVGRGG	KCHADANQTD	ACADEGGGFF
201	HDXVSXFEDY	GIRLFGGFFR	IAAVGIFLGK	TRHEFADKVF	QNHCRGTGYD
251	GVAGSKVFRV	AALLQPDVLL	AQKRSQDLAD	GNVAELILIA	VQIEAHPRLI
301	GFVSKSDSAD	APDQYACGDF	GGSIDLTADV	AEIGINGVSF	VRTAERTAGT
351	HAESEKGNRR	RANODEOSDP	KFOYVLLH*		

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m543/g543

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
g543	MVCRLFAAVFGFQLGNQSPVDAFGFDDFAELVAVHGNQARAFDGDVVGTVFAAALVGGKVH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAAFIDDGIVFDVDVGVFQHRAGIGADQQGLKFFGQRLFLR					
	:  :		:  :			
g543	IDGLLTGDADFGTDDDFLAALIDDGIVFDVDGRVFEQHRAGIGADQQGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180

```

m543 . pep      VGRGAPRVADRQC GHTLEIEIGNRIGFGFLASGVGIAXFXDAQYLSGVLTDLAYRVGRGG
      ||||:|||||
g543            VGRGTFRVADRQC GHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLGCVLADLSHCVGRGG
      130      140      150      160      170      180

      190      200      210      220      230      239
m543 . pep      KCHADAQNTDAQCADEGGFFHDXVSVKFEYDG-IRLFGGFFRIA AVGIFLGKTRHEFADKV
      |||||
g543            KCHADAQNTDAQCADEGGFFHDV---FPENGCVCLFCGFFRIAALSVFLGEAGHEFTDQV
      190      200      210      220      230

      240      250      260      270      280      290      299
m543 . pep      FQNHCRCTGYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAAELILAVQIEAHPRL
      |||||
g543            FQNHCRCTGYGDGVAGSKVFRIAALLQPDVLFQAQKRSQDLRGNVTAELILAVQIKAHPRL
      240      250      260      270      280      290

      300      310      320      330      340      350      359
m543 . pep      IGFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERTTAGHAESEKGNR
      |||||
g543            IGFRVKPDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRAARHAESEKGNR
      300      310      320      330      340      350

      360      370      379
m543 . pep      RRANQDEQSDPKFQYVLLHX
      |||:|||||
g543            RRADQDEQSDPKFQYVLFHX
      360      370

```

```
a543.seq
1   ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGCTCCAC GCCTTTCGCT TTGATAAATT CGCCGCAATTG GTTGCGGTAT
101 ACCGTAACCA GGCTCGCGCC TTCGATGGC AGCTGTAGTG TACGGTATT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATT CTTTGCCGCC TTTATTGACG
251 ATNCGATTGT CTTTGACGTT GACGTTGGCG TTTTTTAAT TCACATCGT
301 GCGCGAATAG GTGCGGATCA GACGGGTTG AAATCTTTG CGCAACGTT
351 GTTTTTCGCG GTCGGACGCG GTGCGCCAAG GGTTGCCGAC CGCCAATGCG
401 GTCATACGTT GGAATTCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 GCGGGCGGTG TTGGCATCAC CGCTTTTAA ATGATCTCAAT ACTTGAGTGG
501 CGTTTTGACG GATTTGGTTT ACCGCGTCGG CAGGGGCCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCTTAGTT TGAATATGAT GGCATACGTT TATTCGCGGG
651 CTTTTTCCGC ATTGCCCGCG TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTTGCCGA TAAGTTTTC CAGAACCATT CGACAAGTGG TACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GATCCAAAAT CCCGAAGTCA GGATTTGCGC GGAAACGTGC
851 CTGCTGAAC TATACTTGCC TGCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTCCGG TCAAGTCCGA GTCCGCCGAC CGCGCCGAC AATACGCGTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTTT GTCCGCAACG CCGAACGCGC CACCGCCGGC
1051 CACCGCGAAA CGGAGAAAAA GACCAGCCGC CGCGCCCAAT AGGACGAACA
1101 GTCCGACCCA AAATTCCAAT ATGTTCTTTT TCATTAA
```

```
a543.ppe
1  MAYGLLAAVX  SLQLXNQSVH  AFRFDNFAEL  VAVHGNQARA  FDGDVVGTVA
51  TAALVGGEVH  VDGFLPGXAD  FGADDDFFAA  FIDDXIVFDV  DVGVF*FQHR
101 AGIGADQQGL  KFFGQRLFLR  VGRGAPRVAD  RQCGHTLEIE  IGRNIGFEGL
151 AGGVGITAF*  DAQYLSGVLT  DLVYRVGRGG  KCHADAQNTD  AQCADEGGFF
201 HD*VS*FEYD  GIRLFGGFFR  IAAVGIFLGK  TRHEFADKVF  QNHCRITYGD
251 GVAGSKSFRV  AALLQPDVLL  AQKRSQDLR  GNVAAELIA  VQIEAHPRLI
301 GFRVKSDSAD  APDQYACGFD  GGIDLOTADV  AEIGINGVSF  TRAERTAG
```

822

351 HAEEKGNRR RANQDEQSDP KFQYVLFH\*

m543/a543 96.0% identity in 378 aa overlap

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
a543	MAYGLLAAVXSLQLXNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAAFIIDGIVFDVDVGVFQFQHRAGIGADQQGLKFFGQRLFLR					
a543	VDGFLPGXADFGADDDFFAAFIIDDXIVFDVDVGVFQFQHRAGIGADQQGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m543.pep	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAXFXDAQYLSGVLTDLAYRVGRGG					
a543	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLAGGVGITAFXDAQYLSGVLTDLVYRVGRGG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m543.pep	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIAAVGI FLGKTRHEFADKVF					
a543	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIAAVGI FLGKTRHEFADKVF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m543.pep	QNHCRTRYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAELILAVQIEAHPRLI					
a543	QNHCRTRYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAELILAVQIEAHPRLI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m543.pep	GFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
a543	GFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
	310	320	330	340	350	360
	370	379				
m543.pep	RANQDEQSDPKFQYVLLHX					
a543	RANQDEQSDPKFQYVLFHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1585>:

g544.seq

```

1  atgaaaaaaa tactcaccgc cgccgcgcgc gactgatcg gcatcctcct
51  cgccaccgct ctcaccccg acagtaaaac cgcccccgc ttctccctgc
101 cgcacctgca cggaaaaacc gtttccaacg ccgacctgca aggcaaagtc
151 accctgatta atttttggtt tccctcctgt ccgggttggt tgagcgaaat
201 gcccaaagtc accaaaacgg caaacgacta caaaaataaa gatttccaag
251 tcctcgccgt tgcccagccc atcgatccga tagaaagcgt ccgccaatac
301 gtcaaagact acggactgcc gtttaccgtc atttatgatg cggacaaagc
351 cgtcggacag gcattcggca cacagggtta tccgacttec gtccttatcg
401 gcaaaaaagg cgaaatcctc aaaacttatg tcggcgaaac cgatttcggc
451 aaactctacc aagaaatcga taccgcgctg gcgcaatag

```

This corresponds to the amino acid sequence &lt;SEQ ID 1586; ORF 544.ng&gt;:

g544.pep

```

1  MKKILTAAAV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGV
51  TLINFWFPC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

```

151 KLYQEIDTAL AQ\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1587>:

m544.seq

```

1  ATGAWAAAAA TACTCACCGC CGCCGTCGTC GCACTGATCG GCATCCTCCT
51  TGCCATCGTC CTCmTCCCCG ACAGCAAAAC CGCGCCCGCC TTCTCCmTGC
101 CCGACCTGCA CGGAAAAACC GTTCCAACG CCGACCTGCA AGGCAAAGTA
151 ACCCTGATTA ATTTTGGTT TCCCTCCTGT CCGGGTTGTG TGAGCGAWAT
201 GCCCAAAATC ATTAACACGG CAAATGACTA TAAAACAAA AACTTCCAAG
251 TACTTGCCGT CGCCAGCCC ATCGATCCGA TAGAAAGCGT CCGCCAATAT
301 GTCAAAGACT ACGGTTTGCC GTTACCGTC ATGTATGATG CGGACAAAGC
351 TGTCGGACAG GCGTTCGGCA CACAGGTTA TCCGACTTCC GTCTTATCG
401 GCAATAAGG CGAAATCTTC AAAACCTACG TCGGCGAACC CGATTTCGGC
451 AAACCTTACC AAGAAATCGA TACGCGCGTG GCGCAATAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 1588; ORF 544&gt;:

m544.pep

```

1  MXKILTAADV ALIGILLAIV LXPDSKTAPA FSXPDLHGKT VSNADLQGV
51  TLINFWFPSC PGCVSXMPKI IKTANDYKXK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGK*GEIF KTYVGEPDFG
151 KLYQEIDTRV AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 544 shows 90.7% identity over a 162 aa overlap with a predicted ORF (ORF 544.ng) from *N. gonorrhoeae*:

m544/g544

	10	20	30	40	50	60
m544.pep	MXKILTAADVVALIGILLAIVLXPDSKTAPAFSXPDLHGKT VSNADLQGVTLINFWFPSC					
g544	MKKILTAADVVALIGILLATVLPDSKTAPAFSLPDLHGKT VSNADLQGVTLINFWFPSC					
	10	20	30	40	50	60
m544.pep	PGCVSXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTV MYDADKAVGQ					
g544	PGCVSEMPKVTKTANDYKKNDFQVLAVAQPIDPIESVRQYVKDYGLPFTVIYDADKAVGQ					
	70	80	90	100	110	120
m544.pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
g544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1589>:

a544.seq

```

1  ATGAAAAAAA TACTCACCGC CGCCGTCGTC GCACTGATCG GCATCCTCCT
51  TGCCATCGTC CTCATCCCCG ACAGCAAAAC CGCGCCCGCT TTCTCCCTGT
101 CCGANCTGCA CGGAAAAANC GTTNCAACG CCGACCTGCA AGGCNAAGTT
151 ANCCTGATTA ANTTTGGTT TCCCTCCTGT CCGGGTTGTG TGAGCGAAAT
201 GNCCANAATC ATTAACACGG CAAATGACTA TAAAACAAA AACTTCCAAG
251 TCCTTGCCGT CGCCAGCCC ATCGATCCGA TAGAAAGCGT CCGCCAATAT
301 GTCAAAGACT ACGGTTTGCC GTTACCGTC ATGTATGATG CGGACAAAGC
351 TGTCGGACAG GCGTTCGGCA CACAGGTTA TCCGACTTCC GTCCTTATCG
401 GCAAAAAAGG CGAAATCCTC AAAACTTATG TCGGCGAACC CGATTTCGGC
451 AAACCTTACC AAGAAATCGA TACGCGCGTG GCACAATAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 1590; ORF 544.a&gt;:

a544.pep

```

1  MKKILTAADV ALIGILLAIV LIPDSKTAPA FLSXLHGKX VXNADLQGV
51  XLIXFWFPSC PGCVSXMPKI IKTANDYKXK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

```

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151 KLYQEIDTAL AQ\*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544.pep	MXKILTA	AAVVALIGILLAIVL	XPDSKTAPAFSXPDLHGKTVSNADLQ	QKVTTLINFWFPSC		
a544	MXKILTA	AAVVALIGILLAIVL	IPDSKTAPAFSLSLXHLGKXVKNADLQ	GXVXLIXFWFPSC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVS	XMPKIIKTANDYKXKNFQVL	AVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ			
a544	PGCVS	EMXXIIKTANDYKXKNFQVL	AVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ			
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQVYPTSVLIGKXGEIFKTYVGE	PDFGKLYQEIDTRVAQX				
a544	AFGTQVYPTSVLIGKXGEILKTYVGE	PDFGKLYQEIDTALAQX				
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547.seq  
 1 atgttcgtag ataacggatt taataaaacg gtagcgagtt ttgcccacaaat  
 51 cgtcgaaact ttcgacgtat tcttctttag gaacgattgc gccttttttta  
 101 cgcagatgaa acagcgggtgc ggttgggtct gctcgttggt atatctcggt  
 151 gatattatta caagatgctg cttcgagatt ccgaaccgct cctttaaaga  
 201 gcttgggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg  
 251 ccgaagtcga gatggatgcc cattacttcc cttactcag aaaatatatta  
 301 aaatttataa tttacatat agttacaaat attagagttt tttgtgtgtg  
 351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgtct ccaaacggaa  
 401 aaaagcgggt tggtttttgt tgtaa

This corresponds to the amino acid sequence &lt;SEQ ID 1592; ORF 547.ng&gt;:

g547.pep  
 1 MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV  
 51 DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL  
 101 KFIMLHIVTN IRVFCVCVKE LLTILVKNL PNGKKRFVFC C\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547.seq  
 1 ATGTTCTG TAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCAAAT  
 51 CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTTTA  
 101 CGCAGATGAA ACAGCGGTGC GGTGGGTCT GCTCGTTGGT ATATCTCGTT  
 151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCCT CTTTAAAGA  
 201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG  
 251 CCGAAGTCGA GATGGATGCT CATTACTTCC CTTACTCAG AAAATATTTA  
 301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTWTTGTGT  
 351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTTG TCTCCAAACG  
 401 GAAAAAAGCG GTTGTGTTT TGTGTGTTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1594; ORF 547&gt;:

m547.pep  
 1 MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV  
 51 DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL  
 101 KFIMLHIFTN IKVFXVCVK ELLTILVKNL SPNGKKRFV CC\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

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	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNFKVFXCVCK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIVTNIRVF-CVCK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCX					
g547	ELLTILVKNLSPNGKKRFVFCCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547.seq
1  ATGTTCTAG  ATAACGGATT  TAATAAACG  GTAGCGAGTT  TTGCCCAAT
51  CGTCGAACT  TTCGACGTAT  TCTTCTTTAG  GAACAATTGC  ACCTTTTSTA
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGGT  ATATCTCGTT
151 GATATCTTTC  CAAGATGCGG  CTTGAGATT  CCGAACCGCT  CCTTTAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAATG
251 CCGAAGTCGA  GATAGATGCT  CATTACTTCC  CCTACTCAG  AAAATATTTA
301 AAATTTATAA  TGTTACATAT  ATTTACAAAT  ATTAAAGTT  TTTT.TGTGT
351 GTGCGTCAAG  GAATTGTTGA  CAATTTTAGT  T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547.pep
1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNNC  TFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSFKELGL  LIQISLSERF  RTNAEVEIDA  HYFPLLRLKYL
101 KFILMHIFTN  IKVFXCVCK  ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNFKVFXCVCK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRLKYLKFIMLHIFTNFKVFXCVCK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548.seq
1  atgttttccg  taccgcgttc  ctttttgccg  ggcgttttcg  tacttgccgc
51  gcttgccgcc  tgcaaacctc  aagacaacag  tgcggcgcaa  gccgcttctt
101 caagtgcac  cgcgcggct  gcggaata  cggcaagcc  gcaaacgcgc
151 ggtacggata  tgcgtaagga  agacatcgcc  ggcgatttca  cactgaccga
201 cggcgaagcc  aagcctttca  gcctgagcga  ttgaaagcc  aaggtcgtga
251 ttctgtcttt  cggcctttac  cactgtcccg  atgtctgccc  gacagggctt
```

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```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggtg ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acggggcgccc aaaacctgcc ggtcatcaag cagcaatacc gcgtgggttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccgggtgc gtatcttatc gataaaaacg gtgaggttgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ AASSASAPA AENAAKPQTR
51 GTDMRKEDIG GDFTLTDGEG KPFLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSIDLKQL GGQAKDVVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGGQNLPIVK QQYRVVSAKI NQKDDSENYL VDHSSGAYLI DNKEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTTCGG TACCGCGTTC CTTTGTGCGG GCGGTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAATG CCGCAAAGCA AnACACGCGC
151 GGTACGGATA TCGGTAAGGA AGACATCGGC GCGGATTCA CGCTGACCGA
201 CCGGCAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTCAATCAAG CAGCAATACc GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSASASA AENAAKQXTR
51 GTDMRKEDIG GDFTLTDGEG KPFLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSIDLKQL GGQAKDVVV FVSIDPERDT PEIIGKYAKQ FNPDFIXLTA
151 TGGQNLPIVK QQYRVVSAKV NQXDDSENYL VDHSSGAYLI DNKEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSASASAAENAAKQXTRGTDMRKEDIG					
g548	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQAASSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFTLTDGEGKPFLNLSDLKGKVVILSFGFTHCPDVCPTGLLTYSIDLKQLGGQAKDVVV					
g548	GDFTLTDGEGKPFLNLSDLKGKVVILSFGFTHCPDVCPTGLLTYSIDLKQLGGQAKDVVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTPETIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENYL					
g548	FVSIDPERDTPETIIGKYAKQFNPDFIGLTATGGQNLPIVKQQYRVVSAKVNQKDDSENYL					
	130	140	150	160	170	180

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	190	200	210
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
g548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
	190	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTC CG TACCGCGTTC CTTTTGCGG GCGGTTTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACTC AAGACAACAG TCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TGCCTAAGGA AGACATCGGC GCGGATTTCG CGCTGACCGA
201 CCGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTTCTGTCTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTACGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCAATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAATATTG GTCGACCACT
551 CTTCGGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSF LP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR
51  GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSIDLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIVK QYRVVSAKV NQKDDSENYL VDHSSGAYLI DNGEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

	10	20	30	40	50	60
m548.pep	MFSVPRSF LP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR GTDMRKEDIG					
a548	MFSVPRSF LP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR GTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL LTYSIDLKQL GGQAKDVKVV					
a548	GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL LTYSIDLKQL GGQAKDVKVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDT PEIIGKYAKQ FNPDFIXLTATGGQNLPIVK QYRVVSAKV NQKDDSENYL					
a548	FVSIDPERDT PEIIGKYAKQ FNPDFIGLTATGDQNLPIVK QYRVVSAKV NQKDDSENYL					
	130	140	150	160	170	180
	190	200	210			
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
a548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```



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```

151 caaatctgca atcggacggg ttgccacgcc gctttccatc gctgctttgg
201 cggcagccgt agcgacgca ggcagcaggc gggaatcgaa cggagtagga
251 atcaggtatt ccgcgccgaa ttcgaatttc ttaccgtaag cggcaaccac
301 ttcttcggtt acttcttcca tcgccaaatc tgcgcaagca tacacgcagg
351 cgcgtttcat ttcttcggtt atggtgggtt cgcgcacatc caacgcggcc
401 cggaagatga acgggaagca caatacgttg ttcacttggt tcgggaagtc
451 ggagcgcccg gtaccgataa ccacgtccgg acgggtttct ttcgccagcg
501 gcggcaggat ttccggattc gggttggcca tggcgaacac gatgggtttt
551 tcgttcatcg tgttcaacat ttcaggcgtc agcaggtttg cgcggagag
601 gccaagaag atgtctttgc cttaaccgc atcgcaagt acgcgcggc
651 cgttgtcttc aacggcgtag aatttttttg attcgccat gcggtcttg
701 tcttcggggg ttggtaaat cagcctttg gagttgcaaa cggttacgtt
751 ttcacgtttc aagcccaaat ccagcagttg gttcaggcag gcaatcgcg
801 cggcacctgc gcggagcac accaaagtcg cttcttcgat tttcggccg
851 gtataacgca gggcggtcaa tacggcgcg gcggtaatga tggccgtgcc
901 gtgctggtca tcatgaaata cggggatttt gcagcgtttg cgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:

g550.pep

```

1 MITDRFHLFH FVSPFIYQSD NKMPPESSD GILTTNGLQL PFAQLGSVSF
51 QICNRTGCHA AFHRCFGGSR SDARQQAGIE RSRNQVFRAE FEFLTVSGNH
101 FFGYFFHRQI CQSIHAGAFH FFVDGGCADI QRAPEDEREA QYVVHLVREV
151 GAAGTDNHVR TGFFRQRRQD FRIRVGHGEH DGFFVHRVQH FRRQQVCAGE
201 AQEDVFAFNR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
251 FTFQAQIIQL VQAGNRGGTC AGAHQSRFFD FTAGITQGVQ YGGGGNDGRA
301 VLVIMKYGDF AAFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

m550.seq (partial)

```

1 ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
51 GTTTGGACTC GTCCATACGG TCTTGTCTT CGCGGGTTTG GTAAATCACG
101 CCTTTGGAGT CGCAAACGGT CACGTTTTTCG CGTTTCAAGC CCAAATCCAG
151 CAATTGGwTC AAGCAGGCAA TCGCGGCCGC ACCTGCGCCG GAACACACCA
201 AAGTCGCTTC TTCGATTTTA CGGCCGGTAA AACGCAKGGC GTTCAATACG
251 GCGGCGGCGG TAATGATGGC CGTGCCGTGC TGGTCGTCGT GGAATACGGG
301 GATTTTGCAG CGTTTGCCTA A

```

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

m550.pep (partial)

```

1 ..DGIGKHALAV VFNGVELFGL VHTVFVFAGL VNHAFGVANG HVFAFQAQIQ
51 QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
101 DFAAFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows \_\_\_% identity over a \_\_\_ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

m550/g550

				10	20	30
m550.pep				DGIGKHALAVVFNGVELFGLVHTVFVFAGLVN		
				:       : : : : : : : : :		
g550	DGFFVHRVQHFRROQVCAGEAQEDVFAFNRI	IGKYAPAVVFNGVEFFGFVHAVFVFAGLVN				
	190	200	210	220	230	240
	40	50	60	70	80	90
m550.pep	HAFGVANGHVFAFQAQIIQLXQAGNRGRT	CAGTHQSRFFDFTAGKTXGVQYGGGGNDGRA				
	: : : : : : : : :	: : : : : : : : :				
g550	HAFGVANGYVFTFQAQIIQLVQAGNRGGTC	AGAHQSRFFDFTAGITQGVQYGGGGNDGRA				
	250	260	270	280	290	300
	100					
m550.pep	VLVVVEYGDFAAFAX					
	:					
g550	VLVIMKYGDFAAFAX					

310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1   CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAG ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACGCGCGAA GATGAACGGG AAGCACAATA CATTGTTCAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGTACC GATAACCACG TCCGGACGGG TTTCTTTCGC
451 CAGCGGCGGC AGGATTTCCG GATTCGGGTT GGCCATAGCG AACACGATGG
501 GTTTTTCGTT CATGGTGTTC AGTATTTTTC GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTCCTTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGAGATC GCAAACGGTC
701 ACGTTTTCGC GTTTCAGGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTGCTGCTG GAATACGGGG ATTTTGCAGC GTTTCGCTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1   LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GVSFQICNR TGCHAAFHRC
51  FGGSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQTAE DEREAYIVH LVREVGAAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNVEL FGLVHTVVFV AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYSGG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```

                                     10      20      30
m550.pep                               DGIGKHALAVVFNGLVHTVVFVAGL
                                     |||||
a550      EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGLVHTVVFVAGL
              170      180      190      200      210      220

              40      50      60      70      80      90
m550.pep    VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDG
              |||||
a550      VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYGGGGNDG
              230      240      250      260      270      280

              100
m550.pep    RAVLVVVEYGDFAAFAX
              |||||
a550      RAVLVVVEYGDFAAFAX
              290      300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1   atgaagctga aaaccttggt attgcccttc gccgcactgg catttgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttgcca cggttgctgg
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcggtat cgtgagaatg
251 ttttgaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgtga aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcggtea gtccgtcgtt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcggatc ttggactgca
```

830

451 ttgtcagga aaatcgcg acatcatctg cccgagttta cgaagagtt  
501 acggcgcatc atctcgcg gtatagtga ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep

1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF  
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDIT PEVKQAVRNT  
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA  
151 LSGKIARHHL PEFTEELRRI ICGGIVD\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)

1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC  
51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG  
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT  
151 AATGCCGGAT TTAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA  
201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTAT CGTGAGAATG  
251 TTTTGAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT  
301 TTATTGAAGA ATGCCCGTGA GATATACAG CAAGAAGAAA TTGACGGCAT  
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGT GCCAAAAATC  
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGACTGCA  
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCGAGTTTA CGGAAGAGTT  
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAG  
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)

1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF  
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDIT PEVKQAVRNT  
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA  
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK					
	:     :     :     :     :     :					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	:     :     :     :     :					
g552	ALAEMPEAKKDQAAEFNRYRENVLKDITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
	:     :     :     :     :					
g552	YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIARHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
	190					
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq

1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC  
51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG  
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT  
151 AATGCCGGAT TTAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA

831

```

201 AGCGAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATCGGGC TGTAAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRIKKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

```

              10      20      30      40      50      60
m552.pep      IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
|||||
a552           IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m552.pep      ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
|||||
a552           ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
              70      80      90      100     110     120

              130     140     150     160     170     180
m552.pep      YGSPVGQSVVAKNPRIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
|||||
a552           YGSPVGQSVVAKNPRIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
              130     140     150     160     170     180

              190
m552.pep      CKQAGQVGKRHHQKX
|||||
a552           CKQAGQVGKRHHQKX
              190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51 GTGCACCAAT GCTTTTGCCG CCCGCCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 CCCGGAAGCG AAAAAAGATC AGCGGCAGAG AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCC AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CCGCATGATT GCCTTTTACG GTTCGCCTGT CGTCACTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
1 LNIKLTLLLPFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLKNAREI YTQEEIDGMI AFYGSVPVQS VVAKNPRIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

832

```

1  TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCCGCCCGG CGACGCGTCG TTGGCGCGTT
101 GGCTGGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCG AAGTGAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLTLLP PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLKLNAREI YTQEEIDGMI AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLTLLP	PFATLALCTN	AFAAPPSDAS	LARWLDTQNF	DRDIEKNMIE	GFNAGFKPYA
m552-1	LNIKLTLLP	PFATLALCTN	AFAAPPSDAS	LARWLDTQNF	DRDIEKNMIE	GFNAGFKPYA
	70	80	90	100	110	120
a552-1.pep	DKALAEMPEA	KKDQAAEAFN	RYRENVKDL	ITPEVKQAVR	NTLKLNAREI	YTQEEIDGMI
m552-1	DKALAEMPEA	KKDQAAEAFN	RYRENVKDL	ITPEVKQAVR	NTLKLNAREI	YTQEEIDGMI
	130	140	150	160	170	180
a552-1.pep	AFYGPSVQGS	VVAKNPRLIK	KSMSEIAVSW	TALSGKIAQH	HLPEFTEELR	RIICGGKNPD
m552-1	AFYGPSVQGS	VVAKNPRLIK	KSMSEIAVSW	TALSGKIAQH	HLPEFTEELR	RIICGGKNPD
	190					
a552-1.pep	AGCKQAGQVG	KRHKQKX				
m552-1	AGCKQAGQVG	KRHKQKX				
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaacct gtctttgggc ttgacaaaa agctgcccg
51  tatactgcaa acagaagtag cggagtgttg cttggcatgt ctacggctg
101 tggccggatt ttatggtttc taccggatt tgcgcgact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatg gggctgacgg gacgggctgt gaggttgat ttagacgaat
251 tgggcagttt ggcctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgctgg aatcggatc ttcggacggg gctgccgtca tggatccggc
351 ttcgggacga cgaaagtca agacggagga aatatcgcg aagtttacgg
401 gaattgcttt ggaactgttg ccaaacacgc gtttcgagga aggggaagaa
451 aagcaggaaa tccgcaccc acccatgttg cgcgggattt ctgggctggg
501 gcggaacatt tttcagcttt tggttttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgtttcgg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctccgaat caggcaaat catgataaat gggcacgaca
701 tttacagctt accgcaccc ttattccgc aatttgagtg cgatggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccggt ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1621>:

1	ATGGATTATT	TATCAAGACT	GTCCTTTGGA	TTTAACAAAA	AGCTACCTGT
51	CATTCTGCAA	ACAGAAGTTG	CTGAATGTGG	TTTAGCATGC	CTGACATCCA
101	TCTTGTCTTA	TTATGGCTTT	CACACTGATT	TAAGAACGTT	ACGCCAAAAA
151	TACACCTCTG	CATTAAAGGG	CGCAAACTTT	GCAGACATCA	TGAGATTTGG
201	CAATGAAATG	AAATTAAACG	CACGAGCTTT	GCGTTTAGAG	TTAGATGAGC
251	TGTCAAAATT	ACAATCAACC	TGCATTCTCC	ATTGGAACCT	AAACCAATTT
301	TGTGTACTTT	GTTCCATTTC	CAAAGACAGT	ATCGTCATTA	TGGACCCTGC
351	TGTCGGTATG	CGAAAAATCA	AAATGGACGA	AGTTTCACAA	AAATTCACAG
401	GGATTGCCCT	AGAATTATTC	CCCAATACCC	ATTTTGAAGA	GAAAAAAGAA
451	ACAAAGAAAA	TCAAAATATT	ATCTCTATTA	AGGGGGGG. T	CAGGCTTAAA
501	ACGCTCTATT	ATTCAAATGC	TTATATTAGC	TATTTCTTTG	GAAGTCTTTG
551	CATTG...				

m553.pep (partial)

```

1  MDYLSRLSFG FNKKLPVILQ TEVAECLGLAC LTSILSYGYF HTDLRTLROK
51  YTLSLKGANL ADIMRFGNEM NLTPTRALRE LDELSNLQLP CILHWNLNHF
101 VVLCSSISKDS IVIMDPAVGM RKIKMDEVSQ KFTGIALELF PNTHFEKKKE
151 TKKIKILSL LRGXSGLKRS L IOMLILAI SLEVFAL...

```

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m553/q553

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1623>:

a553.seq

1 ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAAA AGCTGCCTGT  
51 TATCCTGC AA ACAGAAATAT CAGAATGCGG CTGGGCATGT CTGGCGGCTG  
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA  
151 TAC

```
a553.pep
  1 MPHLQNLISLG LKKKLPVILQ TEISEGLAC LAAVAGFHGF HTNLRALRSK
 51 Y
```

	10	20	30	40	50	60
m553.pep	MDYLSRLSFGFNKKLPVILQTEVAECGLACLTSLSYYGFTDLRTLRLQKYTLSLKGANL					
	:   :     :   :               :   :         : :   :     :   :					
a553	MPHLQNLSLGLKKKLPVILQTEISECGLACLAAVAGFHGFHTNLRLRLSKY					
	10	20	30	40	50	
	70	80	90	100	110	120
m553.pep	ADIMRFGNEMNLTPRALRLLEDELSNLQLPCILHWNLNHFVVLCSISKDSIVIMDPVGM					

```
g554.seq.
1 atgacagcac ataaaaatcct gcccgtcctt cttcccatca tcttaggcgt
51 ttctcaccga acgggtgcatt gccccgcggc caacagaccg acggtacacg
101 ccgccccccac gctccaaaca ccgaaatccc tcacggcggc acacatcgtt
151 atcgaccttc aaagcaggca gactttatcc gccaaaaaca ccaatacccc
201 tgtcgaaccg gcggcactaa cccaactgat gaccgcata tttggttttc
251 aaaacatgaa atcgggaaat atccaatctg aagaaaactt aaaaatcccc
301 gaatccgcatt gggcttcaga aggaagcaga atgtttgtac gtccccgcga
351 tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
401 acgatgcccc cctaaccctt gccgacggcg tgggcaacgg ctcgattgaa
451 aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gcatgaagaa
501 caccgtattc aaaaacccga caggcttggg tagagaagga caggtttcca
551 ccgccaagaa cctctccctg ctgtctgaag cattgtatgc cgactttccg
601 gaattattcc cgctgttttc catcaaatcg ttaagtttg aaaaatcaga
651 acaaaacaac cgcaatatcc ttttatatg ggacaacaa gtataacggc
701 tgaaagccgg gcacacagaa agcggcggct acaaccttgc cgtgtcatc
751 tccggcaacg gcaggcacat ccttgtcatc aactaggtt cggaatcggc
801 ggaaccccgc gcatcggaca acagcaagct gctgaaccg gcatgtcagg
851 cctctgcata gccaaaaata tatccgaag gcaaacctg tgccccacg
901 caattttccg gaggcagcaa aaaaaccgtc cgcgaggct tctctaaaga
951 agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
1001 tggaaacctat acagccgatt cccgccccgg taaaaaaagg gcagatttta
1051 ggaaaaactca aatcaggca aaacggacat accattgccg aaaaagaat
1101 cgtcgctagc gaaaacgtag aaaaaagaag ccggtggcaa aggcctttgga
1151 cgcgtctgac agggcgataa
```

g554.pep.

1	MTAHKILEPVL	LPILGVSHA	TAASPAPNRP	TVHAAPTLQT	PETLTAHKIV
51	IDLQSRQTL	AKNTNTPVEP	AALTQLMTAY	LVFNKMAKSGN	IQSEENAKIP
101	ESAWASEGR	MFVRPGDTVS	TDKLLKGMIA	LCANDAALTL	ADRLNGSIE
151	NFVQQMKEA	RRLGMKNTVF	KNPTGLGREG	QVSTAKDLSL	LSEALMRDFP
201	EYYPLFSIK	FKFENIEQNN	RNILLYRDNN	VNGLKAGHTE	SGGYNLAVSY
251	SGNGRHILVI	TLGSESAETR	ASDNSKLLNR	ALQAFDTPKI	YPKGKTVAQI
301	QISGGSKKT	V RAGFLKEAYI	TLPHKEAKMA	EQILETIQPI	PAPVKKGQIL
351	GKIKIRONGH	TIAEKEIVAL	ENVEKRSRWO	RLWTRLTGO*	

m554.seq..

```
1  ATGACAGCAC  ATAAAAATCCT  GCCCCTCCTG  CTTTCCATCA  TCTTAGGCGT
51  TTCTCAGCA  ACGGCTGCAT  CGCCGCGCC  CAACAGACCG  ACGGTACACG
101 CCGCCCCAC  GTTCCAAACA  CCCGAAACCC  TCACAGCGGC  ACACATCGTT
151 ATCGACCTT  AAAGCAAACA  GATTTTATCC  GCCAAAAACA  TCAATACCCC
201 TGTGTAACG  GCGGCCTAA  CCCAACTAG  GACCGCATAT  CTGGTTTACA
251 AAAACATGA  ATCGGGCAAT  ATCCAATCTG  AAGAAAAACT  AAAAATACCC
```

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301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTG AAAAACCCTGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATCA AAAATATAGA
651 ACAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAGCCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTCATC ACATTGGGTT CGGAATCGGC
801 GGAACACGCG GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCGAAAG GCAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AACCGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFT PETLTAHV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
101 ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LSANDAALTL AGRNGSIE
151 NRVQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPFLFSIKS FKFNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKQIL
351 GKIKIRONGY TIAEKEIVAL ENVKRSRWQ RLWACLQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554.pep	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFT PETLTAHV IDLQSKQILS					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTFT PETLTAHV IDLQSRQILS					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m554.pep	AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTVS					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTVS					
	70	80	90	100	110	120
	130 140 150 160 170 180					
m554.pep	TDKLLKGMIALSANDAALTLAAGRLNGSIE NRVQMNKEARRLGMKNTVFNPTGLSREG					
g554	TDKLLKGMIALCANDAALTLADRLNGSIE NRVQMNKEARRLGMKNTVFNPTGLGREG					
	130	140	150	160	170	180
	190 200 210 220 230 240					
m554.pep	QVSTAKDLALLSEALMRDFPEYYPFLFSIKSFKFNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLALLSEALMRDFPEYYPFLFSIKSFKFNIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
	250 260 270 280 290 300					
m554.pep	SGGYNLAVSYSGNRHILVITLSESAETR ASDNSKLLNWALQAFDTPKIYPKGKTVAQI					



```

g554      SGGYNLAVSYSGNGRHLVITLGSESAETRASDNSKLLNRLQAFDTPKIIYPKGKTVAQI
           250       260       270       280       290       300
           310       320       330       340       350       360
m554 . pep QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKQGILGKIKIRQNGY
           |||||
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKQGILGKIKIRQNGH
           310       320       330       340       350       360
           370       380       390
m554 . pep TIAEKEIVALENVKKRSRWQLWACLGTGQX
           |||||
g554      TIAEKEIVALENVEKRSRWQLWTRLTGQX
           370       380       390

```

```
a554.seq
1  ATGACAGCAC  ATAAAAATCCT  GCCCGTCCTG  CTTTCCATCA  TCTTAGGCGT
51  TTCTCAGCGA  ACGGCTGCAT  CGCCCGCGCC  CAACAGACCG  ACGGCACAGT
101 CGCGCCCCGC  GTTCCAAAACA  CGCCGAAACCC  TCACAGCGGC  ACACATCGTT
151 ATCGACCTTC  AAAGCAAACA  GATTTTATCC  GCCAAAAACA  TCAATACCCC
201 TGTGCAACCG  GCGGCACTAA  CCCAACTGAT  GACCGCATAT  CTGGTTTTCA
251 AAAACATGAA  ATCGGGAAT  ATCCGATCTG  AAGAAACACTT  AAAAATACCC
301 GAATCCGCTA  GGGCTTCAGA  AGGAAGCAGA  ATGTTTGTA  CTCCCGCGCA
351 TACGGTCAGC  ACCGACAAAC  TCTTAAAGG  CATGATTGCA  CTATCCGCAA
401 ACGATGCGCG  CCTAACCCCT  GCCGCGCGCC  TGGGCAACGG  CTCGATTGAA
451 AATTTTGTGC  AACAAATGAA  CAAAGTAGCC  CGACGCTTGT  GCGATGAAGA
501 CACTTGATT  AAAAATCCGA  CAGGCTGAG  TAGAGAAGGA  CAGGTTTTCCA
551 CCGCCAAAGA  CCTCGCCCAG  CTGTCTGAAG  CATTGATGCG  CGACTTCCG
601 GAATATTACC  CGCTGTTTT  CATCAAATCT  TTCAAATCA  AAAATATAGA
651 GCAAAACAAC  CGCAATATCC  TTTTATATAG  GGACAACAAT  GTAAACGGTC
701 TCGAAGCGCG  ACACACAGAA  AGCGGCGGCT  ACAACCTTGC  CGGTTCATAC
751 TCCGGCAACG  GCAGGCACAT  CTTGTGCATC  ATCTGGGTT  CGGAATCGCG
801 GGAACACAGC  GCATCAGACA  ACAGCAAGCT  GCTGAAGTGG  GCATTGCAAG
851 CCTTCGATAC  GCCCAAAATA  TATCCGAAAG  GCAAAACCGT  TGCCCAAAATC
901 CAAATTTCCG  GAGGCAGCAA  AAAAACCGTC  CGCGCAGGCT  TCCTCAAGA
951 AGCCTACATC  ACTCTGCCAC  ATAAGGAAGC  GAAATATGCA  GAACAATTC
1001 TAGAAACCAT  ACAGCCGATT  CCCGCCCCAG  TAAAAAAGG  GCAAAATTTA
1051 GGAAAAATCA  AAATCAGACA  AAACGGATAC  ACCATTGCCG  AAAAAGAAAT
1101 CGTCGCACCT  GAAATGTAA  AAAAAAGAAG  CCGGTGGCAA  AGGCTTTGGG
1151 CGTGTCTGAC  AGGGCAGTAA
```

```
a554.pep
  1  MTAHKILPVL  LSIILGVSHA  TAASPAPNRP  TAHAAPTFQT  PETLTAAHIV
51  IDLQSKQILS  AKNINTPVEP  AALTQLMTAY  LVFKNMKSGN  IRSEENLKIP
101 EAWASEGSR  MFNVRPGDVS  TDKLLKGMIA  LSANDAALT  AGRLLNGSIE
151 NNVQQMNKEA  RRLGMKNTVF  KNPTGLSREG  QVSTAKDLAQ  LSEALMRDFF
201 EYYPLFSIKS  FKFKNIEQNN  RNILLYRDNN  VNGLKAGHTE  SGGYNLAVSY
251 SGNRHILVI  TLGSESAETR  ASDNSKLLNW  ALQAFDTPKI  YPKGKTVAQI
301 QISGGSKKTV  RAGFLKEAYI  TLPHKEAKMA  EQILETIQPI  PAPVKKGQIL
351 GKIKIRONGY  TIAKEIIVAL  ENVKKRSRWO  RLWACLTGQ*
```

	10	20	30	40	50	60
m554.pep	MTAHKILPVLLSIIILGVSHATAASPAPNRPTVHAAPTFTQTPETLTAAHIVIDLQSKQILS					
	:					
a554	MTAHKILPVLLSIIILGVSHATAASPAPNRPTAHAAPTFTQTPETLTAAHIVIDLQSKQILS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m554.pep	AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTVS					
	:					
a554	AKNINTPVEPAALTQLMTAYLVFKNMKSGNIRSEENLKIPESAWASEGSRMFVRPGDTVS					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m554.pep	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQOMNKEARRLGMKNTVFKNPTGLSREG					
a554	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQOMNKEARRLGMKNTVFKNPTGLSREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m554.pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKEKNIEQNNRNILLYRDNNVNLKAGHTE					
a554	QVSTAKDLAQLSEALMRDFPEYYPLFSIKSFKEKNIEQNNRNILLYRDNNVNLKAGHTE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m554.pep	SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
a554	SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m554.pep	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRONGY					
a554	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRONGY					
	310	320	330	340	350	360
	370	380	390			
m554.pep	TIAEKEIVALENVKKRSRWQRLWACLTGQX					
a554	TIAEKEIVALENVKKRSRWQRLWACLTGQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1 atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51 cgccgtttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccatacctgct tgccgcgctc atcgctcgccg ccgctgcggg cggctttgtt
151 tggacatccc gccgacagca acgccagttt atcgaacgtc tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcggacaa caccagaaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cagcgtatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1 MDNKTCLRIG GLILLTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51 WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKRPRTR QEINQMAAQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1 ATGGACAATA AGACCAAAC GCGCTTGGGC GGCCTGATTT TACTGACCAC
51 CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAaaaaatt
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTCGCAAA AATGTTTCGGT GGACGAGGCG CACGCTATGT TCAaaaaacg
351 CCCGACACGT CAGGAAATCA ATCAAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1 MDNKTCLRIG GLILLTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51 WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

101 LSQKCSVDEA HAMFKRPTR QEINQMAAQ SRGQKRPHR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKT	KLRLG	LILLT	AVLSL	IIVLIV	DSWPLA
g556	MDNKT	KLRLG	LILLT	AVLSL	IIVLIV	DSWPLA
	10	20	30	40	50	60
m556.pep	IERLKK	FDIDPE	KGRINE	ANLRR	MYHSGG	QHOKDA
g556	IERLKK	FDIDPE	KGRINE	ANLRR	MYHSGG	QHOKDA
	70	80	90	100	110	120
m556.pep	ATLICS	QKCSV	DEAHAM	FKKR	PTR	
g556	ATLICS	QKCSV	DEAHAM	FKKR	PTR	
	70	80	90	100	110	120
m556.pep	QEINQ	MAAQ	SRGQ	KRPH	RX	
g556	QEINQ	MAAQ	SRGQ	KRPH	RX	
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACAAACT	CGCCTTGGGC	GGCCTGATTT	TACTGACCAC
51	CGCCGTTT	AGCCTCATT	TCGTATTGAT	TGTCGATTCC	TGGCCGCTTG
101	CCATCCTGCT	TGCCGCCGTC	ATCGTCGCCG	CCGCTGCGGG	CGGCTTTGTT
151	TGGACATCCC	GCCGACAGCA	ACGCCAGTTT	ATCGAACGTC	TGAAAAAATT
201	CGACATCGAT	CCCGAAAAAG	GCAGAATCAA	CGAGGCAAAC	CTGCGCCGTA
251	TGTACCACAG	CGGCGGACAA	CACCAAAAAG	ATGCGATTAC	CCTGATCTGC
301	CTGTGCAAAA	AATGTTCCGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG
351	CCCGACACGT	CAGGAAATCA	ATCAAATGGC	GGCAAAACAG	TCGCGCGGTC
401	AGAAACGTCC	GCACCGTTAA			

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKT	KLRLG	GLILLT	AVL	SLIIVL	IVDS	WPLAIL	LAIV	IVAAA	AGGFV
51	WTSRR	QQRQF	IERLKK	FDID	PEKGR	INEAN	LRRMY	HSGGQ	HQKDA	ITLIC
101	LSQKC	SVDEA	HAMFKR	PTR	QEINQ	MAAQ	SRGQ	KRPHR	*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKT	KLRLG	LILLT	AVLSL	IIVLIV	DSWPLA
a556	MDNKT	KLRLG	LILLT	AVLSL	IIVLIV	DSWPLA
	10	20	30	40	50	60
m556.pep	IERLKK	FDIDPE	KGRINE	ANLRR	MYHSGG	QHOKDA
a556	IERLKK	FDIDPE	KGRINE	ANLRR	MYHSGG	QHOKDA
	70	80	90	100	110	120
m556.pep	ATLICS	QKCSV	DEAHAM	FKKR	PTR	
a556	ATLICS	QKCSV	DEAHAM	FKKR	PTR	
	70	80	90	100	110	120
m556.pep	QEINQ	MAAQ	SRGQ	KRPH	RX	
a556	QEINQ	MAAQ	SRGQ	KRPH	RX	
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pcp..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pcp..

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

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a557.seq  
 1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGC GG  
 51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA  
 101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG  
 151 CTGTATCAGG CTTCCGGTAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC  
 201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC  
 251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG  
 301 GTATTGAAAC GCGGCGAGCC GGTGCGCAA CCGATGACCG TGTCCTCCG  
 351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAA CAGGAAGAGG  
 401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC  
 451 CGCCGCCTGA CCTTTCTGAA GCGGAATGA

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

a557.pep  
 1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA  
 51 LYQASGRVDD AAGQMTLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ  
 101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEEALWAE MRQDAAEQIV  
 151 RRLTFLKAE\*

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA LYQASGRVDD					
a557	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA LYQASGRVDD					
	10	20	30	40	50	60
m557.pep	AAGQMTLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
a557	AAGQMTLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
	70	80	90	100	110	120
m557.pep	AAGQMTLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
a557	AAGQMTLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
	70	80	90	100	110	120
m557.pep	AYADNEILGK QEEEEALWAE MRQDAAEQIV RRLTFLKAE X					
a557	AYADNEILGK QEEEEALWAE MRQDAAEQIV RRLTFLKAE X					
	130	140	150	160		
m557.pep	AYADNEILGK QEEEEALWAE MRQDAAEQIV RRLTFLKAE X					
a557	AYADNEILGK QEEEEALWAE MRQDAAEQIV RRLTFLKAE X					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

g558.seq..  
 1 ATGGATGCTT GTTTTTCGT CATTCGCCA CAGGCGGGA TTCGGAGATT  
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA  
 101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA  
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG  
 201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA  
 251 AGTCCATTTC CGACACCTCT CGGCGCATGC CGTCTGAAAA CCAATCTCCA  
 301 CTTTCAGACG GCATTGTTA G

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

g558.pep..  
 1 MDACFFVIPA QAGIRRFIV FKRSGRILAG AGMPLYTFS ELYMLQQGTA  
 51 HQAPHCVLPE RGCPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSENQSP  
 101 LSDGIV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

m558.seq..  
 1 ATGAATGCTT GTTTTTCGT CATTCGCCA CAGGCGGGA TTCGGAGATT  
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA  
 101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA  
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG  
 201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA  
 251 AGTCCATTTC CGACATCTsT CGGCGCATGC CGTCTGAAAA CCAATCTCCA  
 301 CTTTCAGACG GCATTGTTA G

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

m558/q558

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1647>:

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

m558/a558 70.2% identity in 141 aa overlap

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1649>:

g560.seq  
1 atgctcatca tccgcaacct gatttactgg ctgatactct gttccaqcct

g560.pap..

m560.seq

m560.pep

m560/g560

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWILICSTLIFLFPFMLLASPFDRGAHKMARVWVGILNWSLKHIVGLKYRII					
	:					
g560	MLIIRNLIYWILICSSLIFLFPFMLLASPFDRGAHKMARVWVGILNWSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	:					
g560	GAEHIPDRPSVICAKHQSGWETLALQEIIPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEKCEHLIETQQPLISGAGPFAA					
	:					
g560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```

a560.seq
1  ATGCTCATCA TCCGCAACCT GATTACTGG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTGCCTTTC CGAGACGGGG
101 CGCACAAAGAT GGCGCGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCGG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAAATCC CCTTTTTCGG CTGGGGCTTG AACTGGTCA AAACCATAGG
351 CATAGCCGC AACAAACGCC GCGAAGCCAA CGAGCAGCTC ATAAACAGG
401 GGTGGCGCG CAAAACGAA GGCTATTGGA TTACCATTTC CCCCAGGCG
451 ACACGCCTTG CGCCCGGAAA ACGCGGCAA TACAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCCCGTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGGAAAA TCGGAACACC TCATCGAAAC GCAGCAGCCG CTCATTTCGG
701 GCGCAGGCC GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```

a560.pep
1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAKHSGW ETALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGARMAM MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMGK CEHLIETQQP LISGAGPFAA KMPSETA*

```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK HIVGLKYRII					
a560	MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK HIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPA VICAKHSGW ETALQDIFP PQVYVAKREL FKIPFFGWGL KLVKTIGIDR					
a560	GAENIPDRPA VICAKHSGW ETALQDIFP PQVYVAKREL FKIPFFGWGL KLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					



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	130	140	150	160	170	180
m560.pep	190	200	210	220	230	240
	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPF	FAA				
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMGKCEHLIETQQPLISGAGPF	FAA				
	190	200	210	220	230	240
m560.pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

m561.seq.

```

1   ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCGGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCGTGCGC AAATTGACAA TCAGGTGACC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCT
301 TCGGACACCC CTCTTGCTTA TGATTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCGCTCCA GTCCTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAAAATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTGCTC TGTACTGATG CTGTTTGGC
551 ACCGATTTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTCGGGC GTTGTTCCTA TCAAATGGGC GGCAGGTGTA
701 AAATTTTATA TGATGATTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCTG CTGTACCAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTT CATTATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTTG GGGAGTACC ATGAGGAAAT CTTCCCAT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTCTCTTT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GGCACAAAAC AGGAGGAAGA AAAACGCCTG CTTGCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGACAAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAA CCGCCTTTGC
1251 CGAAAACAAA CGGAGGAAG CCGCAGAAAA CATCAGCTTT ATCAAAACAG
1301 GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTTCCGT
1351 ACCAAAATCA GCAATAAAGA ATTTCCCGAA GCCGTTGCCG ACCTATTCCG
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAAACG
1451 GTTCGTTTCT GCCGCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCCTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAACAC GCCCGCGCCA CCCATGTAAA
1551 ATTCACCCTT TCCGAACACG CGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTGACACG GAGAAAATAG GAGAACCCAC GGGCAGCCAT
1651 GTCGGAATGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

m561.pep

```

1   MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLTLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
251 LEKQNQNLTL LYOTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFAENK REEAENISF IKTGVQECYE DVRELLLNFR
451 TKISNKEFFE AVADLFARFT QQTGITVETA WENGSLFPQ EAQLQMIFIL

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501 QESLSNIRKH ARATHVKFTL SEHGGRFTMT IQDNGQGFD T EKIGEPTGSH  
 551 VGLHIMQERA KRIHAVLEIR SQAQQGTTVS LTVASEESLK \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLVWGLAALS	VVLTLLLSRL	LENAASVIEE	EAGNLR	MQAY	
g561	MILPTRFSDGIPLSRLKLLTGLVWGLAALS	VVLTLLLSFRL	LENAASVIEE	EAGNLK	MQAY	
	10	20	30	40	50	60
m561.pep	RLAYMAGEGSPRAQIDNQVAEF	EKSLKRIAQSDAIHPLIPSDT	PLAYDLIQSMLIIDWQA			
g561	RLAYMAGEGSPRAQIDNQIAEF	EKSLKRISQSDAIHPLIPSDN	PLAYDLIQSMLIIDWQA			
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAEF	EKSLKRIAQSDAIHPLIPSDT	PLAYDLIQSMLIIDWQA			
g561	RLAYMAGEGSPRAQIDNQIAEF	EKSLKRISQSDAIHPLIPSDN	PLAYDLIQSMLIIDWQA			
	70	80	90	100	110	120
m561.pep	HILPPLQSYRRPTQVDLYRF	AGNIELFLOALENANEKNTW	WLRRFQWAIMLMTLVSSVLM			
g561	NILPPLQAYRRPTQIELYRF	AGNIELFLOALENAGEKNTW	WLRRFQWVIMLMTLVSSVLM			
	130	140	150	160	170	180
m561.pep	LFWHQIWVIRPLQALREGAER	IGRRCFDIPVPEGGTPEFKQV	GRCFNQMGGR	LKILYDDL		
g561	LFWHQIWVIRPLQALREGAER	IGRRHFDIPVPEDVRPN	SNRSGGVSTK	WRSXG		
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAER	IGRRCFDIPVPEGGTPEFKQV	GRCFNQMGGR	LKILYDDL		
g561	LFWHQIWVIRPLQALREGAER	IGRRHFDIPVPEDVRPN	SNRSGGVSTK	WRSXG		
	190	200	210	220	230	
m561.pep	EGQVAEQTRSLEKQONLTL	LYQTTRDLHQSYIPQQA	AHFLNRILPAVGADSGR	VCCLDG		
g561	EGQVAEQTRSLEKQONLTL	LYQTTRDLHQSYIPQQA	AHFLNRILPAVGADSGR	VCCLDG		
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTTGCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCTT
301	TCGGACACCC	CTCTTGCTTA	TGATTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCCTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	GCCGGAACA	TCGAACTGTT	TTTGACGGCA
451	TTGGAATATG	CCAACGAAA	AAACACATGG	TGGCTCAGGC	GTTTTCAATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCGTC	TGTACTGATG	CTGTTTGGC
551	ACCAGATTTG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAATTCAAA	CAGGTCGGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTG	GAAGGACAAG	TCGCGGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAATCAAAA	CCTGACCCCTG	CTGTACCAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCCGATTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCAT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCTG	CTTGACAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCTTTGCG
1251	CGAAACAAA	CGGAGGAAG	CCGCAGAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTTCCGT
1351	ACCAAAATCA	GTAATAAGA	ATTTCCTGAA	GCCGTTGCCG	ACCTATTCTC

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1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGGCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATCAAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

a561.pep

```

1 MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51 EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRKILYDDL EGQVAEQTRS
251 LEKQNQNLTLYQTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGRLLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFENK REEAAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQGFDT ENIGEPSGSH
551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK *

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m561/a561 96.9% identity in 590 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALS					
a561	MILPARFSDGISLSRLKLLTGLWVGLAALS					
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA					
a561	RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA					
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM					
a561	HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM					
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRKILYDDL					
a561	LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRKILYDDL					
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQNQNLTLLYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG					
a561	EGQVAEQTRSLEKQNQNLTLLYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG					
	310	320	330	340	350	360
m561.pep	GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT					
a561	GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT					
	370	380	390	400	410	420
m561.pep	LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK					
a561	LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK					

847

	370	380	390	400	410	420
m561.pep	430	440	450	460	470	480
	REEAAENISFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFARFTQQTGITVETA					
a561	REEAAENIGFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFSRFTQQTGTTVETA					
	430	440	450	460	470	480
m561.pep	490	500	510	520	530	540
	WENGSLPFPQEAQLQMIFILQESLSNIRK HARATHVKFTLSEHGGRFTMTIQDNGQGFD					
a561	WENGTHLPTQDEQLQMIFILQESLSNIRKHAHATHIKFRLKQDGSFTMTIQDNGQGFD					
	490	500	510	520	530	540
m561.pep	550	560	570	580	590	
	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSQAQGGTTVSLTVASEESLKK					
a561	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSQAQGGTTVSLTVASEESLKK					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

```

1  atggcaagcc cgctcagtcct gcctttcaat tcgggcaaga ccaaaccgac
51  ggcttttgcc ggcgcggttt tggtcggaat catgttttcc acgcgcgtgc
101 gggcgcgccg caggtcctttg tggcgcacgt cggtaacggt ttggtcgttg
151 gtcagtgcgt ggatggtggt cattgcgcct ttgacgatgc cgacgctttc
201 gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251 tggaaacgac ggatcatgctg gcggtcagga cgctgtcggt caccgcgtac
301 acgacgggtg catcgacatc gtcgccgccc ggtgcggaat tgaggacttt
351 tttcgcgcgg ctttcgaggt ggattttggc tttttctttg ctggtgaacg
401 cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451 tcggcagggg tcggggtcga gaagaagggg attttgcgcg cgttgacgat
501 gaggttgccg ccgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551 tgtcgaattt ggatcagatg gcgttggttt caaggctgcc gctggcgttg
601 acggcgacga tttgagattg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

```

1  MASPSSLPFN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLNT LATGERQLVV QEALTTVMS AVRTLSETPY
101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSM TSTPSSFHGS
151 SAGLRVEKKG ILSPLTMR LPSWDTASAKR PCTVSNLVRW ALVSRPLPLAL
201 TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

```

1  ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51  GGCTTTTGCC GCGCCGGTTT TGGTCGGAAT CATGTTTTC ACGCCGCTGC
101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGTCATGTCG GCGGTCAGGA CGCTGTCGTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
351 TTTCCGCGCG CTTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TGCGGGTCGA GAAGAAGGGG ATTTTGTGCG CGTTGACGAT
501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG
551 TGTCGAATTT GGTGAGATGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA GTTGGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

```

1  MASPSSLPFN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLNT LATGERQLVV QEALTTVMS AVRTLSETPY

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848

101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS  
 151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL  
 201 TATSWSWS\*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSG	STKPTAFAAPVL	VGIMFSTPLRARR	RLWRTSVTVW	SLVSAWMVVIAP	
g562	MASPSSLPFNSG	STKPTAFAAPVL	VGIMFSTPLRARR	RLWRTSVTVW	SLVSAWMVVIAP	
	10	20	30	40	50	60
	70	80	90	100	110	120
m562.pep	LTMP	TLNLTATGERQL	VVQEALETTVM	SAVRTLSFTPY	TTVASTSSPP	GAEMRTFFAP
g562	LTMP	TLNLTATGERQL	VVQEALETTVM	SAVRTLSFTPY	TTVASTSSPP	GAEMRTFFAP
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSL	LVNAPVHSMTK	STPSSFHGS	SAGLRVEKKG	ILSPLTMLRP	PPSWDTASAKR
g562	LSRWILAFSL	LVNAPVHSMTK	STPSSFHGS	SAGLRVEKKG	ILSPLTMLRP	PPSWDTASAKR
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRW	ALVSRLPLALT	TATSWSWSX			
g562	PCTVSNLVRW	ALVSRLPLALT	TIWSWSX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

a562.seq  
 1 ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC  
 51 GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTCC ACGCCGCTGC  
 101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG  
 151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC  
 201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT  
 251 TGGAAACGAC GGTCATGTCG GCGGTCAGGA TGCTGTCGTT CACGCCGTAC  
 301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT  
 351 TTTGCGGCCG CTTTCCAGAT GAACTTTGGC TTTTCTTTG CTGGTGAACG  
 401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT  
 451 TCGGCAGGGT TCGGGTCNA GAAGAANGG ATTTTGTGCG CGTTGACGAT  
 501 GAGGTGCGCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGACGCG  
 551 TGTCGAATTT GGTGAGGTGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG  
 601 ACGGCGACGA TTTGGAGTTG GTCTTGA

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

a562.pep  
 1 MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL  
 51 VSAWMVVIAP LTMP

m562/a562 96.6% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSG	STKPTAFAAPVL	VGIMFSTPLRARR	RLWRTSVTVW	SLVSAWMVVIAP	
a562	MASPSSLSFN	SGSTKPTAFAAP	VLVGIMFSTPLR	ARRRSLWRTSV	TVWSLVSAWMV	VIAP
	10	20	30	40	50	60

849

	70	80	90	100	110	120
m562 . pep	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R T L S F T P Y T T V A S T S S P P G A E M R T F F A P					
a562						
	70	80	90	100	110	120
	130	140	150	160	170	180
m562 . pep	L S R W I L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V E K K G I L S P L T M R L P P S W D T S A S K R					
a562						
	130	140	150	160	170	180
	190	200	209			
m562 . pep	P C T V S N L V R W A L V S R L P L A L T A T S W S W S X					
a562						
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563 . seq

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1  ATGAACAAAA CCCTCTATCG TGTGATTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAGC TGTGCCGATA
101 GTGGTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTCTTTAT GTTTGGCTTT
201 GGGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCcc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCCAAGTT GATGTGGGTA ATegcGGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GCGGTTGGA TCCAAGGCAA TCCTTGCTTG
451 ACAAGGGGCG AAGCACGTGT GGTGTAAAC CAAATCAACA GCAGCCATCC
501 TTCACAACTG AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAAGTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTTAAGATAA GGCAAGGCAA TGCTGTAATC GCCGGACAG
701 GTTTGGATGC CCGTGATACC GATTTCACAC GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTG GTAATCAAGG
801 GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCACGATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAGTCAA TATCCGCACT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 ACACTGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTGAGG CAAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAAACTGGAT ATTGCGTTAC AAGATGATT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACCTTGC AAGCAGGAAA ACGCATTTCG
1351 ATTAAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCCG
1401 CGGTACGACA GACATTGGCA CGCAGCACA TTTAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAACCAAA ATCCAAGCCG GGCAATGAA TAATATCGGT
1501 ACAGGTCGGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTTAGG CATTGAACAA TTAAATAACC GTGAAAACAG TCTGATTTAC
1651 AGCGGTAACG ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCCAAAGGA TACACAATGC CGGCGCAATC ATTGAAGCTG
1751 CAGGCAAAAT GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT
1801 TTGAAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATTG TTGATTACGA
1851 AGCATTTTGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
1901 GCTGGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAACCTG CGCCTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

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2101 GGCGGCCAAT TGCTTG TGCA AACAGAAAA GACGGTTTGC ATAACGAGCA  
2151 AACCTTTGGC GAGAAGAAAG TCTTCAGCGA AAATGGTAAG TTGCACAAC  
2201 ACTGGCGTGC GCGTCGTAAA GGACATGATG AAACAGGGCA TCGTGAACAA  
2251 AATTATACTT TGCCGGAGGA AATCACACGC GACATTTCAC TGGGTTTCAAT  
2301 TGCCTATGAA TCGCATAGCA AAGCATTAAAG CCGTCATGCG CCCAGCCAAG  
2351 GCACTGAGTT GCCACAAAGT AACCGGGATA ATATCCGTAC TGCAGAAAAGC  
2401 AACGGTATTT CGCTACCCTA TACGCCCAAT TCTTTTACCC CATTACCCGG  
2451 CAGCAGCTTA TACATTATCA ATCCTGCCAA TAAAGGCTAT CTTGTTGAAA  
2501 CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGGGTAG TGAATATATG  
2551 CTGGGCAGCC TCAAACTAGA CCCAAACAAT TTACATAAAC GTTTGGGTGA  
2601 TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA GAGCTGACAG  
2651 GGATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA ATTTAAAGCC  
2701 TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC TCAGCGTTGG  
2751 CATTCGATTA AGTGCCGAGC AAGCAGCGCA ACTGACCAGC GATATTGTTT  
2801 GGTGGGTACA AAAAGAAGTT AAACCTTCCTG ATGGCGGCAC ACAAACCGTA  
2851 TTGATGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGGCA TAGACGGTAA  
2901 AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT TCAGGCAGCC  
2951 TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT TATCAATACC  
3001 GATACGCTAG ACAATATCGG TGGCGTATT CATGCGCAAA AATCAGCGGT  
3051 TACGGCCACA CAAGACATCA ATAATATTGG CGGCATTCTT TCTGCCGAAC  
3101 AGACATTATT GCTCAATGCG GGTAACAACA TCAACAACCA AAGCACGGCC  
3151 AAGAGCAGTC AAAATGCACA AGGTAGCAGC ACCTACCTAG ACCGAATGGC  
3201 AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA GCGCAGGCAG  
3251 GCAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA ATCAGATCAA  
3301 GGGCAAAACC GGCTGCAGGC AGGACGCGAC ATTAACCTGG ATACGGTACA  
3351 AACCGGCAAA TATCAAGAAA TCCATTTTGA TGCCGATAAC CATACCATCC  
3401 GAGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA AGGCGATGTT  
3451 ACCCTatTGT CAGGGAATAA TCTCAATGCC AAAGCTGCCG AAGTCGGCAG  
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This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pcp..

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 751 NYTLPEBITR DISLGSFAYE SHSKALSRHA PSQGTQLPQS NRDNIRTAKS  
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The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

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This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pep..

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951 TQTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEEITR NISLGSFAYE
1051 SHRKALSHHA PSQGTLPQS NGISLPYTSN SFTPLPSSSL YIINPVNKGY
1101 LVETDPRFAN YRQWLGS DYM LDSLKLDPNN LHKRLGDGY EORLINEQIA
1151 ELTGHRRLDG YQNDDEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
1201 DIVWLQKEV KLPDGGTQTV LVPQVYVRVK NGDIDGKAL LSGSNTQINV
1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQSAVTAT QDINNIGGML
1301 SAEQTLILLNA GNNINSQSTT ASSQNTQGS TYLDRMAGIY ITGKEKGVLA
1351 AQAGKDINII AQQISNQSEQ QOTRLQAGR INLDTVQTSK HQATHFDADN
1401 HVIRGSTNEV GSSIQTGDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
1451 NISAGINTH VDDASKHTGR SGGGNKLVT DKAQSHHETA QSSTFEGKQV
1501 VLQAGNDANI LGSNVISDNG TOIQAGNHVR IGTOTQSQS ETYHQTQKSG

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### Homology with a predicted ORF from *N.gonorrhoeae*

m563/g563

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10      20      30      40      50
g563.pep MNKTLYRVIFNRKRGAVVAVAETTKREGKSCADSGSGSVYVKSVSFIPTH----SKAFC
|||||
m563.pep MNKTLYRVIFNRKRGAVVAVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
10      20      30      40      50      60
60      70      80      90      100     110
g563.pep FSALGFSLCLALGTVNIAFADGIITDKAAPKTQQATILQTNGNIPQVNIQTPTSAGVSVN
|| |||||:|:| |||||:| |||||
m563.pep FSLLGFSLCLAVGTANIAFADGIADKAAPKTQQATILQTNGNIPQVNIQTPTSAGVSVN
70      80      90      100     110     120
120     130     140     150     160     170
g563.pep QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE
|||||
m563.pep QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQMNGYIE
130     140     150     160     170     180
180     190     200     210     220     230
g563.pep VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIRQGNVIAHGHL
|||||
m563.pep VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLSGFKIRQGNVIAHGHL
190     200     210     220     230     240
240
g563.pep DARDTDFTRIL-----
|||||
m563.pep DARDTDFTRILSYHSKIDAPVWGQDVRVVAGQNDVVATGNAHSPILNNAANTSNNTANN
250     260     270     280     290     300
250     260     270     280     290
g563.pep -----LYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGTM
:|||||
m563.pep GTHIPLFAIDTGLGGMYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGTM
310     320     330     340     350     360

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	300	310	320	330	340	
g563 . pep	AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----					
	::  :             :                            :					
m563 . pep	AAANAKDNTNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLSSGEILIHNSG					
	370	380	390	400	410	420
g563 . pep	-----					
m563 . pep	SLKNETSGTIEAARLAIDTDTLNNQGKLSQTGSQKLHIDAQGMKNRGRMGLQDTAPTAS					
	430	440	450	460	470	480
g563 . pep	-----					
m563 . pep	NGSSNQTGNSYNASFHSSTTTPTTATGTGTATVSI SNITAPT FADGTIRTHGALDNSGSI					
	490	500	510	520	530	540
g563 . pep	-----					
m563 . pep	IANGQTDVSAQQGLNNAGQIDIHQ LNAKGSAFDNHNGTII SDAVHIQAGSLNNQNGNITT					
	550	560	570	580	590	600
g563 . pep	-----EDLAVSGSLNNQNGE IATNQQLIIHDGQQSTVVIDNT					
m563 . pep	RQQLEIETDQLDNAHGKLLSAE IADLAVSGSLNNQNGE IATNQQLIIHDGQQSTAVIDNT					
	610	620	630	640	650	660
g563 . pep	390	400	410	420	430	440
	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERKIVAGNELSLSTRGSLKNS					
m563 . pep	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNS					
	670	680	690	700	710	720
g563 . pep	450	460	470	480	490	500
	HTLQAGKRIRIKANNLDNAVQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQKIAGQMNNIG					
m563 . pep	HTLQAGKRIRIKANNLDNAAQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQKIAGQMNNIG					
	730	740	750	760	770	780
g563 . pep	510	520	530	540	550	560
	TGRIYGDNIAIAATRLDNQDENG TGAAIAARENLNLGIEQLNNRENSLIYSGNDMAVGGA					
m563 . pep	TGRIYGDNIAIAATRLDNQDENG TGAAIAARENLNLGIGQLNNRENSLIYSGNDMAVGGA					
	790	800	810	820	830	840
g563 . pep	570	580	590	600	610	620
	LDTNDQATGKAQRIHNAGAIIEAAGKMRLGVEKLNHTNEHLKTQLVETGRERIVDYEAFG					
m563 . pep	LDTNGQATGKAQRIHNAGATIEAAGKMRLGVEKLNHTNEHLKTQLVETGREHIVDYEAFG					
	850	860	870	880	890	900
g563 . pep	630	640	650	660	670	680
	RHELLREGTQHELGWFFVYNNESDHLRTPDGAHENWHKYDYEKVTQETQVGTGAPAKIIA					
m563 . pep	RHELLREGTQHELGWSVYNDES DHLRTPDGAAHENWHKYDYEKVTQKTQVGTGAPAKIIS					
	910	920	930	940	950	960
	690	700	710	720	730	740

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g563 . pep	GSDLIIDSKAVFNSDSRIIAGGQLLVQTEKDGLHNEQTFGEKKVFSSENGKLHNYWRARRK
m563 . pep	GNDLTIDGKEVFNTDSQIIAGGNLIVQTEKDGLHNEQTFGEKKVFSSENGKLHNYWREKHK
	970 980 990 1000 1010 1020
	750 760 770 780 790 800
g563 . pep	GHDETGHREQNYTLPEEITRDISLGSFAYESHKALSRHAPSQGTLPQSNRDNIRTAKS
m563 . pep	GRDSTGHSEQNYTLPEEITRNISLGSFAYESHKALSHHAPSQGTLPQSN-----
	1030 1040 1050 1060 1070
	810 820 830 840 850 860
g563 . pep	NGISLPYTPNSFTPLPGSSLYIINPANKGYLVETDPRFANYRQWLGS DYMLGSLKLDPNN
m563 . pep	-GISLPYTPNSFTPLPGSSLYIINPVNKG YLVETDPRFANYRQWLGS DYMLDSLKLDPNN
	1080 1090 1100 1110 1120 1130
	870 880 890 900 910 920
g563 . pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
m563 . pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
	1140 1150 1160 1170 1180 1190
	930 940 950 960 970 980
g563 . pep	SAEQAAQLTSDIVVLVQKEVKLPDGGTQT VLPQVYVRVKNGGIDGKGALLSGSNTQINV
m563 . pep	SAEQVAQLTSDIVVLVQKEVKLPDGGTQT VLPQVYVRVKNGDIDGKGALLSGSNTQINV
	1200 1210 1220 1230 1240 1250
	990 1000 1010 1020 1030 1040
g563 . pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQSAVTATQDINNIGGILSAEQTLLLNA
m563 . pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQSAVTATQDINNIGGMLSAEQTLLLNA
	1260 1270 1280 1290 1300 1310
	1050 1060 1070 1080 1090 1100
g563 . pep	GNNINNQSTAKSSQNAQGSSTYLDRMAGIYITGKEKGVLAAGKDINI IAGQISNQSDQ
m563 . pep	GNNINSQSTTASSQNTQGSSTYLDRMAGIYITGKEKGVLAAGKDINI IAGQISNQSEQ
	1320 1330 1340 1350 1360 1370
	1110 1120 1130 1140 1150 1160
g563 . pep	GQTRLQAGRDINLDTVQTKGYQEIHFADNHTIRGSTNEVGSSIQT KGDVTL LSGNNLNA
m563 . pep	GQTRLQAGRDINLDTVQTSKHQATHFDADNHVIRGSTNEVGSSIQT KGDVTL LSGNNLNA
	1380 1390 1400 1410 1420 1430
	1170 1180 1190 1200 1210 1220
g563 . pep	KAAEVGSAKGT LAVYAKNDITISSGIHAGQVDDASKHTGRSGGKNLVI TDKAQSHHETA
m563 . pep	KAAEVSSANGT LAVSAKNDINISAGINTTHVDDASKHTGRSGGKNLVI TDKAQSHHETA
	1440 1450 1460 1470 1480 1490
	1230 1240 1250 1260 1270 1280
g563 . pep	QSSTFEGKQVVLQAGNDANILGSNVIDSNGTRI QAGNHVRIGTTQTQSQSETYHQTKSG
m563 . pep	QSSTFEGKQVVLQAGNDANILGSNVIDSNGTQI QAGNHVRIGTTQTQSQSETYHQTKSG
	1500 1510 1520 1530 1540 1550
	1290 1300 1310 1320 1330 1340
g563 . pep	LMSAGIGFTIGSKTNTQENQSQSNHEHTGSTVGLKGDTTIVASKHYEQTGSNVSSPEGNN

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m563 . pep	LMSAGIGFTIGSKTNTQENQSQSNEHTGSTVGSLSKGDTTIVAGKHYEQIGSTVSSPEGNN
	1560 1570 1580 1590 1600 1610
g563 . pep	LISTQSMDIGAAQNQLNSKTTQTYEQKGLTVGIQFARYRFGTTSDCRSTQSSKQVQGSKN
	1350 1360 1370 1380 1390 1400
m563 . pep	TIYAQSIDIQAAHNKLSNNTTQTYEQKGLTVAFSSPVTDLAQQA- IAVAQSSKQVQGSKN
	1620 1630 1640 1650 1660
g563 . pep	DRVNAAAAANAGWQAYQTGKGAQNLANGTTNAKQVSISITYEQQNRQTTQVQANQAQAS
	1410 1420 1430 1440 1450 1460
m563 . pep	DRVNAAAAANAGWQAYQTGKSAQNLANGTTNAKQVSISITYEQQNRQTTQVQANQAQAS
	1670 1680 1690 1700 1710 1720
g563 . pep	QIQAGGKTTLYCRRCEQSNINITGSGVSGRAGTGLIADKQIHLQSAEQSNTERSQNKSA
	1470 1480 1490 1500 1510 1520
m563 . pep	QIQAGGKTTLIATGAEEQSNINIAGSDVAGKAGTILIADNDITLQSAEQSNTERGQNKSA
	1730 1740 1750 1760 1770 1780
g563 . pep	GWNAGAAVSFGQGGWSLGAAGGNVKGKGYGDSVTHRHSIHGDKGSQTLIQSGGDTTIK
	1530 1540 1550 1560 1570 1580
m563 . pep	GWNAGAAVSFGQGGWSLGVTAGGNVKGKGYNGDSITHRHSIHGDKGSQTLIQSGGDTTIK
	1790 1800 1810 1820 1830 1840
g563 . pep	GAQVRGKGVQVNAKNLSIQSVQDRETYQSKQONAGAQTGVGYGFSASGDYSQSKIRADHA
	1590 1600 1610 1620 1630 1640
m563 . pep	GAQVRGKGVQVNAKNLSIQSVQDRETYQSKQONASAQVTGVGYGFSAGGDYSQSKIRADHV
	1850 1860 1870 1880 1890 1900
g563 . pep	SVTEQSGIYAGEDGYQIKVGNHTGLKGGIITSSQSAKDKGNRFSTGTLAGSDIQNYSQY
	1650 1660 1670 1680 1690 1700
m563 . pep	SVTEQSGIYAGEDGYQIKVGNHTDLKGGIITSTQSAEDKGNRFQTATLTHSDIKNHSQY
	1910 1920 1930 1940 1950 1960
g563 . pep	EKGSFGLGASVAVSGKTLGQGAQNKPKDKHLTSIADKNGASSSVGYGSDSDSQSSITKSG
	1710 1720 1730 1740 1750 1760
m563 . pep	KGESFGLGASASISGKTLGQGAQNKPKDKHLTSVADKNSASSSVGYGSDSDSQSSITKSG
	1970 1980 1990 2000 2010 2020
g563 . pep	INTPKNIQITDEAAQIRLTGKIAAQTKADIDTNVTTDTAERHSGSLKNIQDKDRVQSELD
	1770 1780 1790 1800 1810 1820
m563 . pep	INT-RNIQITDEAAQIRLTGKTAAQTKADIDTNVTTDTAERHSGSLKNTFNKEAVQSELD
	2030 2040 2050 2060 2070 2080
g563 . pep	LQRTVSQDFSKNVQQTNTEINQHLDKLKADKEAAETAAAEALANGDMETAKRKAHEAQDA
	1830 1840 1850 1860 1870 1880
m563 . pep	LQRTVSQDFSKNVQQAQNTNTEINQHLDKLKADKEAAETAAAEALANGDMETAKRKAHEAQDA
	2090 2100 2110 2120 2130 2140
g563 . pep	AAKADNWQQGVILNMLASGLAEPTQSGAGIAAATASPDVSYAIGQHFQDLAQONANGKL
	1890 1900 1910 1920 1930 1940
m563 . pep	AAKADNWQQGVILNMLASGLAAPTQSGAGIAAATASPAVSYAIGQHFQDLAQONANGKL
	2150 2160 2170 2180 2190 2200

		1950	1960	1970	1980	1990	2000
g563.pep		TASQETAHVLAHAVLGA	AVAAAXGNNAPAGALGAGGSEAA	APIIGKWL	YGKGDGGS	LNAE	
m563.pep		TASQETAHVLAHAVLGA	AVAAVGDNNALAGALSAGGSEAA	PYISKWL	YGKEKGS	DLTAE	
	2210	2220	2230	2240	2250	2260	
		2010	2020	2030	2040	2049	
g563.pep		EKETVSAITRMLGTAAGA	AEGNSSADAVWGC	FQTASDFASSFS	YPINMX		
m563.pep		EKETVTAITNVLGTATGA	AVGNSATDAAQGS	LNAQSAVENNDT	VEQVKFALRHP	RIATAI	
	2270	2280	2290	2300	2310	2320	
m563.pep		GSVHKDPGSTLEPNISTIA	STFQLNLFNPSEFGGEG	GVGNAFRHVLWQATIT	REFGKDIA		
		2330	2340	2350	2360	2370	2380

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m564.seq
1 ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51 GATAGCGGTT GCTGAAAATG CCAAAACGCGA GGGCAAAAAA ACAGCGGCACA
101 CCGAAGCTGT GGTGATTTTG CCAATATGATA TTGCGGGGCTT TCGGGGTTTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTC
201 TGCCCTTATC CTGACTTCTT CTTCGTGTAC TGCCCAAGGT ATCGTTGCCG
251 ACAAAATCCG ACCTGCACAG CAACAGCCTA CCATCTGTCA AACGAGTAA
301 GGCATACCCG AAGTCAATAT TCAACCCCTT ACTTCGGCAG GGGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTGCAGC CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CCTTGTTGG CAAGGGGCGA AGCACGTGTG GTTGTAAACC AAATCACACG
501 CAGCCATTCT TCACAACCTA ATGGCTATAT TGAAGTGGCG GGACGACGTG
551 CAGAAGTCGT TATTGCCAAT CCGCAGGGA TTGCAGTCAA TGGTGGTGGT
601 TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAGATAAG GCAAGGCAAT GTTGTATCTG
701 CCGGACACGG TTTGGATGCA CGTGATACCG ATTACACAGC TATTTCACTG
751 TATCATTCCA AAATTGATGC ACCCGTATGG GGACAAGATG TTCGTGTCTG
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATTC
851 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAAACGGACA
901 CATATCCCTT TATTTGCGAT GTATACAGCG AAATTAGGAG GTATGTATGC
951 CAACAAAATC ACCTTGATCA GTACGGTCTA GCAACGAGCG ATTCGTATATC
1001 AAGGGCAATG GTTTGCCCTC GCCGGCAATG TGGCAGTGAA TGCTGAGGGT
1051 AAACGTGTCA ACACGGGCAT GATTGCAGCG ACGGGAGAAA ATCATGCGGT
1101 TTCCTTTCAT GCCCGCAATG TTCATAATAG CCGTACGGTT GCCTCACAGG
1151 ATGATGCCAA TATTCACAGC CAGACGCTGG ACAATTCCAG TACGGTCTTA
1201 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCCGTCTGA AAAACCAAAA
1251 CAACGGTAGC ATCAGCGGCT CCCGCTTAGA TATGTCAACA GGTGGTTTGG
1301 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGAATTTGTA
1351 TCTGCCGGCA AATTCGATAA CAGTGGCAAG ATTGGTGTA TGTACGTTCC
1401 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACAG ATTCCGAGTA
1451 CTGCAACAGG TTCAGGCAGC AGCACTGTCT CGGTATCTAA GCCTGGTTCA
1501 AACAAATCCG TTTACCTAC AGCACTGTCA AAAAATCAGC CCGTAGGAGC
1551 CATTCAAACA ACAGAGCAT TTGACAACTG AGGATCAAT AATGCGGGTG
1601 GGCAAATTGA CATTGCCGCC CAAAACGGTT TGGGAAATTC GGGTAGTCTG
1651 AATGCGGCTA AACTACGAGT ATCAGGCGAT TCATTTAACA ATACGGTTAA
1701 AGGCAAACTC CAGGCACAGC ATCTGGCTGT TAACTACTAA ACTGCTAAAA
1751 ACAGCGGTCA CTTATTAACT CCAACCGCA AGATTGATAA CCGTGAATCA
1801 CATAATGCCG GAGAAATTGC CGCCAACAAT CTGACACTCA TTCATTGGG
1851 CGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTTACAGC
1901 TTGATACCGC CGGTTTACAT ATGTCAGTA ACATTCTTGC CGATAGTGG
1951 ACCGTTACCA CCAAGATAAA TCTTCGCAAT ACAGAAAAG TTTCTGTTG
2001 ACAGCTGAAT ACCGAAGGTC AGACTCTAGA TAATACGGCG GCAGCTATAG
2051 AGGCTGAAAC GGTTAACATC CAAAGTCAGC AACTGACTAA CCAAGCGGCG
2101 CATATTACTG CTACCGAACA ACTGACTACT AATAGTCGAA ATGTAGACAA
2151 CCAAAACGGC AAACCTCTAT CTGCAAAACA AGCACAATTA GCTGTTTTC
2201 ACGGCTTATA CAACCAACAT GGTGAAATTG CCACCAACCG CAGGTTGTCT
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2251 ATTCACGATA AAAATCAAAA CACTTTGGCG TTAACAATG CGGATGGCAC  
 2301 GATTCAATCT GCCGGTAATG TATCGCTACA AGCCAAATCA CTCGCCAACA  
 2351 ATGGCACATT AACAGCCGGT AACAACTGG ATATTGCTTT GACGGACGAT  
 2401 TTCGTCGTAG AGCGCGACCT CACTGCAGGC AAACAATTAA ATCTAAGCAT  
 2451 AAAAGGCCGT CTGAAAAATA CCCATACCCT ACAAGCAGGC CATACGCTCA  
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 2551 GGAGAACAAA CGGACATCAC ATCCGAACAG CATGTTGACA ACAGGGGCTT  
 2601 GATCAACAGC GACGGTTTGA CCCACATCGG TGCAGGTCAA ACCCTGACCA  
 2651 ACACCGGAC AGGCAAAATC TATGGCAACC ATATTGCCCT GGACGCGCAA  
 2701 ATACTGCTTA ACCGGGAAGA AACGACGGAA GGCAGTACCA AAGCGGGGGC  
 2751 AATAGCTGCA AGGAAACGTT TGGATATTGG AGCGAAAGAG ATTCTAACC  
 2801 AAGAAGGTGC CCTACTATCC AGCGAAGGTA TTTTGGCCGT AgGTAATCGA  
 2851 CTGGATGAAC AACATCATGC GGCAGGCATG GCCGATACCT TTGTTAATGG  
 2901 CAGTGCCGGT TTGGAAGTAC AAGGTGATGC ATTGATGTCC GTTCGGAATA  
 2951 TGAGAAATAT CAATAATCAC TTTAAACAG AGACATACTT AGCCAAAGCG  
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 3101 CTACTGCTAC GTTCCATTTA AAAAATGGTT CTCGTATTGA GGCCAAACCAA  
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 3351 AGGTGCGACA GATGCTGTCT GCACACAGTG GGATTCAGTT AAAAAAAG  
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 3451 CCTTACCATG ATACCCAAT ATTTACCCAC GACTTCGACA CGCCTGTATC  
 3501 CGTCATCCAA CAGAATGCCG CCTCCCCTTC CTTTCAACCC GCCGCATCTG  
 3551 CAATCAAAT GATTGACGGA GTATCCACGG CAGCCGTCAA TGGTCAGCGC  
 3601 ATCCATACCG GTAATGTGGT CTCGTAAAT AACGCTACTG TTACTCTGCC  
 3651 TAACAGCAGC CTCTATACCA CCCATCCTGA CAATAAAGCG TGGTTGGTTG  
 3701 AAACCGATCC TCAATTGCA GACTACCGCC GCTGGTTGGG CAGCGACTAC  
 3751 ATGTTGCAAC AACTGCAATT GGACACCAAT CATCTACACA AACGGCTTGG  
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 3901 GCTCTGATGG ACAACGGCCT TACTGCTGCC AAAACATTGG GTCTCACCCC  
 3951 AGGTATCGCC TTGAGTGCAG AGCAAGTTGC CCGCTTAATC TCAGATATCG  
 4001 TTTGGATGGA AAATCAAACC GTCACCTGT CTGACGGTTC GACTCAAACC  
 4051 GTACTGGTTC CTAAGTCTA TGCCCTGGCG CGCAAAGGTG ATCTCAATAC  
 4101 TAGCCGTGGC CTGATTAGTG CCGAACAGT CTTACTTAAA CTGCAAAACG  
 4151 GCAACCTGAC TAACAGCGGT ACCATTGCGG GGCAGACAGC CGTACTCATC  
 4201 CAGGCACGGA ATATTAACAG CAACGGTAAC ATTCAAGCCG ACCAAATCGG  
 4251 CTTAAAAGCT GAAAAAAGTA TCAATATCGA CGGCGGGCAG GTACAAGCAG  
 4301 GCAGACTGCT GACTGCCCAA GCGCAAAATA TCAACCTTAA CGGTACAACC  
 4351 CAAACTTCCG GTAATGAACG TAACGGCAAT ACCGCCATCG ATCGTATGGC  
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 4451 CAGACGGCAT CCTATCCCTG CATGCCAGCA ACGATATCAA CCTCAATGCG  
 4501 GCCACCGTCT CTAACCAAGT TAAAGACGGC ACTACCCAAA TTACCGCCGG  
 4551 CAATAATCTC AACCTCGGCA CCATCCGTAC CGAACATCGC GAAGCCTATG  
 4601 GTACATTAGA TGACGAGAAC CATCGCCATG TCCGCCAAAG TACCGAAGTC  
 4651 GGCAGCAGTA TCCGCACGCA AAACGGCGCA CTGCTTAGAG CCGGTAACGA  
 4701 CTTAAAAATC CGCCAAGGCG AACTGGAGGC CGAAGAAGGC AAAACCGTCC  
 4751 TTGCCGAGG ACGTGATGTC ACTATCAGCG AAGGACGCCA AATAACCGAA  
 4801 CTGGATACCT CGGTAAGCGG AAAAAGCAA GGCACTCCTT CCAGTACCAA  
 4851 AACACACGAC CGCTACCGCT TCAGTCATGA TGAAGCAGTC GGCAGCAACA  
 4901 TCGGCGGCGG CAAAATGATT GTTGCAGCCG GGCAGGATAT CAATGTACGC  
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 5301 CACTGACTAC GCCCATACCC AGGAACAAA AGGCCTTACC GTCCGCCCTA  
 5351 ATGTCCCGGT TGTCCAAGCT GCACAAAAC TCATACAAGC AGCCCAAAAT  
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 5451 TGCATGGCAG AGTTATCAAG CAACCAACA AATGCAACAA TTTGCTCCAA  
 5501 GCAGCAGTGC GGGACAAGGT CAAACAACA ATCAAAGCCC CAGTATCAGT

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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CCGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAGG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAA AAAAAAGCA
5801 GTGGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
5851 GGAATTACCG CCGGAGGAAA TATCGGTAAA GGTAAAGAGC AAGGGGGAAG
5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
5951 TCCGAAGCGG CGGGGATACC ACCCTCAAAG GTGTGCAGCT CATCGGCAAA
6001 GGCATACAGG CAGATACGCG CAACCTGCAT ATAGAAAGTG TTCAAGATAC
6051 TGAACCTAT CAGAGCAAAC AGCAAACCG CAATGTCCAA GTTACTGTCG
6101 GTTACGGATT CAGTGCAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGCC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAACCCAC AGCCGCTACG AAGGCAGAAG
6351 CTTCCGCATA GCGGCGAGTT TCGACCTGAA CGCGCGCTGG GACGGCAGCG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
6451 TACGGCAGCG ACGGAGACAG CAAAAACAGC ACCACCCGCA GCGGCGTCAA
6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAATT GCCCGAACAG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCG CATCGACACC
6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAACAGCT TCGACAAAGA
6651 CGCGGTCGCC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCG
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCCG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGCG TGGAGGCCGA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAA AGCCGCCTTC CGCGCATCCC
6851 TCGGCCAAGT AAACGCCTAT CTTGCCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GGCCGGCGGC GGCACCTCCC
7001 TTGCCGCACC GTATTGGAC AAAGCGGCGG AAAACCTCGG TCCGGCGGGC
7051 AAAGCGGCGG TCAACGCACT GGGCGGTGCG GCCATCGGCT ATGCAACTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAGATTGG AACAATAGGC
7151 AGCTGCATCC GAAAGAAATG GCGTTGGCCG ACAAATATGC CGAAGCCCTC
7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAGGC AGATACTGCG TTGGGTGGAC AAAGGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 CGTTGCCGAA GGAATGACGA GCCTTGTCAG CCCCAATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAAGGCATC CGCAACCTGA AAAACATCAA GCCGACAGTT
7651 ACCGGCAGCG ATCCCTTATT GCGGGGTGCG GGAATATACC GTATCCCTGC
7701 AAACGGCAAT GTTCCGAAGG GGGACAGGAT TCCGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

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1  MNRTLYKVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51  IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QOPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVIAN PAGIAVNGGG
201 FINASRATLT TAQPOYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW GQDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWFFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVS DVPQTG LNPNPSPVIPQ IPSTATSGS STVS VSKPGS
501 NNPVSPAPPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNLGNSGSL
551 NAAKL RVSGD SFNNTVKGKL QAHD LAVNTQ TAKNSGHLLT QTGKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILADSG
651 TVTTKNNLAN TGKVSVARLN TEGQTLNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVDNQNG KLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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901 ILLNREETTE GSTKAGAI AA RKRLDIGAKE IHNQEGALLS SEGIFAVGNR
951 LDEQHHAAGM ADTFVNGSAG LEVQGDALMS VRNMQNINNH FKTETYLAKA
1001 EKQVRDYTVL GQNTYYQAGK DGLFDNSQGG KDQTTATFHL KNGSRLEANQ
1051 WHVRDYHIET YKERIENRP AHITVGGDLT ASGQNWLNKD SRIVVGGRII
1101 TDDLNQKEIT NQSTTGKGR TAVGTQWDSV TKKGWYSGRK RQRRTERNHT
1151 PYHDTQLFTH DFDTPVSVIQ QNAASPSFQP AASAIKLIDG VSTAAVNGQR
1201 IHTGNVVS LN NATVTLPNSS LYTHPDNKG WLVTDPQFA DYRRWLGS DY
1251 MLQQLQLDTN HLHKRLGDGY YEQKLVNEQI HQLTGYRRLD GYRSDEEQFK
1301 ALMDNGLTAA KTFLTPGIA LSAEQVARLT SDIVWMENQT VTLSDGSTQT
1351 VLVPKVYALA RKGDLNTSGG LISAEQVLLK LQNGNLNLSG TIAGROAVLI
1401 QARNINSNGN IQADQIGLKA EKSINIDGGQ VQAGRLLTAQ AQNINLNGTT
1451 QTSGNERNGN TAIDRMAGIN VVGSHTQVD NRTSDGILSL HASNDINLNA
1501 ATVSNQVKDG TTQITAGNNL NLGTIRTEHR EAYGLDDEN HRHVRQSTEV
1551 GSSIRTQNGA LLRAGNDLKI RQGELEAEEG KTVLAAGRDV TISEGRQITE
1601 LDTSVSGSKS GILSSTKTHD RYRFSDHEAV GSNIGGGKMI VAAGQDINVR
1651 GSNLISDKGI VLKAGHDIDI STAHNRYTGN EYHESKKSGV MGTGGLGFTI
1701 GNRKTTDDTD RTNIVHTGSI IGSNLGDTVT VAGNRYRQTG STVSSPEGRN
1751 TVTAKSIDVE FANNRYATDY AHTQEQKGLT VALNVFVQA AQNFIAAQN
1801 VGKSKNKRVN AMAAANA AWQ SYQATQQMQQ FAPSSSAGQG QNNNQSPSIS
1851 VSTITYGEQKS RNEQKRHYTE AAASQIIGKG QTTLAATGSG EQSNINITGS
1901 DVIGHAGTAL IADNHIRLOS AKQDGSEQSK NKSSGWNAGV AVKIGNGIRF
1951 GITAGGNIGK GKEQGGSTTH RHTHVGGTTG KTTIRSGGDT TLKGVQLIGK
2001 GIQADTRNLH IESVQDTETY QSKQQNGNVQ VTVGYGFSAS GSYRQSKVKA
2051 DHASVTGQSG IYAGEDGYQI KVRDNTDLKG GIITSSQSAE DKGKNLFQTA
2101 TLTASDIQNH SRYEGRSFGI GGSFDLNGGW DGTVTDKQGR PTDRISPAAG
2151 YGSDGDSKNS TTRSGVNTHN IHITDEAGQL ARTGRTAKET EARIYTGIDT
2201 ETADQHSGLH KNSFDKDAVA KEINLQREVT KEFGRNAQA VAAVADKLG N
2251 TQSYERYQEA RTLLEAELQN TDSEAEKAAF RASLGQVNAY LAENQSRYDT
2301 WKEGGIGRSI LHGAAGGLTT GSLGGILAGG GTSLAAPYLD KAAENLGPAG
2351 KAAVNALGGA AIGYATGGSG GAVVGANVDW NNRQLHPKEM ALADKYAEAL
2401 KREVEKREGR KISSQEAAMR IRRQILRWVD KGSQDGYTDQ SVISLIGMKG
2451 EDKALGYTDW YRDYGARNPQ TYNDPKLFEE YRRQDKPEYR NLTWLHSGTK
2501 DTKIRQGERK NEEFALNVAE GLTSLVNP NP RIKVPILAGI RNLKNIKPTV
2551 TGSDDLPLAGA GNIRIPANGN VAKGDRIPTD ALASKGIKHK DRKDQLEKK*

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Computer analysis of this amino acid sequence gave the following results:

#### Homology with fha

m564/fha

ID FHAB\_BORPE STANDARD; PRT; 3591 AA.

AC P12255;

DT 01-OCT-1989 (REL. 12, CREATED)

DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE FILAMENTOUS HEMAGGLUTININ. . . .

SCORES Init1: 190 Initn: 524 Opt: 594

Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

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              10      20      30      40      50      60
m564 .pep  MNRTLYKVVFENKHNRCMIAVAENAKREGKNTADTQAVGILPNDIAGFAGFIHSISVISFS
           || :||::||:: || : : ||:  | ||  :: |  :  : |  : ||: ::
fhab_borpe MNTNLYRLVFSHVRGMLVPVSEHCTV-G-NTFCGRTRG---QARSGARATSLSVAPNALA
              10      20      30      40      50

              70      80      90      100     110     119
m564 .pep  LSLLLG-SALILTSSSATAQGIVADKSAPAQQQPTILQTGNIGIPQVNIQTPTSAGVSVNQ
           :||: :|| :||  ||::|  | ||  :|| || :| ||| ||: ||| ||
fhab_borpe WALMLACTGLPLVTH---AQGLV-----P-QGQTQVLQGGNKVPVVNIADPNSGGVSHNK
              60      70      80      90      100

              120     130     140     150     160     170     179
m564 .pep  YAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSQNLNGYIEV
           : ||: ||: ||::||: : : ||:  | ||  :|| :| :| :| :| :| :| :|
fhab_borpe FQQFNVANPGVFENNGLTDGVSRI GGALTKNPNLTR-QASAILAEVTDTPSPRLAGTLEV
              110     120     130     140     150     160

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	180	190	200	210	220	230	239
m564 .pep	GGRRAEVVIANPAGIAVNGGGFINASRATLTTAQPQYQAGDLSGFKIRQGNVVIAGHGLD						
	: ::          :                 :   :   :             :						
fhab_borpe	YGKGADLIIANPNGISVNGLSTLNASNLTLTGRPSVNGGRI-GLDVQQGTVTIERGGVN						
	170	180	190	200	210	220	
	240	250	260	270	280	290	
m564 .pep	ARDTDYTRILSYHSKIDAPV---WGQ---DVRVVGQNDVAATGDAHSPILNNAANTS						
	:   :   :     :   :           :   :       :						
fhab_borpe	ATGLGYFDVVARLVKLGAVSSKQKPLADIADVAGANRYDHATRRATPI----AAGARG						
	230	240	250	260	270	280	
	300	310	320	330	340	350	
m564 .pep	NTANNGTHIPLFAIDTGKLGMYANKITLISTVEQAGIRNQGWFFASAGNVAVNAEGKLV						
	:   :   :     :   :         :   :   :   :   :   :   :						
fhab_borpe	AAAGA-----YADGTAAGAMYKGHITLVSSDGLGVRQLGS-LSSPSAITVSSQGEIA						
	290	300	310	320	330		
	360	370	380	390	400	410	
m564 .pep	NTGMIAATGENHAVSLHARNVHNSGTVASQDDANIHSQTLDNSGTVLSSGRLTVRNLGRL						
	:   :   :   :   :   :   :   :   :   :   :   :   :   :						
fhab_borpe	---LGDATVQRGPLSLKGAGVVSAGKLAGGGAV---NVAGGGAVKIA---SASSVGNL						
	340	350	360	370	380		
	420	430	440	450	460	470	
m564 .pep	KNQNNGTIQAAARLDMSTGGLDNTGNITQTGSQALDLVSAGKFDNSGKIGVSDVPQTGLNP						
	:   :   :   :   :   :   :   :   :   :   :   :   :						
fhab_borpe	AVQGGGKVQATLLNAG-----GTLVSGRQAVQLGAASSRQALSVNAGGALKADKLSA						
	390	400	410	420	430		
	480	490	500	510	520	530	
m564 .pep	NPSV-IPQIPSTATGSGSSTVSVSKPGSNNFVSPTAPAKNYAVGRIQTTGAFD-NAGSIN						
	:   :   :   :   :   :   :   :   :   :   :   :   :						
fhab_borpe	TRRDVDGKQAVALSASSNALSVRAGGA-----LKAGKLSATGRDLVDGKQAVTLGSA						
	440	450	460	470	480	490	
	540	550	560	570	579		
m564 .pep	AGGQIDIAAQNGLGNSGSLNAAKLRVSG-----DSFNNT-----VKGKLQAHDLAVNT						
	:   :   :   :   :   :   :   :   :   :   :   :   :						
fhab_borpe	SDGALSVSAGGNLRANELVSSAQLEVRGQREVALDDASSARGMTVVAAGALAAARNLQSKG						
	500	510	520	530	540	550	
	580	590	600	610	620	630	
m564 .pep	QTAKNSGHLTQTGKIDNRELH--NAGEIAANNLTLIHSGRLSNDKKGNIRAAHLQLDTA						
	:   :   :   :   :   :   :   :   :   :   :   :   :						
fhab_borpe	AIGVQGGAEVSVANANSDAELRVGRGQVDLHDLAARGADISGEGRVNI GRARS DSDVK						
	560	570	580	590	600	610	
	640	650	660	670	680	690	
m564 .pep	GLHNAGNILADSGTVTTKNNLRNTGKVSVARLNTGQTLDNTRGRIEAE TVNIQS QQLTN						
	:   :   :   :   :   :   :   :   :   :   :   :   :						
fhab_borpe	-VSAHGALSIDSMTALGAIGVQAGGSVSAKDMRSRGAVTVSGGG-----AVNLGDVQ---						
	620	630	640	650	660		
	700	710	720	730	740	750	
m564 .pep	QSGHITATEQLTINSRNVNDNQNGKLLSANQAQLAVSDGLYNQHGEIATNRQLSIHDKNQ						
	:   :   :   :   :   :   :   :   :   :   :   :   :						
fhab_borpe	SDGQVRATSAGAMTVRDV-----AAAADLALQAGDALQAGFLKSAGAMTVNGRDAV						
	670	680	690	700	710		

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760      770      780      790      800      810
m564 .pep TLALNNADGTIQSAGNVSLOAKSLANNGLTAGNKLDIALTDDFVVERDLTAGKQL-NLS
      |  ||: ::||: :: : | |:|: |:| :: : :| :| |:| |:|
fhab_borpe RL-----DGA-HAGGQLRVSSDQQAALGSLAAKGELTVSAAARAATVA-EL---KSLDNIS
              720      730      740      750      760

      820      830      840      850      860      870
m564 .pep IKGRLLK-NTHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLNSDGLT
      : | : ::::: : ::| | :|: : ::| | : | ::||:
fhab_borpe VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE----GWGAVGADSL-
              770      780      790      800      810

      880      890      900      910      920      930
m564 .pep HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETEGSTKAGATAARKRLDI-GAKEIHN
      |: :: :| : : : |:| |: :|: :|: | |:| :|: :|:
fhab_borpe --GSDGAISVSGRDAVRVDQARSLADISLG----AEGGATLGAVEAAGSIDVRGGSTV--
              820      830      840      850      860

      940      950      960      970      980      990
m564 .pep QEGALLSSEGIFAVGNRLDEQHHAAAGMADTFVNGSAGLEVQGDALMSVRNMQNNHFEKT
      ::| :: : :| : | : :|: : :|: :|: :|: :|: :|:
fhab_borpe AANSLHANRDVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV
              870      880      890      900      910      920

      1000      1010      1020      1030      1040      1050
m564 .pep ETYLAKAEK--QVRDYTVLGQNTYYQAGKDGFLDNSQGGQKQDTTATFHLKNGSRIEANQ-
      ||| :|: :| :| :| :| :| :| :| :| :| :| :| :| :|
fhab_borpe ALQSAKASGTLHVQGGHEHLDLGTAAVGAVDV----NGTGDVRVAKLVSDAGADLQAGRS
              930      940      950      960      970

      1060      1070      1080      1090      1100
m564 .pep --WHVRDYHIETYKERIIEENRPAHITVGGDLTASGQNWLNKDSRIVVGGRITDDLNQKE
      : | : : : :| | |:| :|: :|: :|: :|: :|
fhab_borpe MTLGIVDTTGDQLQARAQQKLELGSVKSDDGLQAAAGGALSAAAEEVAGALELS---GQGV
              980      990      1000      1010      1020      1030

      1110      1120      1130      1140      1150      1160
m564 .pep ITNQSTTGKGRITDAVGTQWDSVTKKGWY--SGRKRQRTERNHTPYHDTQLFTHDFDTPV
      :::::| |:|: :| | : :| |:| | :| | |
fhab_borpe TVDRASASRARIDSTGVSIGALKAGAVEAASPRRARRALR-----QDFFTPG
              1040      1050      1060      1070      1080

      1170      1180      1190      1200      1210      1220
m564 .pep SVI---QQNAASPSFQPAASAIAKLIDGVSTAANGQRIHTGNVVSLLNNATVILPNSSLYT
      ||: | |: :| :: :| :| :| :| :| :| :| :| :|
fhab_borpe SVVVRAGGNVTVGRGDFHQGVLAQGDIIIMDA--KGGTLLLRNDALTENGTVTISADSAVL
              1090      1100      1110      1120      1130      1140

      1230      1240      1250      1260      1270      1280
m564 .pep THPDNKGWLVETD-PQFADYRRWLGS DYMLQQLQDLTNHLHKRLGDGYEQLVNEQIHQ
      | : : : :| : :| : :| | : :|: : : :|
fhab_borpe EHSTIESKISQSVLAAKGDKGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRQIDV
              1150      1160      1170      1180      1190

      1290      1300      1310      1320      1330      1340
m564 .pep LTGYRRLDGYRSDEEQFKALMDNGLTAAKTFLTPG-IALSAEQVARLTSDIVWMENQTV
      : | : :| :| :: :| :| :| :| :| :| :| :|
fhab_borpe VDGRPQI-----TDAVTGEARKDES VSDAALVADGGPIVVEAGELVSHAGGIGNGRNK--
              1200      1210      1220      1230      1240      1250

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[illegible]

		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGEQGGSTTHRHThVGSGTTGKTtIRSGGDttLKGvQLIGkgIQADTRNLH        : :     :: :  : :   :					
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNegVIQAagGHigG-----DVDNRsv- 1870                   1880                   1890                   1900					
		2020	2030	2040	2050	2060	
m564	.pep	IESVQDTETyQSkoqNGNVQtVgYGFSAgsSYRQskVK-----DHASvtQGsgIyaGe ::: :   ::: : : :  : :    : k :  :  :					
fhab_borpe		VRTVSAMEYfKtPLPvSLTALDNrAgLSpatWNfQStYeLLDQNRYeyIWGLPYTy 1910          1920          1930          1940          1950          1960					
		2070	2080	2090	2100	2110	2120
m564	.pep	DGYIKIVRDNTDLKgGIItSSqsAEDkGKNLfQTATLTAsDIQHNS--RYEGrsFGIgGS :::::        : :					
fhab_borpe		TEWSvNtLKnlDL-GYOAKPAptAPMPKA-----PELDLRghTLesAEGRKI-FGEY 1970          1980          1990                         2000          2010					
		2130	2140	2150	2160	2170	
m564	.pep	FdLNgGWdGT-----VDtkQRPTDRISpaAgYGSDgSKNsTTrSGVNtNhIHITDeAg  :  :: : ::  :    :   :: : :  : : :: :					
fhab_borpe		KKLQGEYEkaMAvQAVEAYgeAtRRvhDqlG-----QRygKaLGGMdaEtKEvdGIIQ 2020          2030          2040                         2050          2060          2070					
		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTgrTAketEARiyTGIDtETAdqHSghlKnsFDkdAvAkEINLoREVtkeFGrNAa ::   : :       :    : : :  : :   :  :  :: :					
fhab_borpe		EFAAdLRtvYaKQADQat-IDAEt-DKVaqRYKSQiD--AVRLQAIQPGRVT--LaKALS 2080          2090          2100          2110          2120					
		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAavaDKlgntQsyERYQEartlle-AELQnTDseAEkaAFrasLGqvNaYL-----  ::    ::  ::::: : :   : :   ::   ::					
fhab_borpe		AALGaDWRALghSOLMQRWKDFKAGKRgaEIafYPKeQtVLaaGAGLtLSngATHngenA 2130          2140          2150          2160          2170          2180					
		2300	2310	2320	2330	2340	2350
m564	.pep	AEHQsrYdtWKEggIGRSILHgAAgglTTGsLGGilAGgGTslAAPylDKAAENlGPack  :::  :    : : : :  :					
fhab_borpe		AQNrgRPeglKiGAhsATSvsGSfdAlrdvgLEkrldIdDALAAVLvnPHIFTRIgaAQT 2190          2200          2210          2220          2230          2240					

g565.seq

1	atggacagca	cattgtctaa	aacgtgttgc	gtttcgtgca	tattgttgag
51	cgtaaccacc	accatttttc	cccgctccag	accggcggct	tccaataactt
101	ccctgcggtt	cgcatacgcc	aacgacacgc	gctcgcctgc	gaattctggct
151	acctgcacgc	gtgcgatgtc	caagtcgagc	gcgaaatacg	caatatcctc
201	tttggggcaa	gacgcgtccg	acgtctctgc	cgcacctgcc	gaagccgaca
251	atcgacacat	gatcacagct	gcctatcgct	tccaccaaca	tgctgtgcag
301	atcgagcgac	ttcatgtccc	agcttga		

g565.pap  
1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA  
51 TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ  
101 IERLHVPA\*

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m565.seq
1  ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTCG CCCGTCACAG ACGGCGGCT TCAATACTT
101 CCTCGCGTTT CCAATCGCC AAGACACCG GTTCGCCCC ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC GCGAAATACG GAATATCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCTGCGC AAGCCGACA
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251 TCAGCACATG GTCGGA CTGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTGCG CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAAC TCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTCGC CGACCGAATG TTTCATTTT AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

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This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

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m565.pep
1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTCEFIL KAMANTTSF NTSSSIANSIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
|||||
g565          MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                10      20      30      40      50      60

                70      80      90      100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDL LMVSTSILCRSSDFMSQLDLTKRPTSASLP
|||||
g565          AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51 CGTAACCAACC ACCATTTTCG CCCGTCCAG ACCGGCGGCT TCCAATACTT
101 CCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCG GCCCCTGCCG AAGCCGACAA
251 TCAGCACATG GTCGGA CTGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
351 ATCGTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTGCG CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAAC TCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTCGC CGACCGAATG TTTCATTTT AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTCEFIL KAMANTTSF NTSSSIANSIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
|||||

```



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```

a565      MDSTLSKTCVSCILLSVTTFIFARPRPAASNTSLRFASFNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60
m565.pep  AKYGISSWARTRPTVCPLPKPTISTWSDLLMVSTILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
a565      AKYGISSWARTRPTVCPLPKPTISTWSDLLMVSTILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
m565.pep  PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
a565      PKRKGAIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
m565.pep  KAMANTTSAFNTSSIANSTNCRQPPINAX
           190     200     210
a565      KAMANTTSAFNTSSIANSTNCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct ttccagacgg cattttgtat gggggttaac
51  ggttggtcag cccgagtagc tcctgcatac cgtacaaacc cgttttgccg
101 ttaccctaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggct
151 gccggctttg tgggtgattt ccacgcgttc gccgtcggtg gcgaagaggg
201 cgggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcggcgcc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAAATATCT TTTCAGACGG CATTGTTGTAT GGGGGTTAAC
51  GGTGTTTCAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTGTCCG
101 TTGACCAAAA CTGCGGCGCG GACGGCACCG GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATTT CCACGCCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGTTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDNCGA DGTGGKGHAA
51  AGLVGDHAF AVGGEEGGVV ADDVACADGG KADGRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDNCGADGTGGKGHAAAGLVGDHAF
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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```

g566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           70      80      90      100     110
g566      AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566.seq
1  ATGCCGCTCTG  AACAATATCT  TTTCAGACGG  CATTTTGTAT  GGGGGTTAAC
51  GGTGTGTTTCTG  CCCGAGTACG  TCCTGCATAT  CGTACAAACC  CGTTTACCCT
101 TTTACCCAAA  CTGCGGCGCG  GACGGCGCGC  GCGGCAAAGG  TCATGCGGCT
151 GCTTGCCCTTG  TGGGTGATTT  CCACGCGCTC  GCCGTCGGTG  GCGAAGAGGG
201 CGGTGTGGTC  GCCGACGATG  TCGCCCGCGC  GGACGGTGGC  AAAGCCGATG
251 GTGGACGGAT  CGCGCGGGCC  GGTGTGGCCT  TCGCGCCCGT  AAACGGCGCA
301 TTGTTTGAGG  TCTCTGCCGA  GCGCGCCGCG  GATGACTTCG  CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566.pep
1  MPSEQYLFRR  HFVWGLTVVQ  PEYVLHIVQT  RFTVYPNCGA  DGAGGKGHAA
51  ACLVGDFHAL  AVGGEEGGVV  ADDVARADGG  KADGGRIARA  GVAFAAVNGA
101 LFEVSAERAG  DDFAHA*

```

m566/a566 94.0% identity in 116 aa overlap

```

m566.pep      10      20      30      40      50      60
MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDNCGADGTGGKGHAAAGLVGDFHAL
|||||
a566          10      20      30      40      50      60
MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
|||||
m566.pep      70      80      90      100     110
AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
|||||
a566          70      80      90      100     110
AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567.seq..
1  atgcgacgac  gggcagcggc  atcgacaagg  cgggtttgca  gtccggcggt
51  tatcaggtct  tattgggcga  tgcggacgtg  cagtcggcgg  cggtacgcag
101 caaagagggc  ggatacggcg  tgttggtgac  gaacgcgcgc  gcttgccggc
151 gcggaatcgc  agctggtgca  ggaaatcgcc  cggaagtgc  gttgaaaaa
201 cgcgctcaag  gcagtggcgg  aagattacga  cttatcctg  atcgactgtc
251 cgccttcgct  gacgctgttg  acgcttaacg  gcttggtggc  ggcgggcggc
301 gtgattgtgc  cgatgttgtg  cgaatattac  gcgctggaag  ggatttccga
351 tttgattgcg  accgtgcgca  aaatccgtca  ggcggtcaat  cccgatttgg
401 acatcacggg  catcgtgcgt  acgatgtacg  acagccgcag  caggctggtt
451 gccgaagtca  gcgaacagtt  gcgcagccat  ttcggggatt  tgcttttga
501 aaccgccatc  ccgcgcaata  tccgccttgc  ggaagcgccg  agccacggta
551 tgccggtgat  ggcttacgac  gcgcaggcaa  agggtgccaa  ggcgtatctt
601 gccttgccgg  acgaactggc  ggcgagggtg  tcggggaat  ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567.pep
1  MRRRAAASTR  RVCSPAFIRS  YWAMRTCSRR  RYAAKRADTA  CWVRTRALAG
51  AEIELVQEIA  REVRLKNALK  AVAEDYDFIL  IDCPPSLTLL  TLNGLVAAGG
101 VIVPMLCEYY  ALEGISDLIA  TVRKIRQAVN  POLDITGIVR  TMYDSRSRLV
151 AEVSEQLRSH  FGDLLFETAI  PRNIRLAEAP  SHGMPVMAYD  AQAKGAKAYL
201 ALADELAARV  SGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
1  ATGAGTGCGA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTTCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GCGGGATACG
251 CTGTGTTGGG TGCGAACCGC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGA
351 AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCC GATTGTATTG CGACCGTGCG
501 CAAATCCGT CAGGCGGTCA ATCCCGATTG GGACATCACG GGCATCGTGC
551 GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTCGGGGA TTTGCTTTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCCT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701 ACGCGCAGGC AAAGGGTACC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 GCGGCGAGGG TGTCGGGGAA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
1  MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAEEEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLDT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNL AEAPSHGMPV MAYDAQAKGT KAYLALADEL
251 AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m567/g567 98.2% identity in 168 aa overlap

	60	70	80	90	100	110	119
m567.pep	GVYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAEEED						
g567	AFIRSYWAMRTCSRRYAAKRADTACWVRTRALAGAEIELVQEIAREVRLKNALKAEEED						
	20	30	40	50	60	70	
m567.pep	120	130	140	150	160	170	179
	YDFILIDCPPSLTLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI						
g567	YDFILIDCPPSLTLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI						
	80	90	100	110	120	130	
m567.pep	180	190	200	210	220	230	239
	TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNLAEAPSHGMPVMAYDAQAKG						
g567	TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETAIPRNLAEAPSHGMPVMAYDAQAKG						
	140	150	160	170	180	190	
m567.pep	240	250					
	TKAYLALADELAARVSGKX						
g567	AKAYLALADELAARVSGKX						
	200	210					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
1  ATGAGTGCGA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTTCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GCGGGATACG
```

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```

251 GCGTGTGGG TCGAACC GCCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CCGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TCGGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501 CAAATCCGT CAGCGGTCA ATCCCGATT GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGCGGAGGG TGTGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GGYVGLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

m567/a567 97.7% identity in 257 aa overlap

              10      20      30      40      50      60
m567.pep      MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
a567           |||||
m567           MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
a567           |||||

              70      80      90     100     110     120
m567.pep      VYQVLLGDADVQSAAVRSKEGGYAVLGNR ALAGAEIELVQEIAREVRLKNALKAVEEDY
a567           |||||
m567           VYQVLLGDADVQSAAVRSKEGGYAVLGNR ALAGAEIELVQEIAREVRLKNALKAVEEDY
a567           |||||

              130     140     150     160     170     180
m567.pep      DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
a567           |||||
m567           DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
a567           |||||

              190     200     210     220     230     240
m567.pep      GIVRTMYDSR SRLVAEVSEQLRSHFGDLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
a567           |||||
m567           GIVRTMYDSR SRLVAEVSEQLRSHFGDLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
a567           |||||

              250
m567.pep      KAYLALADELAARVSGKX
a567           |||||
m567           KAYLALADELMARVSGKX
a567           |||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
1 atgctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
51 gataccttgc agaattctgc gattaaagcg ttcgcggctg cccaatattt
101 tcaggcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaaaggc
151 tgtaaaaaca gcccacatcag gaacgaaact tcgtcttcgg ggcgacgcca
201 gttttcgggt gaaaaggcaa acacggctcag atattgcacg cccagtttgg
251 cgcaatgctt caccatattt tccaacgcgt ccaagccgct tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggccgt tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgctg

```

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401 tgctgctctt catatctgcc tttcgcggtt cggcggtcaa atgccgtctg  
451 aacgccgcgc cgtga

This corresponds to the amino acid sequence <SEQ ID 1690; ORF 568.ng>:

g568.pep  
1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA  
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP  
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL  
151 NAAP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1691>:

m568.seq  
1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC  
51 GATGCCTTGC AGAATCTGCC GGTGAAGCG TTCCGGCGTG CCCAATATCT  
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TCGCAAAGCC  
151 TGTAAAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGGCCA  
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG  
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC  
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT  
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG  
401 TGCTGCTTTT CATGTCTGCC TTTCCGGTTC CGGCATTCAA ATGCCGCTCTG  
451 AACGCCGAAC CGTGCAGGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG  
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC  
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTCTT TGTCTTTGAG  
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATAGAGA  
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG  
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC  
751 TGCCGGGTTT AGTCCCAAGT TTGA

This corresponds to the amino acid sequence <SEQ ID 1692; ORF 568>:

m568.pep..  
1 MLRVRPVLFA VNASASSMPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA  
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP  
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL  
151 NAEPCLRNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE  
201 EFFDVVVGIA AHVADRDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS  
251 CRVQSQV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m568/g568 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
g568	MLRVRPVLFAVKASASSIPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIIRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCLRNCHQIFFFGSQEFVGFVGNVFGVQ					
g568	MCLGMAVCSKMVCVLLFISAFRGSFAFKCRLNAAPX					
	130	140	150			
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1   ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTTGAC GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTAAAAACA GCCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTTCGGGTT CGGCATTCAA ATGCCGTCG
451 AACGCCGAAC CGTGACGGTT AAATGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 CTTCTTTCG CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTC AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1   MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVKASASSMPFRIXRLKRSRLPSIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	70	80	90	100	110	120
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	130	140	150	160	170	180
a568	ICLGMVCSKTACVLLFMSAFRGSAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
m568.pep	190	200	210	220	230	240
a568	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	250	HRHADQVADSCRVSQVX				
a568	HRHADQVADSCRVSQVX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1   atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgcgggc
101 tgattgccct gaccgccttg tgggagtatg cccgtatggc cggtttgtgc
```

874

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tggcgtagt
201 tgcctatgcg ggcggctgga tgctgcctaa ttgggtttgg tatgtgttt
251 tggcattttg gctcgccggt atgcctttgt ggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgctcatgcc
351 gttttggttc gcgctcgat ccctggcgcc cgcacccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRPKWR
101 LGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTACGCGC CGCAATGGTT GTGGGCTGCA TTTGCGGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATTG CCTCGCCGCA ACCTTGTTT TCGGCGTGGT
201 TGCTATGCGG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCCTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGTTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCCGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGCGCG CGCGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTGCA TACAGGCTGG
601 TTCGATACCG TGTAAATCGG TTTGGTGCTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAGCTGCTG GCCCGGACAC GCGCGCGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRPKWR
101 LGGWQVYAV GWLLMPFWF ALVSLRPHPD DALPLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAIAPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVSVCGDLL ESWLKRAAGI KDSSKILPGH GGVFDRDTSL
251 IAVISVYAAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLMPFWF					
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLMPFWF					
	70	80	90	100	110	120
m569.pep	ALVSLRPHPDALPLAVMGLVWVADICAYFSGKAFGKHKIAPAISPGKSWEGAIGGAVC					
g569	ALVSLAPASRX					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTACGCGC CGCAATGGTT GTGGGCTGCA TTTGCGGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

```

875

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGGTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCEA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGCGCGTGT TCGACCGEAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569.pep
1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALLIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFTDGTW
201 FDTVLIGLVL TVSVSCGDL ESWLKRAAGI KDSSNLLPGH GGVFDRDTSL
251 IAVISVYAAM MSVLN*

m569/a569 99.6% identity in 265 aa overlap

10 20 30 40 50 60
m569.pep MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALLIALWEYARMGGLCKIKTNHYLAA
|||||
a569 MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALLIALWEYARMGGLCKIKTNHYLAA
10 20 30 40 50 60

70 80 90 100 110 120
m569.pep TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
|||||
a569 TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
70 80 90 100 110 120

130 140 150 160 170 180
m569.pep ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIIAPAI SPGKSWEAIGGAVC
|||||
a569 ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIIAPAI SPGKSWEAIGGAVC
130 140 150 160 170 180

190 200 210 220 230 240
m569.pep VAVYMTAVRSAGWLAFTDGTWFDTVLIGLVLTVSVSCGDLLESWLKRAAGIKDSSKLLPGH
|||||
a569 VAVYMTAVRSAGWLAFTDGTWFDTVLIGLVLTVSVSCGDLLESWLKRAAGIKDSSNLLPGH
190 200 210 220 230 240

250 260
m569.pep GGVFDRDTSLIAVISVYAAMMSVLNX
|||||
a569 GGVFDRDTSLIAVISVYAAMMSVLNX
250 260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

g570.seq..

```

1 atgataccgtt tgacccgcgc gtttgccgcc gccctgatcg gtttatgctg
51 caccacagcg gcgcacgcgc acaccttcca aaaaatcgcc tttatcaaca
101 ccgagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc ccgtcaggac gaattgcaaa aactgcaacg
201 cgaaggcttg gatttgaaa ggcagctcgc cggcgcaaaa cttaaggacg
251 caaaaaagcg gcaagccgaa gaaaaatggc gcgggctggt cgaagcgctc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaacgcaaa ccgcgtcatc gtcaaaatcg

```



876

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac  
 451 acccaatacgc acgttaccga cagcgtcatt aaagaaatga acgcccgcgtg  
 501 a

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

1 MTRLTRFAAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT  
 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF  
 101 RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIIYVN  
 151 TQYDVTDVSI KEMNAR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

1 ATGACCCGTT TGACCCGCGC GTTGGCCGCG GCTCTGATCG GTTGTGCTG  
 51 CACCGCAGGC GCGCAGCGCG ACACCTTCCA AAAAATCGGC TTTATCAACA  
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CCGCAAGAT TCAAAAAACG  
 151 CTGGACAGCG AATTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG  
 201 CGAAGGTCTG GATTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG  
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC  
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA  
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG  
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC  
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG  
 501 A

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

1 MTRLTRFAAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT  
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAF  
 101 RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQNVIIYVN  
 151 TQYDVTDVSI KEMNAR\*

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
g570	MIRLTRFAAAALIGLCCTTAGAHADTFQKIGFINTERIYLESKQARNIQKTLDGEFSARQD					
	10	20	30	40	50	60
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA					
g570	ELQKLQREGLDLERQLAGGKLRDAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRRNEEFA					
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA					
g570	ELQKLQREGLDLERQLAGGKLRDAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRRNEEFA					
	70	80	90	100	110	120
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDVSIKEMNARX					
g570	SLQQNANRVIVKIAKQEGYDVILQDVIIYVNTQYDVTDVSIKEMNARX					
	130	140	150	160		
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDVSIKEMNARX					
g570	SLQQNANRVIVKIAKQEGYDVILQDVIIYVNTQYDVTDVSIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

1 ATGACCCGTT TGACCCGCGC GTTGGCCGCG GCTCTGATCG GTTGTGCTG  
 51 CACCGCAGGC GCGCAGCGCG ACACCTTCCA AAAAATCGGC TTTATCAACA  
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CCGCAAGAT TCAAAAAACG  
 151 CTGGACAGCG AATTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG  
 201 CGAAGGTCTG GATTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG  
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC  
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA  
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG  
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC  
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```
a570.pep
1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
51  LDSEFSAROD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151 TQYDVTDSVI KEMNAR*
```

m570/a570 97.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLTLDSEFSARQD					
a570	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLTLDSEFSARQD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRRKKQAQFEEDYNLRNNEEFA					
a570	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVYVNTQYDVTDSVIKEMNARX					
a570	SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```
g571.seq (partial)
1  atgcgcgttt tccgagtaaa ccgatttgtt gttaccgttt tggcgggcgg
51  tataggttct gccgtccac acgctgcctg cgtcggcaaa caggctcagg
101 cggacggtgc gtgcgtcttt cgcaccgggc atcggaaga gcagctcggc
151 ggagacgttg gctttttgtg tgcgcgcgta gctgatttt tgcgcgtatt
201 cgtcatcac tttcggggcg agcgtgccgc ttctgtagcc gcgcaccgaa
251 cccaggccgc cgcgtagaa gttttcaaa agggggattt ctttggttct
301 gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351 ttttgc...
```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```
g571.pep (partial)
1  MRVFRVNRV VTVFGGGIGS AVPHAACVGK QAQADGACVF RTGHREEQLG
51  GDVGFFVAIV ADFFAVFVIH FRAERAAVFA AHRTQAAAVE VFKEGDFFGS
101 AVAARNADFA AEHQREGFA...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```
m571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTGT AACCTGCGCG CCGGTGCGCG
51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201 TTTTTCGCC GTATTCGTCA TAGACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCAG GCGCGCGCG TAGAAGTTT CAAAGAAGGG
301 GATTTCITTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGGTTTGT CTCAGGGGA AGAACAGGT TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTCGCGCTT
451 CACGCCCGTC AGGTAGCCGC GCGTCGCCCA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```
m571.pep
1  MGIAGAVNVL NPAAGRGTA VVVGFVAPHA ACVGKQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAADVADFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQR EGFAQGEEPG LVVGGGVVLQ FAARQGDGFGV
151 HARQVAARRP *
```

878

m571/g571 93.1% identity in 102 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVLNPAAGRGTAVVVVGFVAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
           :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g571      MRVFRVNRVVTVFVGGIGSAVPHAACVKGQAQADGACVFRTHREEQLGGDVGF
           10      20      30      40      50

      70      80      90     100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g571      FVAAVADFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           60      70      80      90     100     110

      130     140     150     160
m571.pep  EGFAQGEEPLVVGGLVQLFAARQDGFVHARQVAARRPX
           ||||
g571      EGFA
           119

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCGC CCGGTCGCGG
51  AACTGCTGTT GTCGTCGTAG GTTTGCGCGT CCCACACGCT GCCTGCGTGC
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201 TTTTTCGCC GTATTCGTCA TACACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCAG GCCGCCGCCG TAGAAGTTT CAAAGAAGGG
301 GATTCTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGGTTTTG CTTAAGGGGA AGAACCAGGT TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTGCTGCCG GGCAGGGCGA TTTCGGCGTT
451 CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

```

a571.pep
1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVKGQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFVIHFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQ EGFA*GEEPG LVVGGGVVLQ FAAGQDGFV
151 HARQVAARRP *

```

m571/a571 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVLNPAAGRGTAVVVVGFVAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      MGIAGAVNVLNPAAGRGTAVVVVGFVAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
           10      20      30      40      50      60

      70      80      90     100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      FVAAVADFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           70      80      90     100     110     120

      130     140     150     160
m571.pep  EGFAQGEEPLVVGGLVQLFAARQDGFVHARQVAARRPX
           |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      EGFAQGEEPLVVGGLVQLFAARQDGFVHARQVAARRPX
           130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:  
g572.seq..

1	atgtgcgcga	tctgtcggggc	ggcgggggctg	ccttcgcgcg	tcgcagcggc
51	gcaaaaaggt	aaaaccattt	atctggcaca	caaagaaacg	ctggttggtt
101	ccgggcgctt	gtttattgaa	accgcccgcg	caaacggcgc	ggcgattgtt
151	cccgctgcga	gcgaacacaa	cgcatttttc	caagtcttgc	gcgcgatta
201	cacagaccgt	ctgaacgaac	acggcatcga	ttcgattatc	ctgaccgctt
251	ccgggcggcc	gtttttaaca	accgatttaa	gcacgttcga	cagcattacg
301	cccgagcagg	cggctcaaca	ccccaattgt	cgtatggggc	gcataaatcg
351	cgtcgattca	gcacctatgg	caacaagggt	cttggaaact	cttaagcgcg
401	attgctgtgt	caactgtccg	ccgcacaaac	tcgaagtcgt	catccatccc
451	caatccgtga	tacacagtat	ggctgcgtac	cgcgacggct	ccgtgtcggt
501	gcaactgggc	atacccgcat	tgcagacgcc	catcgccatt	tgttctggct
551	tgcccgagcg	catcgattcg	ggctgtcgga	aaactcgatt	cggcgcatgt
601	tccgcgctga	ccttccaaaa	gccgcgattc	ggcgcgtctc	cttcctcgaa
651	gttcgctatt	gaaaccataa	acgcaggcgg	agccgcgcc	tgcgtattga
701	acggcgccaa	cgaaacggcc	tgtgcgcgct	ttttggacgg	acagattaag
751	tttaccgaca	ttgcacaaac	cgtcgcccat	tgcttcagac	aaagcttttc
801	aaacggcatg	ggcgcatatg	aaggactgtt	ggcgcgcaat	gcccggcac
851	qccqcaaacg	gcgggcatct	atcggcacac	tcgcgtga	

g572.pap..

1	MCAIVGAAGL	PSALAAQKG	KTIYLANKET	LUVSGALFME	TARANGAAVL
51	FVDSEHNATF	QVLPRDYTR	LNEHGIDSII	LTASGGFFLT	TDLSTFDSIT
101	PEQAVKHPNV	RMGRKISVDS	ATPMARKTGLE	IEAHWLFENCP	PKDKLEVIHP
151	QSVIHSMWY	RDGSLVALQG	NPDMRKTPIAL	CLGLPERNCIS	VAGGLDFPGL
201	SALTFOKPDF	GRFPCCLKFAY	ETINAGGAAP	CVLNAANETA	VAAFLDGOIK

m572.seq..

1	ATGTGCGCCA	TCGTGCGGGC	GGTGGGGCTG	CCTTCCGCGC	TCGCAGCGGC
51	GCAAAAAGCG	AAAAACCATTT	ATCTGGCAAA	CRAAGAAACG	CTGGTGGTTT
101	CCGGCGCGTT	GTTTATTGAA	ACCGCCGCTG	CAACCGCGCG	GGCAGTGCCTG
151	CCCGTCGCAG	CGGAACACAA	CCCGTTTTC	TAAAGTTTGC	CGCGCGGATT
201	CGCGCGCGGT	CTGAACGAAC	ACGGCATCGC	TTCGATTATC	CTGACCGCTT
251	CGCGCGCGCC	GTTTCTGCC	GCCGATTTGA	ACACGCTTCA	CGCATTTACG
301	CCCGCCCAAG	CGCTCAACA	CCCCAATTGG	CGTATGGGAC	GCAAAATCTC
351	CGTCGATTCC	GCCACCATGA	TGAACAAAGG	TTTGGAGCTG	ATTGAAGCGT
401	ATTGGCTGTG	CAACTGTCCG	CCCGACAAC	TCGAAGTCGT	CATCCATCCG
451	CAATCCGTGA	TACACAGCAT	GTGCGCTAC	CGCGACGGCT	CGGTGCTGGC
501	GCAACTGGCG	AATCCCGATA	TGCGAAGCCG	CATCGCTTAT	GTGTTGGGTT
551	TGCCCGAGCG	CATCGATTCC	GGTGTGCGCG	ACCTGGATT	CGACGCATTG
601	TCGCGCTGA	CCTTCCAAAA	CGCCGACTTT	GACCGCTTCC	CCTGCTGATG
651	GCTCGCCTAT	GAAGCGCATG	ACGACGGCGC	AGCCGCGCCC	TGCGTATTAG
701	ACGCGGCCAA	CGAAGCGCGC	GTGCGCGCCT	TTTGTGACGG	ACAGATTAA
751	TTTACCGACA	TGCGCAAAAC	CGTGCGCCAC	TGCTTCAAGT	AAGACTTTTC
801	AGACGGCATA	GGGCATATAG	GGGGGCTCTT	GGCGCAAGAT	GCCCCGACAC
851	GGCGACAAGC	GCGAGCATTT	ATTGGCAATG	TCGCGTGA	

м572.пер..

1	MCAIVGAVGL	PSALAAQKG	KTIYLANKET	LUVSGALFME	TARANGAAVL
51	PQVSEHNVA	QLPRDYAGR	LNEHGASII	LTASGPGFLT	ADLNTFDTRT
101	PAQAVKHPNW	RVMGRISVDS	AMNMGKLEL	IEAHWLFNCP	PDKTVVHHHP
151	QSVIHSVMRY	RDGSLVAQLG	NPDMRTPIAY	CLGLPERIDS	GVGDLDFDAL
201	SALTQPKQPF	DRFPCCLRLE	EAMNAGGLAP	CVLNAANAEA	VAAFLDQGQTK
251	FTDIKTAHVA	CLADGSDGI	GDIGGAGAAD	ARTRAOARFA	IGTLR*

m572/g572 92.9% identity in 295 aa overlap

	10	20	30	40	50	60
m572 . pep	MCAIVGAVGLPSALAAAKGKTIYLANKETLVVSGALFMETARANGA AVL PVDSEHN AVF					
	:   :	:   :	:   :	:   :	:   :	:   :
g572	MCAIVGAAGLPSALAAAKGKTIYLANKETLVVSGALFMETARANGA AVL PVDSEHNAIF					
	:   :	:   :	:   :	:   :	:   :	:   :
	10	20	30	40	50	60
	70	80	90	100	110	120
m572 . pep	QVLPRDYAGRLNEHGIASIILTASGGPPLTADLNFTDRITPAQAVKHPNWNRMGRIKISVDS					
	:   :	:   :	:   :	:   :	:   :	:   :
g572	QVLPRDYYDRLENGIGDISIILTASGGPPLTTDLSTFDSITPEQAVKHPNWNRMGRIKISVDS					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
g572	ATMANKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDFDALSALTFOKPDFRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVGKLDGALSALTFOKPDFGRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
g572	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIEGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```
a572.seq
1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGGCGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCCGTG CAAACGGCGC GGCAGTGCTG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTCG CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCCC GTTCTGACC GCCGATTAA ACACGTTTCA CAGCATTACG
301 CCCGACCAAG CGGTCAAACA CCCCAATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTTGGCTGT CAACTGTCCG CCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGGC
501 GCAACTGGGC AATCCCGATA TGCGAACGCC TATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCC GGTGTCGGCG ACCTGGATT TCGACGCATTG
601 TCCGCGCTGA CCTTCCAAA GCCCGACTTT GACCGCTTCC CCTGCCTGAA
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCT TTTGGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTTC
801 AGACGGCATA GCGGACATAG GGGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGACAAGC GCGGGCATT ATCGGCACAC TCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```
a572.pep
1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPDYTGR LNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS VVGDLDFDAL
201 SALTFOKPDF DRFPCLLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIAKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*
```

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572.pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL					
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572.pep	QVLPDYAGRLENEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
a572	QVLPDYTGRLNEHGIASII LTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDLFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGDLDLFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1 atgccctggt tgtgccgcct taatcgcaat atcggcagtt tccaaatcac
51 gaatctcacc gaccataatg atgtccgggt cctgacgcag gaaagacttc
101 aaagcagcgg caaaagtcag accctgctta tcattgacgt taacctgatt
151 gatgcccggt aggttaattct cggcagggtc ttccgcggtt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga caccgtctta
251 cccgaaccgg tcggaccggt taccagcacc atcccgttag gacgggtgaat
301 cgcttccaac aacaattttt tctggaacgg ctcaaaaccg agctggtcga
351 tgttcaaaga cggcgcatcg gaattcaaaa tccgcatcac gaccttttcg
401 ccaaacagcg tcggcaatgt gctgacacgg aaatcgacag gcttgccgcc
451 cttttgaaag gtcagctgca tccatccgtc ctgcggtatc cgtttttcgg
501 aaatgtccaa acgcgacatt accttaatcc gggaagcaag ctgccccctt
551 accgcaatgg gggcgctgaac cacctcgagg agctgccgtt ccacacggaa
601 acggatacgc gcatttgtgt cgtaaaactc gaaatggatg tcggatgccc
651 cgctacgcaa ggcattccgac aaagttttat ggataaacct cggaacaggg
701 ccgtcttctg cctcctcgtc gtgatatac aggggtgtgc tttcctcttc
751 ctcttgcccc tccccaaagt cctgaagcag cgatgtcgaa cgcgaaccca
801 cccaatcgag caaacccgcc aactggatc cctcgacaat gaccaactca
851 accgcaatcc ctgcccgcga aaccgttttc tgaatttgcg gcatctgggt
901 cggatcggaa accgcaaaaa atactttgtc gccccacgg aaaaacggca
951 cacagtggaa ctccaccatc tgctcctcgg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgataaac tgaacaccct
1051 cgcaatcaat gccgcaagcg acttgggcga aatgacacgg tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1 MPCLRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNL
51 DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVRTVN
101 RFQQQFFLER LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPTV LRYPFPGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTRIVFVKL EMDVGCPTAQ GIRQSFMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNRNPGCR NRFLNLRHLG
301 RIGNRKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1 ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTACCAAC aCaw.TTTT TCTGAAACGG CTCAAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT

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551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCTTGCCCC TCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTGTG GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

```

m573.pep..
1  MPCLCRNLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
51  DARQVNLGRV FRCNIIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPPAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLF
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

m573/g573 95.9% identity in 364 aa overlap

      10      20      30      40      50      60
m573.pep  MPCLCRNLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV
          |||
g573      MPCLCRNLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV
          |||

      70      80      90     100     110     120
m573.pep  FRCNIIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXFFLKR LKTELVDVQR
          |||
g573      FRCNIIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXFFLKR LKTELVDVQR
          |||

      130     140     150     160     170     180
m573.pep  RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK
          |||
g573      RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK
          |||

      190     200     210     220     230     240
m573.pep  LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRAVFCLLV
          |||
g573      LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRAVFCLLV
          |||

      250     260     270     280     290     300
m573.pep  VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC
          |||
g573      VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC
          |||

      310     320     330     340     350     360
m573.pep  RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR
          |||
g573      RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR
          |||

m573.pep  NDTVX
          |||
g573      NDTVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

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a573.seq  
 1 ATGCCCTGTT TGTGCCGCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC  
 51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC  
 101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT  
 151 GATGCCCGGC AGGTAAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA  
 201 CCGACTCCGT ATTCAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA  
 251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT  
 301 CGCTTCCAAC AACATTTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA  
 351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG  
 401 CCAACACAGC TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC  
 451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG  
 501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGGAAGCAAG CTGCCCCCTT  
 551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA  
 601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC  
 651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG  
 701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTCTCTCTTC  
 751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA  
 801 CCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA  
 851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT  
 901 CGGATCGGAA ACCGCAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA  
 951 CACAGTGGAA CTCCACCATC TGCTCTCCG TCAACACCCC CATCAGCACC  
 1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCTT  
 1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep  
 1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI  
 51 DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN  
 101 RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA  
 151 LLKGQLHPAV LRYPFNGVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE  
 201 TDTGIVFVKL EMDVRCPAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE  
 251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLPNGR NGFLNLRHLC  
 301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP  
 351 RNQCRKRLGR NDTV\*

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573.pep	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRYQHFFLKR LKTELVDVQR					
a573	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
m573.pep	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRYQHFFLKR LKTELVDVQR					
a573	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFNGVQTRHYLNPGSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFNGVQTRHYLNPGSK					
	130	140	150	160	170	180
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAQGIRQSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAQGIRQSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAQGIRQSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAQGIRQSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLPNGRNGFLNLRHLC					
a573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLPNGRNGFLNLRHLC					
	250	260	270	280	290	300



884

	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360

m573.pep	NDTVX
a573	NDTVX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1 atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51 attgtggatt atcctgtctg cgattatcct ttgtcccgtc ttcttcacga
101 tgggctgggt tgccgcccg cgtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc ctctgggatt ttataaaagc ctggacgctt tggctgaccg
201 caacagcggg cgccggcga gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaac cttaccctcg gcaaaacttta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggacaatgc tgcattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccaaag cgccgggtttg gtctgatcgt ccgaacagat ttttttgggg
451 ctgcaagacg gtgaaatggc gctggaagcc agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgttt
651 caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgccccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgcgcgcgtc
751 gaagcctatg ccgcatcgaa gcagcaaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaaccg tctgacagga tatatgcaga cgtttccgca acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg cttaaaggcg agaaagaagc
951 cgccgcaaac gccgtcgcgc ttgtccgcgc caagccgcgc cttaacggcg
1001 tgtaccgcct gctcgggttg aaactcagcg atttggatcc ggcttggaaa
1051 gccgatgccg acatgatgcg ttcggttacc ggacggcagc tccagcgcag
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1 MLPLNLSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51 KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTIGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGMAREAR RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFEIAQFYC
201 ELAQAAALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFFAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVYEKSL LKGEKEAAQT AVELVRRKPD LNGVYRLGL KLSDLDPAAWK
351 ADADMMSRVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1 ATGCCGCCGA ATCTACCAAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51 ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCGGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGAAC CTCACCCTCG GCAAACTTTA CCGCCAGCGT
301 GGCGAAAACG ACAAAGCCAT CAACATACAC CCGACAATGC TCGATTCTCC
351 CGATACGGTC GGCGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTITGGGG
451 CTGCAAGACG GTAAAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACCTTGCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG TCGCGGTTT

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651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGCGGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGA AAA CCTGAAGAAG
851 GCTTGAACCG TGTACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AAATCAGCG ATATGAATCC GGCTTGGA AA
1051 GCCGATGCCG ACATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCT
1151 GGCCTGCCCC CGCCTGCAAC AAATGCGAGA CGTTTACCCC GAATAAAATC
1201 GAAGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```

1  MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVY DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQAAALFES NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNVYRLGL LKLSMDNPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

m573/g573 97.8% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA KSIPSGFYKS					
g574	MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA KSIPSGFYKS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m574.pep	LDALVDRNSG RAARELAEVY DGRPQSYDLN LTLGKLYRQR GENDKAINIH RTMLDSPDTV					
g574	LDALVDRNSG RAARELAEVY DGRPQSYDLN LTLGKLYRQR GENDKAINIH RTMLDSPDTV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m574.pep	GEKRARVLFE LAQNYQSAGL VDRAEQIFLG LQDGKMAREA RQHLLNIYQQ DRDWEKAVET					
g574	GEKRARVLFE LAQNYQSAGL VDRAEQIFLG LQDGEMAREA RQHLLNIYQQ DRDWEKAVET					
	130	140	150	160	170	180
	190	200	210	220	230	240
m574.pep	ARLLSHDDQT YQFEIAQFYCE LAQAALFES NFDVARFNVG KALEANKKCT RANMILGDIE					
g574	AQLLSHDDQT YQFEIAQFYCE LAQAALFES NFDVARFNVG KALEANKKCT RANMILGDIE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGKPEEGLNRLTG YMQTFPELDL					
g574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGKPEEGLNRLTG YMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVEKSL LKCEKEAAQT AVELVRRKPD LNVYRLGL LKLSMDNPAWK ADADMRSVI					
g574	INVVEKSL LKCEKEAAQT AVELVRRKPD LNVYRLGL LKLSMDNPAWK ADADMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI EVX					
g574	GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI EVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1  ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAATCGTC GACGCGCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GCGGAAAACG ACAAGGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TCGGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGGAACC GCCCGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTT AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTGATG CCGCGCGTTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCGGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGCGGAGAAG CTTTACGAAG CCTATGCCG GCAGGGAAGA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGGC AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCCGCC CAAGCCCGAC CTCACGGCG
1001 TGTACCGCCT GCTTGGTTTG AAATCAGCG ATTTGGATCC GGCTTGGAAA
1051 GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTCT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1  MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLSDPDTT GAKRARVLF LAQNYQSAGL VDRAEQIFLG
151 LDQGMAREAR QHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSLDPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHEKSQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

m574/a574 97.5% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLKKADMDNELWI	ILLPIILLPVFFAMGWFAAR	VDMKTVLKQAKSIPSGFYKS			
a574	MRPNLPNSLEKADMDNELWI	ILLPIILLPVFFAMGWFAAR	VDMKTVLKQAKSIPSGFYKS			
	10	20	30	40	50	60
m574.pep	LDALVDRNSGRAARELAEV	DGRPQSYDLNLTGKLYRQR	GENDKAINIHRTMLDSDTV			
a574	LDALVDRNSGRAARELAEV	DGRPQSYDLNLTGKLYRQR	GENDKAINMHQTLSDPD			
	70	80	90	100	110	120
m574.pep	GEKRRARVLFELAQNYQSAGL	VDRAEQIFLGLQDGKMA	REARQHLLNIYQQDRDWEKAVET			
a574	GAKRRARVLFELAQNYQSAGL	VDRAEQIFLGLQDGEMAREAR	QHLLNIYQQDRDWEKAVET			
	130	140	150	160	170	180
m574.pep	ARLLSHDDQTYQFEIAQFYCE	LAQAALFKSNFVARFNVG	KALEANKKCTRANMILGDIE			
a574	ARLLSHDDQTYQFEIAQFYCE	LAQAALFKSNFDAARFNVG	KALEANKKCTRANMILGDIE			
	190	200	210	220	230	240
m574.pep	ARLLSHDDQTYQFEIAQFYCE	LAQAALFKSNFVARFNVG	KALEANKKCTRANMILGDIE			
a574	ARLLSHDDQTYQFEIAQFYCE	LAQAALFKSNFDAARFNVG	KALEANKKCTRANMILGDIE			

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	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGYMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGYMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDINGVYRLLGLKLSDMNPAWKADADMMRSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPDINGVYRLLGLKLSOLDPAWKADADMMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

```

g575.seq (partial)
1  ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51  ccgtcaaaca gtccgccttc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggcaacttc actggctgtt tccgcaacag
151 gttcggaaac ggtgttacgg gtttcgtcgg tcggcggtgc gatggcagaa
201 gcggcggtct cttggggggg cggattcggc agcgggttcc gatgcggcag
251 tatttgacgc gggtagaggt ccgggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggggttcgggt cgaacggcgc gtttttcgcg
351 ttttgcttcg ggcgcgga cttttgcttc aggtttttca accggttttt
401 cgacagggtt ctctatcggt ttctccacag ttgctgtttt ggacggttca
451 gacggcatgg atgcagtttc ggctttgggt ttgcgcgttt gcggtttggg
501 ttgttccgct ttgatttttt tgggtgctgc cgctttgatc ctgttcagat
551 tcggaatgtg a*

```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

```

g575.pep (partial)
1  ..MPCLRRQAAR CTNRRTRQT VRFRLLRQK PVRQVRQVR RQLHWLFPQQ
51  VRKRCYRFR SACRWQKRL LGGADSAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGSG RTAGPSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDSG
151 DGMDAVSALG FAVCGLGCSA LIFLGAALI LFRFGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

```

m575.seq..
1  ATGCTTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTCCCGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201 GTTGACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251 TGGCGTTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTTGCCGG GCTGCCAGGC TGTGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCCGATAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGCTGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATTAATGCC GCGCCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCGCA ACAGACCGTC AAACAGTCCG CTTTCGGTTT
701 CTTCCTTCGG AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGGTGC GCGTGTGAT GGCAGAAGCG GCGGCTTCTT GGGGGGCGGA
801 TTCGGCAGCG GTTTCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTCCG
851 GTCGAACGGC CGGTTTTTCC GCTTTTGCTT CGGGCGCGGC AACTTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTTGGGTT
1001 GTTCCGCTTT GATCCTGTTC AGATTCGGA TGTA

```

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This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

m575.pep  
 1 MVSGEAEFRK PASPEGEAGF AEAVSSVPIW LFEGRLESEK VSTVSGLFSA  
 51 VWAIDSGSGV SMTISTGLYG LKVGSGSYTLS VDSMAFQSAS ARFWVSSSCV  
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF  
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR  
 201 RKSSSRAINA APPPASSKVY EPPNRPNSNP LSVSSSAETC STGSETALPV  
 251 SSVGVSMAEA AASWGADSAA VSDAAVFAAG TSGRTAGFS AFASGAATFA  
 301 SGFSTGFSTV ACLDGS DGM DAVSALGFAVC GLGCSALILF RFGM\*

m575/g575 70.2% identity in 114 aa overlap

	240	250	260	270	280	
m575.pep	SSAETCSTGSETALPVSSVGVSM	AEAAASWGADSAAVSDAAVFAAGTG	-----			
g575	LHWLFPQQRKRCYRFRRSACRWQKRLL	GGADSAAVSDAAVFAAGTGPGWRSVAEAGVS				
	50	60	70	80	90	100

	290	300	309	310	320	
m575.pep	-----SGRTAGFSAFASGAATFASGFSTGFST	-----	VACLDGSDGMDAVSALGFA			
g575	DTAGLGSRTAGFSAFASGAATFASGFSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA					
	110	120	130	140	150	160

	330	340	
m575.pep	VCGLGCSALI-----LFRFGMX		
g575	VCGLGCSALIFLGAALILFRFGMX		
	170	180	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

a575.seq  
 1 ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CCGAGGGTGA  
 51 GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG  
 101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCGGGTTT GTTTTCGGCA  
 151 GTTTGGGCGA CAGATTCCGG TCGGGCGGTG TCGATGACGA TTTCGACAGG  
 201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA  
 251 TGGCGTCCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA  
 301 AGTGCGCCGG ATAAAATGCC GTTTTGCGCG GCTGCCAGGC TGTCGAAATC  
 351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGT  
 401 TTGCGGACAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTT  
 451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CCACTTCGGC  
 501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT  
 551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG  
 601 CGCAAAAGCA GCAGCAGGGC GATCAATGCC GCGCCTCCGC CGGCAAGCAG  
 651 CAAGGTGTAC GAACCGCCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG  
 701 AAACCTGTTC GACAGGTTTC GAAACGGCGT TACCGGTTTC GTCGGTCGGC  
 751 GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT  
 801 TTCCGATGCG GCAGTATTTG CAGCGGGTAC AGGTTCTGGT CGAACGGCCG  
 851 GTTTTCCGCG TTTTGCTTCG GGCGCGGCAA CTTTGTCTTC AGGTTTTTCA  
 901 ACCGGTTTCT CTACCGTTGC CTGTTTGAC GGTTCGGACG GCATGGATGC  
 951 GGTTCGGCT TGGGTTTCG CCGTTTCCGG TTTGGGTTGT TCCGCTTTGA  
 1001 TCCTGTTTCA ATTCGAATG TGA

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

a575.pep  
 1 MVSGEAEFRK PASPEGEAGF AEAVSSVPIW LFEGRLESEK VSTVSGLFSA  
 51 VWAIDSGSGV SMTISTGLYG LKVGSGSYTLS VDSMAFQSAS ARFWVSSSCV  
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF  
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR  
 201 RKSSSRAINA APPPASSKVY EPPNRPNSNP LSVSSSAETC STGSETALPV  
 251 VSMASAAASW GADSAVSDA AVFAAGTGSG RTAGFSAFAS GAATFASGFS  
 301 TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM \*

889

m575/a575 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
m575.pep	MVSGEEAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
a575	MVSGEEAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
	10	20	30	40	50	60
m575.pep	70	80	90	100	110	120
	SMTISTGLYGLKVGSGSYTLSVDSMAFQASARFWVSSSCVSAPDKMPFCAAARLSKSKSM					
a575	SMTISTGLYGLKVGSGSYTLSVDSMAFQASARFWVSSSCVSAPDKMPFCAAARLSKSKSM					
	70	80	90	100	110	120
m575.pep	130	140	150	160	170	180
	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSSAASSR					
a575	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSSAASSR					
	130	140	150	160	170	180
m575.pep	190	200	210	220	230	240
	SGSSSGTDSSVRRARLDWARRKSSSRINAAPPPASSKVYEPNRPNSPLSVSSSAETC					
a575	SGSSSGTDSSVRRARLDWARRKSSSRINAAPPPASSKVYEPN----SPLSVSSSAETC					
	190	200	210	220	230	
m575.pep	250	260	270	280	290	300
	STGSETALPVSSVGVSMAEAAASWGADSAVSDAAVFAAGTSGRGTAGFSAFASGAATFA					
a575	STGSETALPVSSVGVSMAEAAASWGADSAVSDAAVFAAGTSGRGTAGFSAFASGAATFA					
	240	250	260	270	280	290
m575.pep	310	320	330	340		
	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
a575	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1 ..atgggcgtgg acatcggacg ctccctgaaa caaatgaagg aacagggcgc
51 ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaatgacc gaagagcagg ccagggaagt gatgatgaaa
151 ttctgcagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaagcccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcgtaa ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactggtca aaatcgcgcg acccgaaaac
601 gcgcccgcca agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence &lt;SEQ ID 1738; ORF 576.ng&gt;:

g576.pep.. (partial)

```

1 ..MGVDIGRSLK QMKEQGAEID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51 FLQEQQAKAV EKHKADAKAN KEKGAEFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLLEKGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1 ..ATGCAGCAGG CAAGCTATGC GATGGCGCTG GACATCGGAC GCTCCCTGAA

```

m576.pep.. (partial)

```

1      ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51     AQEVMVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101    LQYKITRQGE GKQPTKDDIV TYVEYGRLLD GTVFDDSKAN GGPVTFPLSQ
151    VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDFVKLV
201    KIGAPENAPA KOPAONDIIK VN*

```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m576.pep	MQQASYAMGVDIGRSLKQMK	EQGAIEDLKVFTEAMQAVY	DGKEIKMTEEQAQ	EVMMKFLQ		
g576	MGVDIGRSLKQMK	EQGAIEDLKVF	TAMQAVYDGKEIKMTEEQAQ	EVMMKFLQ		
	10	20	30	40	50	
	70	80	90	100	110	120
m576.pep	EQQAKAVEKHKADAKANKE	KGAEFLKENAAKDG	VKTASGLQYKITKQ	GEGKQPTKDDIV		
g576	EQQAKAVEKHKADAKANKE	KGAEFLKENAAEDG	VKTASGLQYKITKQ	GEGKQPTKDDIV		
	60	70	80	90	100	110
	130	140	150	160	170	180
m576.pep	TVEYEGRLIDGTVF	DSKANGGPVTFPLSQ	VI PGWTEGVQLLKEG	GEATFYIPSNLAYRE		
g576	TVEYEGRLIDGTVF	DSKANGGPATFPLSQ	VI PGWTEGVRLLEK	GEATFYIPSNLAYRE		
	120	130	140	150	160	170
	190	200	210	220		
m576.pep	QGAGDKIGPNATLV	FDVKLVKIGAPENAPAKQ	PAQVDIKKVN			
g576	QGAGEKIGPNATLV	FDVKLVKIGAPENAPAKQ	PDQVDIKKVN			
	180	190	200	210		

a576.seq

1	ATGAACACCA	TTTTCAAAT	CAGCGCACTG	ACCTTTTCCG	CCGCTTTTGC
51	ACTTTCCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTTCCGCG	CAGGGCGACA	CCTCTTCGAT	CGGCAGACG
151	ATGCAGCAGG	CAAGCTATGC	GATGGGCGTG	GACATCCGAG	GCTCCCTGAA
201	GCAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAGTCT	TTTACCGAAG
251	CCATGCAGGC	AGTGATGATC	GGCAAGAAAA	TCAAATAGAC	CGAAGAGCAG
301	GCTCAGGAAG	TCATGATGAA	ATTCTTTCAG	GAACAACAGG	CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGACG	CGAAGGCCAA	TAAAGAAAAA	GGCGAAGCCT
401	TTCTGAAAGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCCGGC
451	CTGC AATACA	AAATCACC AA	ACAGGCGCGA	GGCAAAACAGC	CGACCA AAGA
501	CGACATCGTT	ACCGTGAAT	ACGGAAGCCG	CTTGATTGAC	GGTACGGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCGCGG	TCACCTTCCC	TTTAGGCCAA

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```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTGTATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

m576.pep
10 20 30
MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
|||||
a576 CGKKEAAPAS ASEPAASSA QGDTSSIGSTM QQASYAMGV DIGRSLKQMK EQGAEIDLKV
30 40 50 60 70 80

m576.pep
40 50 60 70 80 90
FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
|||||
a576 FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
90 100 110 120 130 140

m576.pep
100 110 120 130 140 150
KDGVKTTASGLQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
|||||
a576 KDGVKTTASGLQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
150 160 170 180 190 200

m576.pep
160 170 180 190 200 210
VIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA
|| |||||
a576 VILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA
210 220 230 240 250 260

m576.pep
220
KQPAQVDIKKVN
|||||
a576 KQPAQVDIKKVN
270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

g576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCGCCG TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGCT TCTGCCGCG CAGGCGGACA CCTTCTCAAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCTGCGAG GAGCAGCAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCAGTACA AAATCACCAA ACAGGGTGAA GGCAACAGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAAC GGCGGCCCGG CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTGACGT GAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```



This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

g576-1.pep  
 1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST  
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ  
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG  
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ  
 201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV  
 251 KIGAPENAPA KQPDQVDIKK VN\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

m576-1.seq  
 1 ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC  
 51 ACTTTCCGCC TCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC  
 101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC  
 151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA  
 201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG  
 251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG  
 301 GCTCAGGAAG TCATGATGAA ATTCCTTCAg GAACAACAGG CTAAGCCGT  
 351 AGAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT  
 401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC  
 451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAACAGC CGACCAAGA  
 501 GCACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT  
 551 TCGACAGCAG CAAAGCCAAC GCGGCGCCCG TCACCTTCCC TTTGAGCCAA  
 601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA  
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTCCGG  
 701 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTGTAGT GAAACTGGTC  
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA  
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

m576-1.pep  
 1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST  
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ  
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG  
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ  
 201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV  
 251 KIGAPENAPA KQPAQVDIKK VN\*

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASAAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASAAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLEKGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

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```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GCGAAGCCT
401 TTCTGAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGGCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCAG
701 GCGACAAAT CGGCCCGAAC GCCACTTGG TATTGTATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pap

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pap	MNTIFKISAL TLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISAL TLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pap	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pap	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pap	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITQGE GKQPTKDDIV TVEYEGRLID					
m576-1	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITQGE GKQPTKDDIV TVEYEGRLID					
	130	140	150	160	170	180
a576-1.pap	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITQGE GKQPTKDDIV TVEYEGRLID					
m576-1	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITQGE GKQPTKDDIV TVEYEGRLID					
	130	140	150	160	170	180
a576-1.pap	GTVFDSSKANG GGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANG GGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pap	GTVFDSSKANG GGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANG GGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pap	ATLVFDVKLV KIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLV KIGAPENAPAKQPAQVDIKKVN					
	250	260	270			
a576-1.pap	ATLVFDVKLV KIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLV KIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

### Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

-- The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577.seq..
1  atggaaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcggt
151 tttatttacg gagcaaacat gaaactatc tataccgtca tcaaatcat
201 tatcctgctg ctcttctgc tgcttgccgt cattaatatg gatgccgtta
251 ccttttcta tcttcgggg cagagtgtca atctgccgt gattgtcgta
301 ttgttcggcg cgttgcgt cgcatcgtg ttcggaatgt ttgccctgtt
351 cggcggtg ctgtccttgc gggcgaaaa cagccgctg cgtgcggaag
401 tgaagaaaag tgcgcgttg agcgacaga aattgactgc accgccgata
451 caaatgctg ccgaatctgc caaacgcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
1  MERSGVFGKI VGNRILRMPS EHAAFYKPK CKSFKLTQSW FRVRSCTGCV
51  FIYGANMKLI YTVIKIILL LFLLLAVINM DAVTFSYLPG QSVNPLIVV
101 LFGAFVVGIV FGMFALFGR LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAESAQKP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577.seq..
1  ATGGAAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAATCGT
101 TTAAGTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTTACG GAGCAAACAT GAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCTGC TGCTTGCCGT CATTAATACG GATGCCGTTA
251 CCTTTTCTA CTGCGGGG CAAAATTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CATTGTAGT CGGTATTATT TTTGGAATGT TTGCCTGTG
351 CGGACGGTTG TTGTCGTTAC GTGGCAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTG ACGGGGAAG AGCTGACCGC ACCACCGCG
451 CAAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGGV
51  FIYGANMKLI YTVIKIILL LFLLLAVINT DAVTFSYLPG QKFDLPLIVV
101 LFGAFVVGII FGMFALFGR LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m577/g577 88.1% identity in 160 aa overlap

	10	20	30	40	50	60
m577.pep	MERNGVFGKIVGNRILRMSS	EHAAASYPKPKCSFKLAQSW	FRVRSCLGGVFIYGANMKLI			
g577	MERSGVFGKIVGNRILRMPSE	HAAAFYKPKCSFKLTQSW	FRVRSCTGCVFIYGANMKLI			
	10	20	30	40	50	60
	70	80	90	100	110	120
m577.pep	YTVIKIILL	LFLLLAVINT	DAVTFSYLPGQKFDL	PLIVV	LFGAFVVGII	FGMFALFGR

895

```

|||||
g577 YTVIKIIILLFLLLAVINMDAVTFSYLPQSVNLPLIVVLFGAFVVGIVFGMFALFGRL
      70      80      90      100     110     120

      130     140     150     160
m577.pep LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQFX
|||||
g577 LSLRGENSRLRAEVKKKSARLSGQKLTAPPIQNAESAQFX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1 ATGGAAAGGA ACGGTGTATT TGGTAAATTT GTCGGCAATC GCATACTCCG
51 TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAACTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCC GGGCGGCGTT
151 TTTATTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCTGT CATTAAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCCGGGG CAAAATTTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CGTTTGTCTG CGGCATCGTG TTCGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTG CGTGCCGAAG
401 TAAAGAAAAA TGC GCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTGC CAAACAGCCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.pep
1 MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSEKLAQSW FRVRSCTPGGV
51 FIYGANMKLI YTVIKIIILL LELLAVINT DAVTFSYLPG QKFDLPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENGR LRAEVKKNARL TGKELTAPPA
151 QNAPESAKQP *

```

m577/a577 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m577.pep MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSEKLAQSWFRVRSCLGGVFIYGANMKLI
|||||
a577 MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSEKLAQSWFRVRSCTPGGVFIYGANMKLI
      10      20      30      40      50      60

      70      80      90      100     110     120
m577.pep YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIFGMFALFGRL
|||||
a577 YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIVFGMFALFGRL
      70      80      90      100     110     120

      130     140     150     160
m577.pep LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQFX
|||||
a577 LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQFX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq..
1 atgggaaagc tcgacatcgg gatattgttt gccgatttct tcaaagattt
51 cgcgccacag ttcggtgggt tccaaaacgt tggctttgcc tacggagcag
101 acttttttgc tgcgtttttg ggcggattgg aaggccacgt gggcgatcgc
151 ggcgatttcg ctttcgtgtg atttcattgt gtttagacct tcggtttcgc
201 cgttttccaa aacacggatg ccgcgcggtt cgcgcaataa aatatcgcgc
251 gtaagttcgc gcacaatcaa aatatccaaa ccggcaacga tttcaggctt
301 gagcgtggag gcgttggtta a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.pep
1 MGKLDIGILF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGHVGDA
51 ADFAFAVFGH VVAFVFAVFQ NTDAARFAEI NIAGKFAHNQ NIQTGNDFRL

```

896

101 ERGGVG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

```
m578.seq..
1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTCG TCGTTTTTTC GCGCGATTGG AAGGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACGCGGATG CCGCGCGGTT CGCCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGGCAACGA TTTCAGGCTT
```

-- This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

```
m578.pep..
1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMGNT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGGVG*
```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
g578	MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAFLGGLEGHVGDADFAFAVFHG					
	10	20	30	40	50	60

	70	80	90	100
m578.pep	VVAFAFAVFQNAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX			
g578	VVAFVFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLERGGVGX			
	70	80	90	100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

```
a578.seq
1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTCG TCGTTTTTTC GCGCGATTGG AAGGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACACGGATG CCGCGCGGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G
```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

```
a578.pep
1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGNT
51  ADFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*
```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
a578	MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGDVGNTADFAFAVFHG					
	10	20	30	40	50	60

	70	80	90	100
m578.pep	VVAFAFAVFQNAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX			
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

```
g579.seq..
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
```

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```

51   TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101  CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151  GCGCGGGGTT TGGCGGTGGC GTTGTCTTA AAAGACCAGC TGTCCAATTT
201  TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCCGTTCAA GTCGGCGACT
251  TTATCCGTGT CGGCGGTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301  CAGACTTCTT TCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351  CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTGCC
401  GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT GAAAGTGGCG
451  AAAGAGGCGG TGTGAAAGC CGCCGCCGAA CACCCTTGA GCGTTCAAAA
501  CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551  TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601  CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651  CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

g579.pep..

```

1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSLRITDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

m579.seq..

```

1   ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCCG CCCGTTCAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

m579.pep..

```

1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSLRITDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
g579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRITDNEEVVLPNSVVM					
g579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRITDNEEVVLPNSVVM					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
g579	GNSIVNRSSLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
g579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```
a579.seq
1  ATGAGGGCGG  CGATGACGCG  CGCGCAGGTC  GATGCCACGC  TGATTAGTTT
51  TTTGTGTAAT  GTTGCCAATA  TCGGGCTATT  GATTTTGGTG  ATTATTGCCG
101 CATTGGGCAG  ATTGGGCGTT  TCCACAACAT  CCGTAACCGC  CTTAATCGGC
151 GCGCGGGGTT  TGGCGGTGGC  GTTGTCTTGT  AAAGACCAGC  TGTCCAATTT
201 TGCCGCCGGC  GCGCTGATTA  TCCTGTTCGG  CCCGTTCAAA  GTCGGCGATT
251 TTATCCGCGT  CGGCGGTTTT  GAAGGATATG  TCCGAGAGAT  TAAATGGTG
301 CAGACTTCTT  TCGGACGAC  CGACAACGAA  GAAGTCGTGC  TGCCCAACAG
351 CGTGGTGATG  GGCAACAGCA  TCGTCAACCG  TTCCACACTG  CCGCTGTGCC
401 GCGCCCAAGT  GATAGTCGGC  GTCGATTACA  ACTGCGATT  GAAAGTGGCG
451 AAAGAGCGCG  TGTGAAAGC  CGCCGTCGAA  CACCCTTGA  GCGTTCAAAA
501 CGAAGAGCGG  CAGGCCGCG  CCTACATCAC  CGCCTTGGGC  GACAATGCCA
551 TCGAAATCAC  ATTATGGGCT  TGGGCAAACG  AAGCAGACCG  CTGGACGCTG
601 CAATGCGACT  TGAACGAACA  AGTGGTCGAA  AACCTCCGCA  AAGTCAATAT
651 CAACATCCCG  TTCCCGCAAC  GCGACATACA  CATCATCAAT  TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```
a579.pep
1  MRAAMTRAQV  DATLISFLCN  VANIGLLILV  IIAALGRLGV  STTSVTALIG
51  GAGLAVALSL  KDQLSNFAAG  ALIILFRPFK  VGDFIRVGGF  EGYVREIKMV
101 QTSRLTTDNE  EVVLPNSVVM  GNSIVNRSTL  PLCRAQVIVG  VDYNCDLKVA
151 KEAVLKAAVE  HPLSVQNEER  QAAAYITALG  DNAIEITLWA  WANEADRWTL
201 QCDLNEQVVE  NLRKVNINIP  FPQORDIHIIN  S*
```

m579/a579 100.0% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
a579	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM					
a579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
a579	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
a579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:

g579-1.seq

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```

1  ATGGACTTCA  AACAATTGA  TTTTACAC  CTGATCAGTG  TTTCCGGTTG
51  GGGGCATCTG  GCTGAAAAGG  CGTGGGCGTT  CGGGCTGAAC  CTTGCCGCCG
101 CGCTGCTTAT  TTTCTTGGTC  GGGAAATGGG  CGGCGAAACG  CATTGTCGCC
151 GTAATGAGGG  CGGCGATGAC  GCGCGCGCAG  GTCGATGCCA  CGCTGATTAG
201 TTTTGTGTGT  AATGTTGCCA  ATATCGGCTT  ATTGATTTTG  GTGATTATTG
251 CCGCATTTGG  ACGGTTGGGC  GTTCCACAA  CATCCGTAAC  CGCCTTAATC
301 GCGCGCGCGG  GTTGGCGGT  GCGTGTGTC  TAAAAGACC  AGCTGTCCAA
351 TTTTGGCGCC  GCGCGCTGA  TTATCCTGTT  CCGCCGTTT  AAAGTCGGCG
401 ACTTTATCCG  TGTCGGCGGT  TTTGAAGGAT  ATGTCCGGGA  AATCAAAATG
451 GTGCAGACTT  CTTGCGGAC  GACCGACAAC  GAAGAAGTCG  TGCTGCCCAA
501 CAGCGTGGTG  ATGGGCAACA  GCATCGTCAA  CCGTTCAGC  CTGCCGCTTT
551 GCGCGCCCCA  AGTGATAGTC  GCGCTCGATT  ACAACTGCGA  TTTGAAAGTG
601 GCGAAAGAGG  CGGTGTTGAA  AGCCGCGCC  GAACACCCCT  TGAGCGTTCA
651 AAACGAAGAG  CGGCAGCCCG  CCGCTACAT  CACCGCCTTG  GCGGACAATG
701 CCATCGAAAT  CACATTATGG  GCTTGGGCAA  ACGAAGCAGA  CCGCTGGACG
751 CTGCAATGCG  ACTTGAACGA  ACAAGTGGTC  GAAAACCTCC  GCAAAGTCAA
801 TATCAACATC  CCGTCCCGC  AACGCGACAT  ACACATCATC  AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQDFDLH  LISVSGWHL  AEKAWAFGLN  LAAALLIFLV  GKWAAKRIVA
51  VMRAAMTRAQ  VDATLISFLC  NVANIGLLIL  VIIALGRLG  VSTTSVTALI
101 GGAGLAVALS  LKDQLSNFAA  GALIILFRPF  KVGDFIRVGG  FEGYVREIKM
151 VQTSRLTTDN  EEVLPNSVV  MGNSIVNRSS  LPLCRAQVIV  GVDYNCDLKV
201 AKEAVLKAA  EHPLSVQNEE  RQPAAYITAL  GDNAIEITLW  AWANEADRWT
251 LQCDLNEQVV  ENLRKVNINI  PFPQDIHII  NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.sseq

```

1  ATGGACTTCA  AACAATTGA  TTTTACAC  CTGATCAGTG  TTTCCGGTTG
51  GGAGCATCTG  GCTGAAAAGG  CGTGGGCGTT  CGGGCTGAAC  CTTGCCGCCG
101 CGCTGCTTAT  TTTTGTGGTC  GGGAAATGGG  CGGCGAAACG  CATTGTCGCT
151 GTGATGAGGG  CGGCGATGAC  GCGCGCGCAG  GTCGATGCCA  CGCTGATTAG
201 TTTTGTGTGT  AATGTTGCCA  ATATCGGCTT  ATTGATTTTG  GTGATTATTG
251 CCGCATTTGG  CAGATTGGGC  GTTCCACAA  CATCCGTAAC  CGCCTTAATC
301 GCGCGCGCGG  GTTGGCGGT  GCGTGTGTC  CTGAAAGACC  AGCTGTCCAA
351 TTTTGGCGCC  GCGCGACTGA  TTATCCTGTT  CCGCCGTTT  AAAGTCGGCG
401 ATTTTATCCG  CGTCGGCGGT  TTTGAAGGAT  ATGTCCGAGA  GATTAATG
451 GTGCAGACTT  CTTGCGGAC  GACCGACAAC  GAAGAAGTCG  TGCTGCCCAA
501 CAGCGTGGTG  ATGGGCAACA  GCATCGTCAA  CCGTTCACA  CTGCCGCTGT
551 GCGCGCCCCA  AGTGATAGTC  GCGCTCGATT  ACAACTGCGA  TTTGAAAGTG
601 GCGAAAGAGG  CGGTGTTGAA  AGCCGCGCTC  GAACACCCCT  TGAGCGTTCA
651 AAACGAAGAG  CGGCAGGCTG  CCGCTACAT  CACCGCCTTG  GCGGACAATG
701 CCATCGAAAT  CACATTATGG  GCTTGGGCAA  ACGAAGCAGA  CCGCTGGACG
751 CTGCAATGCG  ACTTGAACGA  ACAAGTGGTC  GAAAACCTCC  GCAAAGTCAA
801 TATCAACATC  CCGTCCCGC  AACGCGACAT  ACACATCATC  AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQDFDLH  LISVSGWEHL  AEKAWAFGLN  LAAALLIFLV  GKWAAKRIVA
51  VMRAAMTRAQ  VDATLISFLC  NVANIGLLIL  VIIALGRLG  VSTTSVTALI
101 GGAGLAVALS  LKDQLSNFAA  GALIILFRPF  KVGDFIRVGG  FEGYVREIKM
151 VQTSRLTTDN  EEVLPNSVV  MGNSIVNRST  LPLCRAQVIV  GVDYNCDLKV
201 AKEAVLKAAV  EHPLSVQNEE  RQAAAYITAL  GDNAIEITLW  AWANEADRWT
251 LQCDLNEQVV  ENLRKVNINI  PFPQDIHII  NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQDFDLH	LISVSGWEHL	AEKAWAFGLN	LAAALLIFLV	GKWAAKRIVA	VMRAAMTRAQ
g579-1	MDFKQDFDLH	LISVSGWEHL	AEKAWAFGLN	LAAALLIFLV	GKWAAKRIVA	VMRAAMTRAQ
	70	80	90	100	110	120
m579-1.pep	VDATLISFLC	NVANIGLLIL	VIIALGRLG	VSTTSVTALIG	GAGLAVALS	LKDQLSNFAA
g579-1	VDATLISFLC	NVANIGLLIL	VIIALGRLG	VSTTSVTALIG	GAGLAVALS	LKDQLSNFAA
	130	140	150	160	170	180
m579-1.pep	GALIILFRPF	KVGDFIRVGG	FEGYVREIKM	VQTSRLTTDN	EEVLPNSVV	MGNSIVNRST



900

```

|||||
g579-1  GALLILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRRTDNEEVVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180
          190      200      210      220      230      240
m579-1.pep LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
g579-1  LPLCRAQVIVGVVDYNCDLKVAKEAVLKAEEHPLSVQNEERQPAAYITALGDNAIEITLW
          190      200      210      220      230      240
          250      260      270      280
m579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
          |||||
g579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

```

a579-1.seq
1  ATGGACTTCA AACAATTTGA TTTTTCAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGCGGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGGTTC GGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTGATGAGGG CGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGTT GCGGTTGTCC TTGAAAGACC AGCTGTCCAA
351 TTTTCCGCCG GCGCGCGTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGCGGTT TTTGAAGGAT ATGTCCGAGA GATTAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTCCACA CTGCCGCTGT
551 GCGCGCGCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCCG CCGCTACAT CACCGCCTTG GGCACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACGCGACAT ACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

```

a579-1.pep
1  MDFKQDFDLH LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKQQLSNFAA GALLILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRRTDN EEVVLPSVSV MGNSIVNRST LPLCRAQVIV GVDYNCDLKV
201 AREAVLKAAY EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRW
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
a579-1.pep MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          |||||
m579-1  MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          10      20      30      40      50      60
          70      80      90      100     110     120
a579-1.pep VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||
m579-1  VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120
          130     140     150     160     170     180
a579-1.pep GALLILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRRTDNEEVVLPNSVVMGNSIVNRST
          |||||
m579-1  GALLILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRRTDNEEVVLPNSVVMGNSIVNRST
          130     140     150     160     170     180
          190     200     210     220     230     240
a579-1.pep LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
m579-1  LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190     200     210     220     230     240
          250     260     270     280
a579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX

```

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```

|||||
m579-1  AWANEADRWTLQC DLNEQVVENLRKVNINIPFPQRDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

```

g580.seq
1  atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
51  cgcgtcgcag cccatttcga tggcaaggca gacttcgccg atcatgtcgc
101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
151 tcgaaaatca gcttggtaaa gccgttgctc caaccgttgg caatcgcacg
201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg
251 ctttggcaga caattcgggt tcaccgaccc atgccacttc gggggaagtg
301 tag

```

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

```

g580.pep..
1  MDSPKVGC GW MVLPM S AASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
101 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

```

m580.seq..
1  ATGGATTTCG CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCGGCA
151 TCAAAAATCA GCTTGGTAAA GCCGTGTCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCC GCCACGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCGGA CAGTTCGGTT TCGCCACCC ACGCCACTTC GGGGGAAGTG
301 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

```

m580.pep..
1  MDSPKVGC GW MVLPM S AASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
101 *

```

m580/g580 97.0% identity in 100 aa overlap

```

          10      20      30      40      50      60
m580.pep  MDSPKVGC GW MVLPM S AASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA SKISLVKPLS
          |||||
g580      MDSPKVGC GW MVLPM S AASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA SKISLVKPLS
          10      20      30      40      50      60

          70      80      90      100
m580.pep  QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEVX
          |||||
g580      QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEVX
          70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

```

a580.seq
1  ATGGATTTCG CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCCG
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCAGCA
151 TCAAAAATCA GCTTGGTGAA ACCATTGTCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCAGA CAATTCGGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG
301 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

```

a580.pep
1  MDSPKVGC GW MVLPM S AASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

```

902

101 \*

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMASQFISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPMASQFISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
	10	20	30	40	50	60

	70	80	90	100
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX			
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSGEVX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1  atgcacttcg cccagcttgt gggctcaaacc ggtatagaac aaaatacgtt
51  ctgtcgtcgt ggttttaccg gcatcgatat gggcggaat accgatgttg
101 cggtacaggg tgatcggggt cttacgagcc attttattag cctttcaaaa
151 ttagaaacgg aagtggagga atgctttgtt ggcttcagcc atacgggtga
201 cttcttcacg ttttttcaac gcaccgccac ggccttcgga cgcacatc
251 aactcgctcg ccaaacgcag atccatggat ttctcaccac gtttcggggc
301 cgcgtcgcca acccaacgca ttgccaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG
101 RVANPTHQCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTCTTTCACG TTTTTCACAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTGCGCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGSLTSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAQADRGSLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60

	70	80	90	100	110
m581.pep	GFSHTVYFFTFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX				
g581	GFSHTVYFFTFQRTATAFGRINQLACQTQIHGFLTTFAGRVANPTHQCSQTAX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

903

```

a581.seq
  1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
 51 CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTGTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGAG GTCCATGGAT TTCTCACCAC GTTTGCGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
  1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTVQADRG LSHFISLSK
 51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTVQADRG	LSHFISLSKLETEVRECFV				
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTVQADRG	LSHFISLSKLETEVRECFV				
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFG	RINQFACQTQVHGFLLTFAG	RINPAHCQSQTAX			
a581	GFSHTVYFFTFFQRTATAFG	RINQFACQTQVHGFLLTFAG	RINPAHCQSQTAX			
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
  1 atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
 51 agagaccgcg ctgcaatgcg ccgcttttgac ggacaatggt acgcttttgg
101 cgtgttacga caggattttt gggcacagc ttccgtcttc ggcagggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttgatg aagggcgagg cggtcattgt tggtaaaaa ggcggggatg
251 cgcttcctgc cgacagtgcg ggcgaacccg ccgatattta tacgccttgc
301 agcctgatgt acgacttggc caaaaacgat ttgcgcgggc tgttgggcgt
351 acgcgaacac aatccgatgt accttatgcc gttttggtat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttcggacagc agaaacgtgc ggaacccaaa ttgcagggtt cgttcaaaag
501 caaaattgcc gaaaatttgc ttaaaacccg ccgggatctg tggttcggct
551 acaccctaac atccgatggc cagatttaca accaaggcag gaaatccgcg
601 ccgttcgcga atacggatta caaacctgaa attttcctga ccagcctgt
651 gaagggcagg ttgccgttcg gcggcaggct gcgtatgctc ggtgcgggtt
701 ttgtccacca gtccaacgga cagagccgct ccgaatcgcg ttcgtggaac
751 aggatttatg ccatggcagg catggaatgg ggcgaattga cggtgattcc
801 gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggatatggc acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgctaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacgggt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
  1 MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
 51 EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMVDLDKND LRLLGVREH NPMYLMPPFWY NNSPNYAPSS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA ENLFKTRADL WFGYTQRSW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGLRLML GAGFVHQSNG QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDIDYDM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGVVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDWDGI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGCGAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCGAG
201 CAGCCTGGAT AAGGGCGAGG CCGTCATTGT TGTGTAAAAA GCGGGGGATG
251 CGCTTCTCTG CGACAGTGC GGGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGGGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTTC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCCGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TTTAAACCCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCGA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTACG CCATGGCAGG CATGGAATGG GGCAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCCT TCGATCAGAG CGCGGATAAA AACGACAATC
851 CCGATATTGC CACTATATG GGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGATGT GTATTCCGTA TTCCGCTACA ACCCAAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTCCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
1  MRYILLTGLL PMSAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYX GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

	10	20	30	40	50	60
m582.pep	MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
g582	MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
	10	20	30	40	50	60
m582.pep	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
	70	80	90	100	110	120
m582.pep	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
	70	80	90	100	110	120
m582.pep	NPMYLMPLWYNNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL					
g582	NPMYLMPLWYNNNSPNYAPSSPTRGTTVQEKFGQKRAETKLQVSFKSKIAENLFKTRADL					
	130	140	150	160	170	180
m582.pep	NPMYLMPLWYNNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL					
g582	NPMYLMPLWYNNNSPNYAPSSPTRGTTVQEKFGQKRAETKLQVSFKSKIAENLFKTRADL					
	130	140	150	160	170	180
m582.pep	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
g582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
	190	200	210	220	230	240
m582.pep	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
g582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
	190	200	210	220	230	240
m582.pep	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR					
	250	260	270	280	290	300
m582.pep	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR					
	250	260	270	280	290	300
	310	320	330	340	350	360

905

```

m582.pep  LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          |||||
g582       LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          |||||
g582       GLMFNDWDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GGCAGGGGATG
251 CGCTTCTGCG CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGGG CAAAAACGAT TTGCGCGGGC TGTGGGCGGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATCGC
401 CCAACTATGC CCCGGGTTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TTAACCCCG CCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTCG GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTTCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACGCG
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ATCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTCCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVRH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPIRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGLKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

```

m582/a582 100.0% identity in 370 aa overlap

```

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||||
a582       MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
          |||||
a582       LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
          70      80      90      100     110     120

          130     140     150     160     170     180

```

906

```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
a582          NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
              130      140      150      160      170      180

              190      200      210      220      230      240
m582.pep      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
a582          WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
              190      200      210      220      230      240

              250      260      270      280      290      300
m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVQLQYR
a582          QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVQLQYR
              250      260      270      280      290      300

              310      320      330      340      350      360
m582.pep      LNDQRNVSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
a582          LNDQRNVSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
              310      320      330      340      350      360

              370
m582.pep      GLMFNDLDGIX
a582          GLMFNDLDGIX
              370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatattacc catcttgccct tctgtgcctt
51  ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgtaaccgat gccacgaggt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg aaatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaaacga ctcaacgcat cgctcatcgc cgcgcccggg ttgtcggcgg
351 ttacgcccgt tactgcgacc aacccgacgg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcgcca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAA GIGRGNGSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRRLP VGYGQCQNQG AQYCGNGEGY RFETQFHHD LKKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGTTG ACCAAAGCCA AATATTACC CATCTTGCCT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCCGAA AGAGCGAGAC TGTAAACGAT GCCACGCGT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAAGCGA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTGGCGCG
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCGCCC
401 AACCGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCGGGC GCACAATACT GCGGCAATGS CGAGGGGTAT CGGTTTGAAA

```

907

551 CCCAATTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG  
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..  
1 MIVDQSQIFT HLAFCAF CGI GAVTAGNRLH NRMYNAAAAA GIGRNGSQQ  
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI  
101 GERTQRIHR RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG  
151 QQRPSLR LDP VGYGQCQNG AQCNGEGY RFETQFHHID LRKKDRPEKS  
201 EK\*

m583 / g583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT HLAFCAF CGI GAVTAGNRLH NRMYNAAAAA GIGRNGSQQ QFGKSETVTD					
g583	MIVDQSQIFT HLAFCAF CGI GAVTAGNRLH NRMYNAAAAA GIGRNGSQQ QFGKSETVTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m583.pep	AQRFSKNGDKQISDTHPQP CFEQTARNHN CDGNQPNQRI GERTQRIHR RARFVGGYAG					
g583	AQRFSKNGDKQISDTHPQP CFEQTARNHN CDGNQPNQRI GERTQRIHR RARFVGGYAG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m583.pep	YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG QQRPSLR LDP VGYGQCQNGA QYCNGEGY					
g583	YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG QQRPSLR LDP VGYGQCQNGA QYCNGEGY					
	130	140	150	160	170	180
	190	200				
m583.pep	RFETQFHHID LRKKDRPEKSEKX					
g583	RFETQFHHID LRKKDRPEKSEKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq  
1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCTT TCTGTGCTT  
51 TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT  
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG  
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA  
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC  
251 AAACCGCGCG AAATCATAAC TGCATGGCA ATCAGCCAAA TCAACGGATT  
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTCGGCGG  
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC  
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC  
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA  
501 AAACCAAGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA  
551 CCCAATTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG  
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep  
1 MIVDQSQIFT HLAFCAF CGI GAVTAGNRLH NRMYNAAAAA GIGRNGSQQ  
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI  
101 GERTQRIHR RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG  
151 QQRPSLR LDP VGYGQCQNG AQCNGEGY RFETQFHHID LRKKDRPEKS  
201 EK\*

m583/a583 99.0% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT HLAFCAF CGI GAVTAGNRLH NRMYNAAAAA GIGRNGSQQ QFGKSETVTD					



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```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQQFGKSETVTD
           10      20      30      40      50      60

           70      80      90      100     110     120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQNPNQRIGERTQRIAHRRARFVGGYAG
           |||||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQNPNQRIGERTQRIAHRRARFVGGYAG
           70      80      90      100     110     120

           130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
           |||||:|||||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
           130     140     150     160     170     180

           190     200
m583.pep  RFETQFHHIDLRKKDRPEKSEKX
           |||||
a583      RFETQFHHIDLRKKDRPEKSEKX
           190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

```

g584.seq..
1  atgctgctgt ctattttggc ggcttcctcg ctggcggtat cttttccggc
51  ggcggctgag gcattgaatt acaatatgtg cgaattttcc gaatcggcgg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcgcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttgta aaaaattcaa
201 caatttcacc agaaaatcga aaaatgtag ctttaaaacc gaattggtat
251 cgcgcagtgc gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag ggcgaggcca gggatttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgcgcgttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcggttct ggtgcgtccc gttataaaat cgtcaaatg aattttgggc
551 aaatcggcag ccatattgcg ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggta cggattcagc
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

```

g584.pep  Length:..
1  MLRSILAASL LAVSFPAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNAVNA EFVKKFNNFT RSKSNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK AEGRDFDALN RFIADVQTD SLEDTDFSVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NFGQIGSHIA GDGA VRKML
201 RAMPMAASVN MKGTDSAAPG VEEISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

```

m584.seq..
1  ATGTTGCGTC TTGTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG AAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAAATCAA
201 CAAGTTCATC AGAAAATCGA AAAATGTTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTAAAG GTCGAAGGTA GAGATTTGA
351 TGAGTTAAAC CGTTTATTG CCGATATTCA AGCAGATGCC GCGTTGGMAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCKATCAG
451 GTCAGCAAGG ATGCCGTTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCGCG
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

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m584.pep..

```

1  MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNKFI RSKKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

	10	20	30	40	50	60
m584.pep	MLRLVLAASL	SAVSFPAAAE	ALNYNIVEFS	ESAGVEVAQD	TMSARFQVTA	EGRDKNVNA
	:					
g584	MLRSILAASL	LAVSFPAAAE	ALNYNIVEFS	ESAGIEVAQD	TMSARFQVAAE	EGRDKNVNA
	10	20	30	40	50	60
	70	80	90	100	110	120
m584.pep	EFVKKFNKFI	RIRKSKNGSF	KTELVSRSAM	PRYQYTNRR	IQTGWEEA	EFKVEGRDF
g584	EFVKKFNFT	RIRKSKNGSF	KTELVSRSAM	PRYQYTNRR	IQTGWEEA	EFKAEGRDF
	70	80	90	100	110	120
	130	140	150	160	170	180
m584.pep	RFIADIQADA	ALXYTDFHVS	RERRNEVIXQ	VSKDAVLRFK	KARAEKLAV	LGLASGYKIV
g584	RFIADVQD	ASLEDTDFS	VSRERRNEV	IDQVSKDAV	LRFKARAEK	LAVLGLASGY
	130	140	150	160	170	180
	190	200	210	220	230	
m584.pep	NLGHIGSHIA	GAGGAAQAK	MLRAMPMAA	SVNMEGAD	SAAPGVEE	ISISVNGTV
	:					
g584	NFGQIGSHI	AGDGA VR	AKMLRAMP	MAASVMK	GTDSAAPG	VEEISISIN
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

a584.seq

```

1  ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51  ..... ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTCAAC AGAAAATCAA AAAATGGTAG CTTTAAACCC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TGCCTGAAC CGTTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATT CCATGTGTCG CGCGAACGCC GCAACGAGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTT GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATCCGC
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1802; ORF 584.a&gt;:

a584.pep

```

1  MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNFT RSKKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRNFDAVN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

	10	20	30	40	50	60
m584.pep	MLRLVLAASL	SAVSFPAAAE	ALNYNIVEFS	ESAGVEVAQD	TMSARFQVTA	EGRDKNVNA
	:					
a584	MLRSILAASL	-----	IVEFS	ESAGVEAVQD	TMSARFQVTA	EGRDKNVNA
	10		20	30	40	

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	70	80	90	100	110	120
m584.pep	EFVKKFNKFIRKSKNGSFKTELVSRSAMP	RYQYTN	GRRIQT	GWEERA	EFKVEGRD	FDELN
a584	EFVKKFNNFTRKSKNGSFKTELVSRSAMP	RYQYTN	GRRIQT	GWEERA	EFKVEGRN	FDALN
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLR	FKARA	EKLAGVL	GASGYKIVKL		
a584	RFIADVQADAALXYTDFHVSRRERNEVIDQVSKDAVLR	FKARA	EKLAGVL	GASGYKIVKL		
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNM	EGADSAAPGVEE	ISISVNGTVQFX			
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNM	EGADSAAPGVEE	ISISVNGTVQFX			
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1 atgaaactgt tccaacgcat tttcgccaca ttttgcgcgg ttatcgctctg
51 cgcaatcttt gtggcgagtt tttctttttg gctgggtgcag aacacccttg
101 ccgaaaacca attcaaccaa cgccgcacca tcgaaaccac attgatgggc
151 agcattattt cgcatttcaa gacacggggc gacaacggcg cgcgcgaaat
201 cctgaccgaa tggaaaaaca gccccgtctc atccgcggtt tacgtcatac
251 agggcgacga gaaaaagac atcttaaac gctatatcga caattacacc
301 atagaacgcg cccggtgtt tggcgcaac aaccccgatt ccaacctgtt
351 cgcacgcgaa tacgaccgtt tcggcggaaga atacctgttc ttcatataag
401 gctgggacaa ccaccaggca caacgcctgc ccagcccgct gtttatcccg
451 ggcctgccgc ttgccccgat ttggcacgaa ttcacatccc tctccttcac
501 catcattgtc ggactgctga tggcatatat ccttgccggc aacattgcca
551 aacccatcag aatcttaggc aacggcatgg acaggggtgc agaacgagaa
601 cttgaagacc gcgtttgcca acaggttcgc gaccgcgacg acgaattggc
651 cgatgttgcc atgcaattcg acacaatggt ggaaaaactg gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFKTRG DNGAREILTE WKNSPVSSAV YVIQGEKKD ILNRYIDNYT
101 IERARLFAAN NPHSNLVRIE YDRFGEEYLF FIKGWDNHQA QRLPSPFLFIP
151 GLPLAPIWHE FIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVAERE
201 LEDRVCCQVR DRDELADVA MQFDTMVEKL E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1 ATGAAACTGT TCCAACGCAT TTTGCCACA TTTTGCGCGG TTATCGTCTG
51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCTTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCGTACGGAA TGGAAAGACA GCCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCCTGAACC GGTATATCGA CAGCTATACC
301 ATCGAACGCG CCCGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCCGAT TTGGCACGAA CTCATCATAT TGTCTTTCAT
501 CATCATCGTC GGACTGCTGA TGGCATATAT CCTCGCCGGC AACATTGCCA
551 AACCACATCA AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCA ACAGGTCGAC GACGCGGACG ACGAATTGTC
651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAAGA ACGCCACCTG CTCCATCAGC TCTCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTGAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAAGTG ACCCGCATGG
851 ATACGCTGCG CGGGGAACTG TTAACCCCTG CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCCGAAAACA CAACCATCCT TGCCAACGAA

```

```

1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCT TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

m585.pep..

```

1 MKLFQRI FATCAVIVCAIFVASFSFWLVQNTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKID ILNRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLI
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDDELHLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPKQKE QYLKRLEGEL TRMDTLAGEL LTLRLTSN
301 MALEKESLKL LPFLGNLVED NQSIQKNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFQNV IRNAVNSPE GSTILINIGQ DHKHWIDVT DNGPGVDEMQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
451 RFLPKKKTG SKTEKSAN*

```

m585 / g585 88.3% identity in 231 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQRI FATCAVIVCAIFVASFSFWLVQNTLAENQFNQ RRTIETTLMG SIISAFRARG					
g585	MKLFQRI FATCAVIVCAIFVASFSFWLVQNTLAENQFNQ RRTIETTLMG SIISAFKTRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGDEKID ILNRYIDSYTIERARLFAAGHPHNSNLVHIE					
g585	DNGAREILTEWKNSPVSSAVYVIQGDEKID ILNRYIDNYTIERARLFAANNPHNSNLVRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGEEYLF FTKDWDKLQARRLPSPLLI PGLPLAPIWHE LIILSFIIIVG LLMAYILAG					
g585	YDRFGEEYLF FIKGWDNHQAQLPSPLFI PGLPLAPIWHEFIILSFIIIVG LLMAYILAG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAKPIRILGNMGMDRVANGELETRISQQVDDRDELHLAIQFDKMVEKLEKLVAKERHL					
g585	NIAKPIRILGNMGMDRVAERELEDRCQVDRDRDELADVAMQFDTMVEKLEX					
	190	200	210	220	230	
	250	260	270	280	290	300
m585.pep	LHHVSHEMRSPLARMQAIVGLIQAQPKQKEQYLKRLEGELTRMDTLAGELLTLRLTSN					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

```

1 ATGAAACTGT TCCAACGCAT CTTGCCACA TTTGCGCGG TTATCGTCTG
51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGAG AACACCCTTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCGG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAAGACA GCCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC
301 ATCGAACGCG CCCGCTTTT CGCCGCGGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGCGGAAGA ATACCTGTTC TTCACCAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCTGC CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCGGAT TTGGCAGCAA CTCATCATAT TGTCTTCAT
501 CATCATCGTC GGACTGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
551 AACCCATCAG AATCTTAGGC AACGCGATGG ACAGGGTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCCA ACAGGTGCGAC GACCGCGACG ACGAATTGTC

```

```

651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAAGA ACGCCACCTG CTCCATCAG TCTCCCATGA AATGCGTTC
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTCAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAAGT TTAACCCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGCTGCGGA CGGAAAAATC CCCGAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

```

a585.pep
1 MKLFQIRIFAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKDD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLI
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDELHSLA IQFDKMVEKL EKLVAKEHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPKQEQ QYLKRLEGEL TRMDTLAGE LTLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNSPE GSTILINIGQ DHKHWIIDVT DNGPGVDEM
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585/a585 99.8% identity in 468 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG					
a585	MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG					
	10	20	30	40	50	60
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGDEKDDILNRYIDSYTIERARLFAAGHPHNSLVHIE					
a585	DAGAREILTEWKDSPVSSGVYVIQGDEKDDILHRYIDSYTIERARLFAAGHPHNSLVHIE					
	70	80	90	100	110	120
m585.pep	YDRFGEEYLF FTKDWDKLQARRLPSPLLIPLPLAPIWHELIILSFIIIVGLLMAYILAG					
a585	YDRFGEEYLF FTKDWDKLQARRLPSPLLIPLPLAPIWHELIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
m585.pep	NIAKPIRILGNMDRVANGELETRISQQVDDRDELHSLAIQFDKMVEKLEKLVAKEHL					
a585	NIAKPIRILGNMDRVANGELETRISQQVDDRDELHSLAIQFDKMVEKLEKLVAKEHL					
	190	200	210	220	230	240
m585.pep	LHHVSHEMRSPLARMQAIVGLIQAQPKQEQYLKRLEGELTRMDTLAGE LTLRLETSN					
a585	LHHVSHEMRSPLARMQAIVGLIQAQPKQEQYLKRLEGELTRMDTLAGE LTLRLETSN					
	250	260	270	280	290	300
m585.pep	MALEKESLKL LPFLGNLVEDNQSIAQKNGQTVTSLADGKI PENTTILANESYLYRAFDNV					
a585	MALEKESLKL LPFLGNLVEDNQSIAQKNGQTVTSLADGKI PENTTILANESYLYRAFDNV					

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	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPGEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPGEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1 atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatattt
51 ttggaaaacc acgggcaaat ggctgtttgc cctgctgatt ttggcggcac
101 tcggctactt gggatacacg gtttaccaa accgtgcggc ttcccaaat
151 caggaagcgg cggcggtgct ggcaaacatc gtggaaaagg cgcaaaacaa
201 agcccccga aagcgaatca atgccgaact gtccaaactc caacaagct
251 acccccattc catttccgcc gcccaagcca cgctgatggc ggcggaacc
301 gaatttgacg cgcagcggtt cgatgttgcc gaaggtcatt tgaatgggt
351 gttgtccaac caaaaagaca gcctgatcca ggcgttgccg gcgcagcgtc
401 ttggcgttgt gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451 ctgcacacgc cggttgagggc ggacttcgcc cccctgctga tggaaactaa
501 aggcgatggt tatgccgcac agggaaaaag ccaggaagcc ttaaaaaact
551 acggacaggg ttgggaaaaa atgcctcaag attctgtcgg tcgcgaattg
601 cttcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1 MAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRAASQN
51 QEAAAVLANI VEKAQNKAPQ SEINAELSKL QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHLKWVLSN QKDSLIQALA AQLRGVLLQ QKKYDAALAA
151 LDTFVEADFA PLLMETKGDV YAAQEKSQEA LKNYGQALEK MPQDSVGREL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1 ATGCAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAACT TTAATATTT
51 TTGGAAAACC ACGGGCAAAT GGCTGTTTGC CTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAAA ACCGTAAAGT TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTAGAAAAGG CGCAAGCAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GACCAAACTC CAACAAAGCT
251 ACCCGCATTC CATTTCGCCC GCCCAAGCCA CACTGATGGC GGCGGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 GTTGTCCAAC CAAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGCGTGTGT GTTGTGCAA CAAAAAAAT ACGATGCCGC GCTTGCCGCG
451 CTCGATACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TTAAAAAACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAAATGA AACTTGATTC GCTGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1 MAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRKVSQN
51 QEAAAVLANI VEKAQSKAPQ SEINAELTKL QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHLKWVLSN QKDSLIQALA AQLRGVLLQ QKKYDAALAA
151 LDTFVEADFA PLLMETKGDV YAAQGKSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAHLEEQQE LDNFKYFWKT TGKWL <del>FALLI</del> LAALGYLGYT VYQNRKVSQN QEAAAVLANI					

914

```

g586      MAAHLEEQQE LDNFKYFWKTTGKWLFA LLILAALGYLG YTVYQNRAASQNQEAAAVLANI
          10      20      30      40      50      60

          70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAEFDAQRYDVAEGHLKWLNSN
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      VEKAQNKA PQSEINAELSKLQQSYPHSISAAQATLMAAAEFDAQRYDVAEGHLKWLNSN
          70      80      90      100     110     120

          130     140     150     160     170     180
m586.pep  QKDSL IQALAAQRLGVVLLQ QKKYDAALALDTPVEADFAPLLMETKGDVYAAQGSQEA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      QKDSL IQALAAQRLGVVLLQ QKKYDAALALDTPVEADFAPLLMETKGDVYAAQGSQEA
          130     140     150     160     170     180

          190     200     210
m586.pep  LKNYGQALEKMPQDSV GRELVQM KLD SLKX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      LKNYGQALEKMPQDSV GRELLQM KLD SLKX
          190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1   ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTT
51  TTGGAAACC  ACGGGCAAAT GGCTGTTGC  CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTACCAAA  ACCGTGCGGC TCCCCAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAACATC  GTGGAAAAGG CGCAAAACAA
201 AGCCCCGCAA AGCGAATCA  ATGCCGAATT GGCCAAGCTC CAACAAAGCT
251 ACCCCCATTC CATTTCCGCC GCCCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 ATTGTCCAAC CAAAAGACA  GCCTGATCCA GGCCTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA  CAAAAAAT  ACGATGCCGC GCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGAATTCGCC CCCCTGCTGA TGGAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAGGAG CCAGGAAGCC TAAAAAACT
551 ACGGACAGGC TTAGAAAAA  ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAAATGA AACTTGATT  GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1   MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLG YTVYQNRAASQN
51  QEAAAVLANI VEKAQNKA PQ SEINAELAKL QQSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKLKWLNS QKDSL IQALA AQLGVVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQGSQEA LKNYGQALEK MPQDSV GREL
201 VQMKLDSLK*

```

m586/a586 97.6% identity in 209 aa overlap

```

          10      20      30      40      50      60
m586.pep  MAAHLEEQQE LDNFKYFWKTTGKWLFA LLILAALGYLG YTVYQNRAASQNQEAAAVLANI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      MAAHLEEQQE LDNFKYFWKTTGKWLFAVLI LAALGYLG YTVYQNRAASQNQEAAAVLANI
          10      20      30      40      50      60

          70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAEFDAQRYDVAEGHLKWLNSN
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      VEKAQNKA PQSEINAELAKLQQSYPHSISAAQATLMAAAEFDAQRYDVAEGHLKWLNSN
          70      80      90      100     110     120

          130     140     150     160     170     180
m586.pep  QKDSL IQALAAQRLGVVLLQ QKKYDAALALDTPVEADFAPLLMETKGDVYAAQGSQEA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      QKDSL IQALAAQRLGVVLLQ QKKYDAALALDTPVEADFAPLLMETKGDVYAAQGSQEA
          130     140     150     160     170     180

```

915

```

                190      200      210
m586.pep      LKNYGQALEKMPQDSVGRELVMKLDLKLX
                |||||
a586          LKNYGQALEKMPQDSVGRELVMKLDLKLX
                190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
1  atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 gccgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
201 ccccatctcg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251 ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301 ggcagcggca gctatctgtg gcacgaagaa cgcaaaactc acggcaacgg
351 caaaacccgc aacaaacgga tgtccgacat atccgccggc atcagccaca
401 ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501 gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSNSNR
51  AALAAPVYIQ TGATSFIPIP TEIQENGST DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151 TVYEKSRNKA SLIKKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACTTG CCGCACCAGG TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGCTGCTG
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGST DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60



916

```

m587.pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587           MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSITYLNSENSRAELAAPVYIQ
                10      20      30      40      50      60

                70      80      90      100     110     120
m587.pep      TGATSFIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587           TGATSFIPTEIQENGSDMLAGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
                70      80      90      100     110     120

                130     140     150     160     170     180
m587.pep      NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587           NKRMSDISAGISHTFLKDGKNPALISFLESTVYEKSRNKASLIKRRGLCPFYNLRYNEY
                130     140     150     160     170     180

                190     200     210     220     230     240
m587.pep      LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRDQK
g587           X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1819>:

```

a587.seq
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACTTG CCGCACCAGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAGGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATTGA
551 CCGTGCCCTA CCGTATCAAC GGCAGCAAAA CCCTTCAAG CAACACCAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CCTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1820; ORF 587.a>:

```

a587.pep
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS ITYLNSENN
51 AELAAPVYIQ TGATSFIPTE IQENGSDML VGTGLGLR YGLTGNTDI
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

m587/a587 95.2% identity in 289 aa overlap

```

                10      20      30      40      50      60
m587.pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a587           MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                10      20      30      40      50      60

                70      80      90      100     110     120
m587.pep      TGATSFIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a587           TGATSFIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
                70      80      90      100     110     120

```

917

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLKGQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

g588.seq

```

1   atgcttaaac atctcgcatc cctactgccc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaaaagac gggcttcctt caggcaaagg catatggcgt
151 tgcgggatg  ggcgcggtta taccggttca ttcaaaaacy gcaaattcga
201 cgggcaaggc gtttataacc ttgccgccgg ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaacaag  gcttggcaca cggcagggtc gccgcctcgc aaaacggcga
351 aacctctttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

g588.pep..

```

1   MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRNYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

m588.seq..

```

1   ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCCTGA CTTCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAAGAC GGTAAACCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGTTTCG TTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAG  GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

m588.pep..

```

1   MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FLEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMK EVKLPKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10            20            30            40            50            60

918

```

m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g588        MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGKPSGKGIWRCRDGRGYTGS
             10      20      30      40      50      60

             70      80      90      100     110     120
m588.pep    FKNGKFDGQGQVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g588        FKNGKFDGQGQVYTVAAAGREVFLEPFNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
             70      80      90      100     110     120

             130     139
m588.pep    IMKCENGMKEVKLPKNKX
g588        YYEMRTRHDX
             130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CGCCGCGTCC GCCGTTCTGA CTCCTATCA AGAACCCGGC TGCACCTACG
101 AAGCGGATGT CGGCAAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTTCG TTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAAG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAA GAAGTGAAGC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1  MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPKAGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMKEV EVKLPKNK*

```

m588/a588 96.4% identity in 138 aa overlap

```

             10      20      30      40      50      60
m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a588        MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGKDGKPKAGKGTWRCQDGRNYTGS
             10      20      30      40      50      60

             70      80      90      100     110     120
m588.pep    FKNGKFDGQGQVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a588        FKNGKFDGQGQVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
             70      80      90      100     110     120

             130     139
m588.pep    IMKCENGMKEVKLPKNKX
             |||||:|||||:|||||:|||||:|||||:|||||:|||||
a588        IMKCENGMKEVKLPKNKX
             130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq..
1  atgcaacaaa aaatccgttt ccaaatcgag gcgatgacct gtcaggcatg
51  tgcttcgcmc attgaaaaag tgttgaacaa aaaagatttt gtcgaatcgg
101 cgggagtga ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgcggaaggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251 atatcggtcg gcggttgtgg cttttgctga ccatcaatat cccgttcctt

```

919

```

301 atcgggtatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
351 ttggatgatt ccgcctgtat ggcagtttgt actggcaagc atagtgaac
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaaggc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatcg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggctgta tggatgacgg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcacaaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgccgaccca agtcaactcg caacgcaacg
701 gcgaatggaa acaactgcc atcgaccaag tgcaaatcgg cgaccttacc
751 gcaccaacc acggcgaacg catcgtgccc gacggcatta tcgaaagcgg
801 cagcgtttgg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggc gggcgcaaaa gtgttggcgg gcgcgtgât gaccgaaggc
901 acgtggtgt accgcgccgc gcagctcggc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagttaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaaactg cgtgggcatc
1051 gcgctcttga cttttatcgt tgcttggctg attaaggcgg attggacggg
1101 cgcactgatg cagccggttg ccgttttggg gattgcctgc ccgtgcgcgc
1151 tcggtctggc gacccctgcc gcgattatgg tcggcatggg caaagcggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtatttg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc cgccgtttat tacgttcccg acagcggctt tgacgaagac
1351 gcttgttacc gcatcgccgc cgccgtcgag caaaacgcgc cccaccgct
1401 cgcccgccgc atcgtctccg ccgcacaagc gcgcggtttg gagattcccg
1451 ctgcacaaaa tgcgcaaac gttgtcggag caggcattac cgccgaagtg
1501 gaaggcgtgg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacgc atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccgaagc cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 acaactggg catcgcacac gccttcggta atatgagtc gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaaaccc tggcgatggg
1851 cgccgacggc atcaacgacg cgcccgcgct tgccgcggcc aacgtcagct
1901 tcgccatgaa aggcggtgcg gacgttgcg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacggtt gaaaacatca agcaaaacct atttttcgcc ttctctaca
2051 atatatggg cattccgctc gccgcgctcg gctttttaa tcccgtcata
2101 gcaggcgcg caatggcggc aagctcgggt tcggtatttg gcaatgccct
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADI AKI IEKTYGYAKE KTEDTLPOPE AEHHIGWRLW LLLTINIPFL
101 IGMVGMLKG LNWTRHDWMI PPVWQFVLAS IVQLWLAI PF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
201 LGKFLHRTK KSSINSLG LL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVALM HAVAVLVVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPQVAAVY YVPDSGFDED
451 ALYRIAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGA DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFEA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTGAAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCGC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTCTT

```

m589.pap..

1	MQQKIRFQIE	GMTQCACASR	IEKVLNKKDF	VESAGVNFAS	EEAQVVFDD
51	KTSVADIARI	IEKTFGWAKE	KTEDTLPOPE	AEHHIGWRWL	LLFTINVPEL
101	<u>IGMAGMMIGR</u>	HDWMIPLGL	FALASVVQLW	LAIFPKYSAW	ASIKGGGLAN
151	DVLVTIGTWS	IYLYSVMYLF	FSPHAAVGYM	HVYFEVGVMS	IGFSLKGFEL
201	EHRTKKSSIN	SLGLLKLTP	TQVNVQRNGE	WKQLPIDQVQ	IGDLIRANHG
251	ERTAADGIEI	SGSGWADESH	LTGESINPEEK	KAGGKAVLAGA	LMTEGSSVYR
301	ATQLGSGTQL	GDMNNALESA	QGSKAPIARV	ADKAAAVFVP	AVVGIALTFH
351	IVFWLIKGDW	TVALMHAAVAV	LVIAACPALG	LATPAAIMVG	MKGAVKHGTW
401	FKDAAAMEEA	AHVDAVVLDK	TGTLTEGSPQ	VAAVYCVPDS	GFDEDALYRI
451	AAAEQONAAH	PLARATVSAA	QARGLLDIPAA	QNAQTVVVAG	ITAEEVGVLG
501	VKAGKAEFAE	LALPKFLDGV	WDIASIVAVS	VDNKPIGAGA	LADALKADTA
551	EAIGRLKKHN	IDVYIMSGDN	QGTVEYVAKQ	LGIAHAFGNM	SPRDKAAEVQ
601	KLKAAGKTVA	MVYGDINDAP	ALAAANVSFA	MKGGADVAEH	TASATLMQHS
651	VNQLADALLV	SQATLKNIKP	<u>NLFFAFFYNI</u>	LGIPLAALGF	LNPVIAGAAM
701	AASSVSVLSN	ALRLKRVKID	*		

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

m589.pep                    10                    20                    30                    40                    50                    60  
 MQQKIRFQIEGMTQACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKT~~SVADI~~AKI  
 |||||:|||||

921

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g589      MQQKIRFQIEAMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADIKI
           10      20      30      40      50      60

           70      80      90      100     1      110
m589.pep  IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLLIGMAGMMIG-----RHDWMI
           ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g589      IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLLTINIPFLIGMVGMMMLKGLNWTRHDWMI
           70      80      90      100     110     120

           120     130     140     150     160     170
m589.pep  PPLWQFALASVVQLWLAI PFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
           ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: ||
g589      PPVWQFVLASIVQLWLAI PFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA
           130     140     150     160     170     180

           180     190     200     210     220     230
m589.pep  AYGMAHVYFEVGMVIGFVSLGKFEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           |:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g589      AHGMAHVYFEAGVMVIGFVSLGKFEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           190     200     210     220     230     240

           240     250     260     270     280     290
m589.pep  IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g589      IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           250     260     270     280     290     300

           300     310     320     330     340     350
m589.pep  SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFFIVTWL
           ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g589      SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVVGIALLTFFIVAWL
           310     320     330     340     350     360
```

922

m589.pep	360	370	380	390	400	410
	IKGDWTVALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	370	380	390	400	410	420
	IKGDWTVALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
m589.pep	420	430	440	450	460	470
	VVLDKTGLTEGSPQVAAYVCVPDSGFDALYRIAAVEQNAAHPLARAIIVSAAQARGL					
g589	430	440	450	460	470	480
	VVLDKTGLTEGRPQVAAYVVPDSGFDALYRIAAVEQNAAHPLARAIIVSAAQARGL					
m589.pep	480	490	500	510	520	530
	DIPAAQNAQTVVGAGITAEEVGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	490	500	510	520	530	540
	EIPAAQNAQTVVGAGITAEEVGVGLVKSGKAEFAELTLPKFSDGVWEIASAVTVSVNGKP					
m589.pep	540	550	560	570	580	590
	IGAFALADALKADTAEAGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	550	560	570	580	590	600
	IGAFALSDALKADTAEAGRLKKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
m589.pep	600	610	620	630	640	650
	AAEVQKLKAAGKTVAMVGDGINAPALAAANVSFAMKGGADVAHTASATLMQHSVNQLA					
g589	610	620	630	640	650	660
	AAEVQKLKAAGKTVAMVGDGINAPALAAANVSFAMKGGADVAHTASATLMQHSVNQLA					
m589.pep	660	670	680	690	700	710
	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPFVIAGAAMAASSSVSLNALRLK					
g589	670	680	690	700	710	720
	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPFVIAGAAMAASSSVSLGNALRLK					
m589.pep	720					
	RVKIDX					
g589						
	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

```

a589.seq
1  ATGCAACAAA AAGTCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCATG
51  TGCTTCGCGC ATTGAAAAG TGTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCTC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GAGGTTGTGG CTTTGTCTGG CCATCAATAT CCCGTTCTTT
301 ATCGGTATGG TAGGGATGAT GCTAAAAGGG CTGAATTGGA CACGGCATGA
351 TTGGATGTTG TCGCCCTTGT TGCAGTTTGC ATTGGCGAGT GTGGTGCAGC
401 TTTGGCTGGC GGTGCCATTT TACAAAAGCG CGTGGGCGAG CATTAAAGGC
451 GGGCTGGCGA ATATGGACGT ACTCGTTACC ATCGGCACGG TCTCGATTTA
501 CCTGTATTCC GTCTATATGC TGTTTTTCAG CCCGCACGCG GCGTACGGTA
551 TGGCGCATGT GTATTTTGAA GTAGGCATAA TGGTGATTGG TTTTGTGTCA
601 CTGGGTAAAT TTTTGGAAAC CCGCACCAAA AAATCCAGCC TGAACAGCTT
651 GGGCTTGCTG CTCAAACCTCA CGCAAACCA AGTCAACGTG CAACGCGATG
701 GCGAATGGCG GCAGCTACCC ATCGACCAAG TGCAAATCGG CGACCTAATC
751 CGCGCCAATC ACGGCGAACG CATTGCCGCC GACGGCATCA TAGAAAGCGG
801 CAGCGGCTGG GCGGACGAAA GCCATCTTAC CGGCGAATCC AATCCCGAAG
851 AGAAAAAGGC AGGCGGCAAA GTATTGGCGG GCGCGCTGAT GACTGAAGGC
901 AGCGTGGTGT ACCGCGCCGC GCAGCTCGGC AGCCAAACCC TGCTCGGCGA
951 CATGATGAAC GCGCTCTCCG AAGCGCAAGG CAGTAAAGCA CCGATTGCGC
1001 GTGTGGCGGA CAAGGCGGCG GCGGTATTCTG TGCCTGCCGT TGTGGGCATC
1051 GCACTTTTGA CTTTATATCG TACTTGGCTG ATTAAGGGCG ATTGGACGCT
1101 CGCATTGATG CACGCCGTCG CCGTTTGGT GATTGCCTGC CCGTGTGCAC

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1151	TCGGTTTGGC	AACCCCTGCT	GCGATTATGG	TCGGTATGGG	CAAAGCGGTT
1201	AAACACGGTA	TTTGGTTTAA	AGACGCGGCA	GCAATGGAAG	AAGCCGCCCA
1251	CGTTGATGCC	GTCGTGCTGG	ACAAAACCGG	CACGCTGACC	GAAGGCAAGC
1301	CGCAGGTTGC	CGCCGTTTAT	TGTGTTCCCG	ACAGCGGCTT	TGACGAAGAC
1351	GCTTTGTACC	GCATCGCCGC	CGCCGTCGAA	CAAAACCGCC	CCCATCCGCT
1401	CGCCCGTGCC	ATCGTCTCCG	CGCCCAAGCG	CGCGGTTTGG	GAGATTCCCA
1451	CCGCACAAAA	TGCCCAAACC	ATTGTCGGCG	CGGGCATTAC	CGCCGAAGTA
1501	AAAGGCGCGG	GTTTGGTAAA	AGCAGGCAAA	GCCGAATTTG	CCGAACGTAC
1551	CTTGCCGAAG	TTTTCAGACG	GCGTTTGGGA	CTCGGCCAGT	GTGGTTGCCG
1601	TATCTGTAAA	CGGCAAACTT	ATCGGCGCAT	TTCGCACTGC	CGACGCGTTG
1651	AAAGCCGATA	CGCCCGAAGC	CATAGCCCGT	CTGAAAAAAC	ACAATATCGA
1701	TGTCTATATT	ATGAGCGGCG	ATAACCAAGG	CACGGTCGAG	TACGTCGCCA
1751	AACAACGGGG	CATCGCACAC	GCCTTCGGTA	ATATGAGTCC	GCGCGACAAA
1801	GCCGCCGAAG	TGCAGAAACT	CAAAGCCGCC	GGCAAAACCG	TGGCGATGGT
1851	CGGCGACGGC	ATCAACGACG	CGCCCGCGCT	CGCCGCGCGC	AACGTCAGCT
1901	TCGCCATGAA	AGGCGGTGCA	GACGTTGCCG	AACACACGCC	ATCGGCCACA
1951	CTGATGCAGC	ATTCGGTCAA	CCAGCTCGCC	GATGCGCTAT	CGGTATCGCG
2001	AGCGACGTTG	AAAAACATCA	AGCAAAACCT	GTTTTTCGCC	TTCTTCTACA
2051	ATATTTTGGG	CATTCCGCTC	GCCGCGCTCG	GCTTTTTAAA	CCCCGTATC
2101	GCAGGCGCGG	CAATGCGGCG	AAGCTCGGTT	TCCGTGTTGA	GCAACGCCTT
2151	GCGCCTGAAA	CGGGTAAAAA	TAGATTGA		

a589.pcp

1	1	MQQKVRFOIE	GMTQACASR	TEKVLNKKDF	VESAGVNFAS	EEAQVVFDD
51		KTSVADIARI	IEKTTYGAK	KTEDTLQPPE	AEHHIGWRWL	<u>LLLAINIPFL</u>
101		<u>IGVMGVMLKG</u>	LGNWRHDWML	SPLLQFALAS	VQVQLWAVPF	YKSAAWSTKG
151		GLANMDVLVT	IGTVSYLYLS	VYMLFESPHA	AYGMAHVYFE	VGIMVIGFVS
201		<u>LKGFLEHRTK</u>	KSSLNSLGLL	LKLTPTQVNV	QRDGEWRQLP	<u>IQDVQIGDLI</u>
251		RANHGERIAA	DGIIESGSGV	ADESHLTGS	NPEEKKAGKG	VLAGALMTEG
301		SVVYRAAQLG	SQTLGLDDMM	ALSEAESGSKA	PIARAVDKAA	<u>AVFVPAVVGI</u>
351		<u>ALLTFIATWL</u>	IKGDTLLTALM	HAVAVLVIAI	PCALGLATPA	AIMVMGKGAV
401		KHGIWFKDAA	AMEEAAHVDA	VVLDKTGTLT	EGKPQVAAYV	CVPDSGFDED
451		ALYIRIAAAE	QNAAHPLARA	IVSAAQAQRL	EIPTAQNAQT	IVGAGITAEV
501		KGAGLVKAGK	AEEAETLTPK	FSDGVWEIAS	VVAVSVNGKP	IGAFALDAEV
551		KADTAEAIGR	LKKHNIDVYI	MSGDNQGTVE	VYVAKQLGIAH	AFGNMSPRDK
601		AAEVQVKLAA	GKTVSMVGDG	INDAPALAAA	NVSFAMKGGG	DVAEHTASAT
651		LMQHSVNQLA	DALSVSRATL	KNIKQNLFFA	FFYNILG1PL	<u>AALGF1NPVI</u>
701		AGAAMAAASV	SVLSNALRLK	RVKTD*		

m589/a589 94.9% identity in 725 aa overlap

		10	20	30	40	50	60
m589.pep		MQQKIRFQIEG	MTCCACASRIE	KVLNKKDFVES	SAGVNFASEE	AQVVFDDSKT	SVADI
a589		MQQKVR	FQIEG	MTCCACASRIE	KVLNKKDFVES	SAGVNFASEE	AQVVFDDSKT
		10	20	30	40	50	60
		70	80	90	100	1	110
m589.pep		IEKTGYGAKE	KTEDTLPQPEA	EHGIGRWLW	LLFTINVPFL	IGMAGMMIG	-----RHDWMI
a589		IEKTGYGAKE	KTEDTLPQPEA	EHGIGRWLW	LLLLAINIP	FLIGMVGMM	LKGLNWRH
		70	80	90	100	110	120
		120	130	140	150	160	170
m589.pep		PPLWQF	FALASVVQL	WLAI	PFYKSAWAS	IKGGLANMD	VLVTIGT
a589		SPLLQF	FALASVVQL	WLAV	PFYKSAWAS	IKGGLANMD	VLVTIGT
		130	140	150	160	170	180
		180	190	200	210	220	230
m589.pep		AYGMAHV	YFEVGV	MVIGFV	SLGKFL	EHRTKSS	LNLSLGL
a589		AYGMAHV	YFEVGIM	VIGFV	SLGKFL	EHRTKSS	LNLSLGL
		190	200	210	220	230	240



924

m589.pep	240	250	260	270	280	290
	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
a589	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
	250	260	270	280	290	300
m589.pep	300	310	320	330	340	350
	SVVYRATQLGSQTLGDMMNAL	SEAQGSKAPIARVADKAAAV	FVPAVVGIAL	LTFFIVTWL		
a589	SVVYRAAQLGSQTLGDMMNAL	SEAQGSKAPIARVADKAAAV	FVPAVVGIAL	LTFFIATWL		
	310	320	330	340	350	360
m589.pep	360	370	380	390	400	410
	IKGDWTVALMHAVAVLVIA	CPALGLATPAAIMVGM	KAVKHGIWFKDAAAMEE	AAHVDA		
a589	IKGDWTLALMHAVAVLVIA	CPALGLATPAAIMVGM	KAVKHGIWFKDAAAMEE	AAHVDA		
	370	380	390	400	410	420
m589.pep	420	430	440	450	460	470
	VVLDKTGTLTGESPQVAAV	YCVPSGFEDEALYRIA	AAVEQNAAHPLA	RAIVSAAQARGL		
a589	VVLDKTGTLTGEGKPQVAAV	YCVPSGFEDEALYRIA	AAVEQNAAHPLA	RAIVSAAQARGL		
	430	440	450	460	470	480
m589.pep	480	490	500	510	520	530
	DIPAAQNAQTIVGAGITA	EVGVLVKAGKAEFAEL	LPKFLDGVWDIA	SVAVSVDNKP		
a589	EIPTAQNATIVGAGITA	EVGVLVKAGKAEFAEL	LPKFSFGVWEIA	SVAVSVNGKP		
	490	500	510	520	530	540
m589.pep	540	550	560	570	580	590
	IGAFALADALKADTAE	IGRLKKNHNDVYIMSG	DNQGTVEYVAKQLG	IAHAFGNMSPRDK		
a589	IGAFALADALKADTAE	IGRLKKNHNDVYIMSG	DNQGTVEYVAKQLG	IAHAFGNMSPRDK		
	550	560	570	580	590	600
m589.pep	600	610	620	630	640	650
	AAEVQKLKAAGKTVAMV	GDGINDAPALAAANVS	FAMKGGADVAEHTA	SATLMQHSVNQLA		
a589	AAEVQKLKAAGKTVAMV	GDGINDAPALAAANVS	FAMKGGADVAEHTA	SATLMQHSVNQLA		
	610	620	630	640	650	660
m589.pep	660	670	680	690	700	710
	DALLVSQATLKNIKQNL	FFAFFYNILGIPLAAL	GFLNPVIAGAAMA	ASSVSVLSNALRLK		
a589	DALSVSRAATLKNIKQNL	FFAFFYNILGIPLAAL	GFLNPVIAGAAMA	ASSVSVLSNALRLK		
	670	680	690	700	710	720
m589.pep	720					
	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:  
g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcggca gtattgctcg gcgttgcttt
51  ggggtacacct tattatttgg gtgtcaaacg agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctggtttac ctctacggaa acgacggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtgttggg acagccggtt acgctggtaa accatatcac gcacggccct
301 ttgcgcggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgcctgaa acggaaaaag ttttggaacg ctttttggg aaacaagttc
401 cgggtttccct tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtgttc ccgctttcga ttatgaagaa ctgtcgggca tcaggctgca

```

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501 ctgggaaggc ctgacggggg aaacgggtta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttggtca aaatcaagct ggcagacaaa
601 ggcgatgccg cgtttgaaaa agcgcatctc gattcggaaa cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggg gtcgattaca acgtcaaatt gaacgaactg
751 gtcaacctcg ttaccgatct gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttcacaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccggggg atcggggcgg tttatcgaca gcgaaggcgg gttccgtttc
901 gatacgttgg tgcacggcga tgaaaaatac ggcccgtgg acatccatat
951 cgctgccgaa cacctcgatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgcgg cagtcaaagg cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag ggaaaaattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tccacaaaa atgttgaag atttggcggg aagtcaggct ggaaatattt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgcct gatggtggac agtacgggtc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgccctg aagttaaacg gaaaacgct gcaaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttcggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:  
g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGVKAES LTQQQKILQK TGFLTIVESHQ
51 YDRGWFSTSE TTIVRLKPEL LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 FAGGFGTQAH IETEFKYAPE TEKVLRFPG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLT EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGDYKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTTEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMMKEDLN
401 QLGLMLKTE ANIRMSIPQK MLEDLAVSQA GNIPSVNAED EAEARASIAE
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNNAL KLNKTLQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

```

m590.seq (partial) ..
1 ..TGGTTTACCT CTATGGAAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAAATACC TGCCGGATAA CCTGAAACA GTGTTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGGCACGC AGGCGTACAT TGAACCGAG TTCAAATACG CGCCTGAAAC
201 GGAATAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG. CTGCACT GGGAAGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTGTGTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCCGG
451 TTTGAAAAG TGCAATTCGA TTCGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGA AAAATCTCC CTAGAATGGA
551 AAGAGGTGT CGATTACAAC GTCAAGTTAA ACGAATCGT CAATCTTGT
601 ACCGATTGTC AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTCGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTCAAC AACAAATCCG TATTGGACAT
951 TAAACTTTC CGATTACGC TGCCATCGGG AAAATCGAT GTGGGCGGAA
1001 AATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCCAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTT AGCGTCAATG
1151 CCGAAGATGA GCGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATC TGCCATTTCT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGGT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

m590 / g590 93.1% identity in 462 aa overlap

m590.pep  
g590

VKAEESLTQQQKILQKTGFLTVESHQYDRGWFTSTETTIVIRLKPPELLHNAQKYLPDNLKI

m590.pep  
g590

VLEQPVTLVNHITHGPFAGGFGTQAIIETEFKYAPETEKVLERFFGKQVPASLANTVVFN

m590.pep  
g590

GSGKMEVSVPAPFDYEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA

m590.pep  
g590

FEKVHFDSSETSDGINPLALGSSNLTLEKFSLEWKEGV DYNVKLNELVNLTDLQIGAFIN

m590.pep  
g590

PNGSIAPSKIIEVGKLAFSTKTGESGAFINSEGOFRFDTLVYGDEKYGPLDIHIAEHLDA

m590.pep  
g590

SALTVLKRKFQAISAKKMTEE QIRNDLIAAVKGEASGLFTNNPVLIDIKTFRFTLPQSKID

m590.pep  
g590

VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG

m590.pep  
g590

RASLDDINETLRMLVDSTVQSMAREKYLTLDGNQIDTAISLKNNQLKLNKGT LQNEPPDP

m590.pep  
g590

FDEGGMVS-EPQQX

FDEGDMVSGQPHX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCCA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCTT
301 TTTGCCGGCG GATTGCGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CCGGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACCG CTATGATGCC CCCTTGTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCCG CGTTTGAAAA AGTGCATTTC GATTGCGAAA CTTCAGACGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGT
751 GTCATCTTTC TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCCTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAATACTT TCCGATTACG GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTAAAGACA TGAAGAAGGA AGATTGAAAC
1201 CAATTGGGTT TGATGCTGAA GAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCGCCT GATGTTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGAAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1  MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE AGFLTVESHQ
51  YERGWFSTTE TTVIRLKEPE LHNAQKYLDP NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSRYNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLT EKFSLEWKEG VDVNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTNLGDQID TAILSKNNQL KLNGKTLQNE
501 PEPDFDEGGM VSEPQQ*

m590/a590 97.8% identity in 462 aa overlap

m590.pep
10 20 30
WFTSMETTVIRLKEPELLNARKYLPDNLKT
a590 VKAEESLTQQQKILQEAGFLTVESHQYERGWFSTETTVIRLKEPELLHNAQKYLDPNLKT
30 40 50 60 70 80

m590.pep
40 50 60 70 80 90
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
a590 VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
90 100 110 120 130 140

m590.pep
100 110 120 130 140 150
GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGFKSRYNGYDAPLFIKIKLADKGDAA
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928

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|||||
a590  GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDA
      150      160      170      180      190      200

      160      170      180      190      200      210
m590.pep FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKNELVNLVTDLQIGAFIN
      |||||
a590  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKNELVNLVTDLQIGAFIN
      210      220      230      240      250      260

      220      230      240      250      260      270
m590.pep PNGSIAPSKIEVGKLAFFSTKTGESGAFINSEGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
      |||||
a590  PNGSIAPSKIEVGKLAFFSTKTGESGAFIDSEGQFRFGTLVYGDEKYGPLDIHIAAEHLDA
      270      280      290      300      310      320

      280      290      300      310      320      330
m590.pep SALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSPGKID
      |||||
a590  SALTVLKRKFARISAKKMTEEQIRNDLIAAVKGEASGLFTHNPVLDIKTFRFTLPSPGKID
      330      340      350      360      370      380

      340      350      360      370      380      390
m590.pep VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
      |||||
a590  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
      390      400      410      420      430      440

      400      410      420      430      440      450
m590.pep RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQLKLNKGTQLONEPEPD
      |||||
a590  RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQLKLNKGTQLONEPEPD
      450      460      470      480      490      500

      460
m590.pep FDEGGMVSEPQQX
      |||||
a590  FDEGGMVSEPQQX
      510

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCAGCCTT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCGAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGTCTGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGGCG GATTCCGGAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTGGGA AAACAAGTCC
401 CGGCTTCCCT TGCCAAATACC GTTTATTTTA ACGGCAGCGG TAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCATGCCCG CGTTTGAAAA AGTGCAATTC GATTGCGAAA CTTGAGACGG
651 CATCAATCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGCT
751 GTCAATCTTG TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901 GATACACTGG TGTACGGCGA TGA AAAATAC GGGCCGCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTTCA CCAACAATCC
1101 CGTATTGGAC ATTA AAACCT TCCGATTCAC GCTGCCATCG GGA AAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTGGAAT
1201 CAATTGGGAT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT

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929

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1251 TCCCCAAAAA ATGCTGGAAG ACTTGCGCGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A

```

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

```

1 MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQOKILOE TGFLTVESHQ
51 YERGWFSTME TTIVRLKPEL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTLEKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KKKFAQISAK KMTEEQIRND
351 LIAAVKGEAS GLFTNPNVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRMLVD STVQSMAREK YLTNGDQID TAISLKNQL KLNKLTQNE
501 PEPDFDEGGM VSEPPQ*

```

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAA	ALLGVALGTP	YYLGVKAES	LTQQOKILOE	TGFLTVESHQ	YERGWFSTME
g590	MKKPLISVAA	ALLGVALGTP	YYLGVKAES	LTQQOKILOE	TGFLTVESHQ	YERGWFSTME
	70	80	90	100	110	120
m590-1.pep	TTIVRLKPEL	LNNARKYLPD	NLKTVLEQPV	TLVNHITHGP	FAGGFGTQAY	IETEFKYAPE
g590	TTIVRLKPEL	LNNARKYLPD	NLKTVLEQPV	TLVNHITHGP	FAGGFGTQAY	IETEFKYAPE
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFG	KQVPASLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
g590	TEKVLERFFG	KQVPASLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDA	PLFKIKLADK	GDAAFEKVHF	DSETSDGINP	LALGSSNLTLEKFSLEWKEG	
g590	FKSYRNGYDA	PLFKIKLADK	GDAAFEKVHF	DSETSDGINP	LALGSSNLTLEKFSLEWKEG	
	250	260	270	280	290	300
m590-1.pep	VDYNVKLNEL	VNLVTDLQIG	AFINPNNGSIA	PSKIEVGKLA	FSTKTGESGA	FINSEGQFRF
g590	VDYNVKLNEL	VNLVTDLQIG	AFINPNNGSIA	PSKIEVGKLA	FSTKTGESGA	FINSEGQFRF
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KKKFAQISAK	KMTEEQIRND	LIAAVKGEAS
g590	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KKKFAQISAK	KMTEEQIRND	LIAAVKGEAS
	370	380	390	400	410	420
m590-1.pep	GLFTNPNVLD	IKTFRFTLPS	GKIDVGGKIM	FKDMKKEDLN	QLGLMLKKE	ADIRMSIPQK
g590	GLFTNPNVLD	IKTFRFTLPS	GKIDVGGKIM	FKDMKKEDLN	QLGLMLKKE	ADIRMSIPQK
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQA	GNIFSVNAED	EAEGRASLDD	INETLRMLVD	STVQSMAREK	YLTNGDQID
g590	MLEDLAVSQA	GNIFSVNAED	EAEGRASLDD	INETLRMLVD	STVQSMAREK	YLTNGDQID
	490	500	510			
m590-1.pep	TAISLKNQL	KLNGKLTQNE	PEP	DFDEGGM	VSEPPQ	

930

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      |:||||| |||||:||||| ||:|:
g590  TVISLKNNALKLNGKTLQNEPDPDFDEGDMVSGQPHX
      490      500      510

a590/m590-1  98.3% identity in 516 aa overlap

      10      20      30      40      50      60
a590.pep  MKKPLISVAAALLGVALGTPYYLGVKAEESLTQQQKILQEAGFLTVESHQYERGWFTSTE
m590-1     MKKPLISVAAALLGVALGTPYYLGVKAEESLTQQQKILQETGFLTVESHQYERGWFTSME
      10      20      30      40      50      60

      70      80      90     100     110     120
a590.pep  TTVIRLKPELLHNAQKYLDPNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
m590-1     TTVIRLKPELLNNAQKYLDPNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
      70      80      90     100     110     120

      130     140     150     160     170     180
a590.pep  TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
m590-1     TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
      130     140     150     160     170     180

      190     200     210     220     230     240
a590.pep  FKSyrNGYDAPLFKIKLADKGDAAFEKVHFDSETS DGINPLALGSSNLTLEKFSLEWKEG
m590-1     FKSyrNGYDAPLFKIKLADKGDAAFEKVHFDSETS DGINPLALGSSNLTLEKFSLEWKEG
      190     200     210     220     230     240

      250     260     270     280     290     300
a590.pep  VDYNVKNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFTKTGESGAFIDSEGQFRE
m590-1     VDYNVKNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFTKTGESGAFINSEGQFRE
      250     260     270     280     290     300

      310     320     330     340     350     360
a590.pep  GTLVYGDEKYGPLDIHIAAEHLDA SALT V LK R K F A R I S A K K M T E E Q I R N D L I A A V K G E A S
m590-1     DTLVYGDEKYGPLDIHIAAEHLDA SALT V LK R K F A Q I S A K K M T E E Q I R N D L I A A V K G E A S
      310     320     330     340     350     360

      370     380     390     400     410     420
a590.pep  GLFTHNPVLDIKTFRFTLP SGK I D V G G K I M F K D M K K E D L N Q L G L M L K K T E A D I R M S I P O K
m590-1     GLFTNNPVLDIKTFRFTLP SGK I D V G G K I M F K D M K K E D L N Q L G L M L K K T E A D I R M S I P O K
      370     380     390     400     410     420

      430     440     450     460     470     480
a590.pep  MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLR L M V D S T V Q S M A R E K Y L T L N G D Q I D
m590-1     MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLR L M V D S T V Q S M A R E K Y L T L N G D Q I D
      430     440     450     460     470     480

      490     500     510
a590.pep  TAISLKNNQLKNGKTLQNEPEPDPDFDEGDMVSEPQOX
m590-1     TAISLKNNQLKNGKTLQNEPEPDPDFDEGDMVSEPQOX
      490     500     510

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1841>:

```

g591.seq
1  TTGCAAACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG GTTGTGCGGC GTCAAGGTTG
101 TCGGTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGCT ACGTCAAAAT
201 GGTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCGCCC AAGCGCATCG CCATCGTCGC CGCCGGTCCG
301 CTGACCAACC TCGCActggc ggTTTGTCTG TACGGACTGa gctTttcctt
351 cggcgtaaCC GAACTGCGGC Cctatgtcgg cacagtcgaA cccgacaccg

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931

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401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTATCGc ctcaTGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCCg ggcAAAAAAA Tcaccctgac
801 ctacgAaCGC GCgggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAacagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTCAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CCAAAACATC GGTTTGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCTT CTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

```

g591.pep..
1  LQTLIAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRGR
51  DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSFAEKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWKTVS HSWTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFGLALMM LMMAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

```

m591.seq
1  TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CTTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTATCG CTGATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTGAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTTGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTGCGCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..



932

```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRK
51 DTEWCLAPIP LGGYVKMVD REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTIARAGF QSGDKIQSVN
151 GTPVADWGS QTEIVLNLEA GKAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLNYER AGQHTADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNLL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVONI GLRFGALMM LMAVAFFND VTRLLG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

m591.pep	10	20	30	40	50	60
	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRK	GDTEWCLAPIP
g591	10	20	30	40	50	60
	LQTLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRK	GDTEWCLAPIP
m591.pep	70	80	90	100	110	120
	LGGYVKMVD	REGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
g591	70	80	90	100	110	120
	LGGYVKMVD	REGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
m591.pep	130	140	150	160	170	180
	ELRPYVGTVE	PDTIARAGF	QSGDKIQSVN	GTPVADWGS	AQTEIVLNLEA	GKAVGVQTA
g591	130	140	150	160	170	180
	ELRPYVGTVE	PDTVAARTG	FQSGDKIQSVN	GVQDWSSA	QTEIVLNLEA	GKAVGVQTA
m591.pep	190	200	210	220	230	240
	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
g591	190	200	210	220	230	240
	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
m591.pep	250	260	270	280	290	300
	ADGKPIASWQ	EWANLTRQSP	GKKITLNYER	AGQHTADIR	PDTVEQSDHT	LIGRVGLRPQ
g591	250	260	270	280	290	300
	ADGKPIASWQ	EWANLTRQSP	GKKITLTYER	AGQHTADIR	PDTVEQPDHT	LIGRVGLRPQ
m591.pep	310	320	330	340	350	360
	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
g591	310	320	330	340	350	360
	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
m591.pep	370	380	390	400	410	420
	IAGQSAELGL	QSYLEFLALV	SISLGVNLNLL	PVPVLDGGHL	VFYTAEWIRG	KPLGERVONI
g591	370	380	390	400	410	420
	IAGQSAELGL	QSYLEFLALV	SISLGVNLNLL	PVPVLDGGHL	VFYTVIEWIRG	KPLGERVONI
m591.pep	430	440				
	GLRFGALMML	MMAVAFFND	VTRLLGX			
g591	430	440				
	GLRFGALMML	MMAAFND	VTRLLGX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:  
a591.seq

933

```

1  TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TCGGTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCTTCG CCGGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGACACAG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTGCG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAACCC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGCGCGC GTGGAAGGAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AACTAATCA GCGCAACGC CTCCGTCAGC
1051 CATATTCCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT GGCACCTGGT AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGACCG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACCGCT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTTGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```

a591.pep
1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG
51  DTEWCLAPIP LGGYVKMVD TREGVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV PDTIARAGF QSGDKIQSVN
151 GTPVADWGS QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLN PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFLALMM LMAVAFFND VTRLLG*

```

m591/a591 99.6% identity in 446 aa overlap

```

          10      20      30      40      50      60
m591.pep  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG DTEWCLAPIP
          |||||
a591       LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG DTEWCLAPIP
          10      20      30      40      50      60

          70      80      90      100     110     120
m591.pep  LGGYVKMVD TREGVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT
          |||||
a591       LGGYVKMVD TREGVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT
          70      80      90      100     110     120

          130     140     150     160     170     180
m591.pep  ELRPYVGTV PDIARAGF QSGDKIQSVNGT PVDWGSQAQTEIVLNLEAGKVAVGVQTA
          |||||
a591       ELRPYVGTV PDIARAGF QSGDKIQSVNGT PVDWGSQAQTEIVLNLEAGKVAVGVQTA
          130     140     150     160     170     180

          190     200     210     220     230     240
m591.pep  SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLPGDRLTA
          |||||
a591       SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLPGDRLTA
          190     200     210     220     230     240

```

934

	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQTHADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQTHADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVVISLGVNLNLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVVISLGVNLNLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLGX					
a591	GLRFGALMMLMMAVAFFNDVTRLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1 atgattccgg acgtgttcgg tcagattttt tcgggcgcgt tcaaattcga
51 cgcggcagca ggcggcttac tcggcggtct gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaacg aggcgggtat gggttccgcg
151 ccgaacgccg ccgcgcgcgc cgaagtgaag caccctgttt cgcaaggtat
201 gattcaaatg ctgggcgtgt ttgtcgatac catcatcggt tgttcttgca
251 ccgccttcat catcttgatt taccaacagc cttatggcga ttgagcggt
301 ggcgcgtcga cgcaggcggc gattgtcagc caagtggggc aatggggcgc
351 gggtttcctc gccgtcatcc tgtttatggt tgccctttcc accgttatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttccg tatgctggtt ttggcgtggg tctatttcgg
501 cgcggttgcc aatgtgcctt tggctcggga tatggcggat atggcgatgg
551 gcatcatggc gtggatcaac ctgctcgcca tcctgctgct ctgcgcattg
601 gcgtttatgc tgctgcgcga ttacaccgcc aagctgaaaa tgggcaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcatacaat
701 ccgatgtttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1 MIPDVFGQIF SGAFKFDAAA GGLLGGGLISQ TMMGIKRG LYSNEAGM GSA
51 PNAAAAAEVK HPVSQGM IQM LGVFVD TIIV CSCTAFI ILI YQQPYGDL SG
101 AALTQAAIVS QVGQWGAGFL AVILFMFAPS TVIGNYAYAE SNVQFIKSHW
151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1 ATGATTCCGG ACGTGTTCGG TCAGATTTT TCGGGCGCGT TCAAATTCGA
51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGCATCAA ACGCGGCTTG TATTCCAACG AGGCGGGTAT GGGTTCGCGG
151 CCGAACCCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTGAGCGGT
301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
351 GGGCTTCCTC GCCGTCATCC TGTATTATGT TGCCCTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTATCAA AAGCCATTGG
451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCGG
501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG

```

935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA  
 651 CCCCAGATTG AACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT  
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..  
 1 MIPDVFGQIF SGAFKFDAAA GLLGLISQ TMMGIKRL YSNEAGMGSA  
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDIIIV CSCTAFIILI YQQPYGDLG  
 101 AALTQAAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW  
 151 LITAVFRMLV LAWVYFGAVA NVPLVDMAD MAMGIMAWIN LVAILLLSPL  
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW\*

m592 / g592 100.0% identity in 237 aa overlap

m592.pep	10	20	30	40	50	60
	MIPDVFGQIFSGAFKFDAAAGLLGLISQTMMGIKRLGLYSNEAGMGSAAPNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGLISQTMMGIKRLGLYSNEAGMGSAAPNAAAAAEVK					
	10	20	30	40	50	60
m592.pep	70	80	90	100	110	120
	HPVSQGMQIMLGVFVDIIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVGQWAGFL					
g592	HPVSQGMQIMLGVFVDIIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVGQWAGFL					
	70	80	90	100	110	120
m592.pep	130	140	150	160	170	180
	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVDMAD					
g592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVDMAD					
	130	140	150	160	170	180
m592.pep	190	200	210	220	230	
	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq  
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTT TCGGGCGCGT TCAAATTCGA  
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA  
 101 TGGGCATCAA ACGCGGCTG TATCCAACG AGGCGGGTAT GGGTCCGCG  
 151 CCGAACGCGC CCGCCGCCG CGAAGTGAAA CACCCTGTT CGCAAGGTAT  
 201 GATTCAAATG CTGGGCGTGT TTGTCGATC CATCATCGTT TGTCTTGCA  
 251 CCGCCTTCAT CATCTTGAT TACCAACAG CTACGCGCA TTTGAGCGGT  
 301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGCGC  
 351 GGGCTTCCTC GCCGTCATCC TGTATTGTT TGCCTTTCC ACCGTTATCG  
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG  
 451 CTGATTACCG CCGTTTCCG TATGCTGGT TTGGCGTGG TCTATTTCGG  
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGA TATGGCGGAT ATGGCGATGG  
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG  
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA  
 651 CCCCAGATTG AACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT  
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep  
 1 MIPDVFGQIF SGAFKFDAAA GLLGLISQ TMMGIKRL YSNEAGMGSA  
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDIIIV CSCTAFIILI YQQPYGDLG  
 101 AALTQAAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW  
 151 LITAVFRMLV LAWVYFGAVA NVPLVDMAD MAMGIMAWIN LVAILLLSPL  
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW\*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMGMGIKRGYLSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMGMGIKRGYLSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDEPKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDEPKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1   atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggtcgc
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101 ggcggtcggg ctgcggcaaa tccaccctgc tgaatatgat tgcgggcatc
151 gtcgggcggg acggcggcga aattcggctg aacggggaaa acattacctg
201 tatgccgccg gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaagccga agccgaacgc ctgcgcctgt cggcacttgc
351 cgaagtcggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacggttg gcaactggcg gcgctttggt tgtccgccct
451 tccctgctgt tgctggatga atcgttttcc agtttggaac cgcatttgcg
501 cgaccggctg cgccgtatga ccgccgaacg catccgcaag ggcggcatcc
551 ctgccgtttt ggtaacgcat tcgcccgaag aggcctgcac ggcggcggac
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcy gtacgccga
651 aaccttgatt caaacgcctg ccggcgtgca ggtcgcccg ctgatggggc
701 tgccaatac cgacgatgac cgccatattc cgcaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctctg tccctcgtcc gcctgccga
801 ctgctccgg cttccgccg tccatccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacggta tttccggaaa cggtagcggtc
901 cgcacccgcy tcgatgaagg gcgtatcgct cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1   MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSLR LSAVHPEHGE LTLNLTVGQH TDGISGNGTV
301 RIRVDEGRIV RFR*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

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1   ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGCGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGGAGAAA ACATTACCCG

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